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Resumen corto

Prediction and evaluation of potentially immunogenic T cell epitopes against the SARS-CoV-2 coronavirus using reverse vaccinology studies

Aguayo-Martinez, E. [1,2], Lara-Ramírez, E. [3]

[1] Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano Del Seguro Social, Zacatecas, México, [2] Laboratorio de Inmunología y Biología Celular y Molecular, Facultad de Ciencias Químicas, Universidad Autónoma de San Luis Potosí, San Luis Potosí, México. [3] Laboratorio de Biotecnología Farmacéutica, Centro de Biotecnología Genómica, Instituto Politécnico Nacional, 88710, Reynosa, México
eyamelie.amtz@gmail.com

The recently discovered Coronavirus SARS-CoV-2 is the etiological agent of the disease COVID-19. The structural proteins encoded in its genome: M, E, S, and N are conserved among the 3 β-CoVs that infect humans, in addition, Domain-motif interactions (DMIs) are an essential means by which viruses mimic and hijack the biological processes of host cells. To disentangle how viruses achieve this process can be useful to develop new rational therapies. We evaluated the motifs that correspond to epitopes against the Nucleocapsid of SARS-CoV-2, in addition it was evaluated whether these epitopes are found in disordered regions within the nucleocapsid protein, since the disordered regions of the proteins tend to be related to protein-protein interactions and so, the immune system tends to recognize epitopes within these regions with greater affinity, indicating the potential of these amino acid sequences as the mechanism by which the virus is capable of mimicking and hijacking the cellular machinery of the host cell to fulfill its cycle of replication and survival. Finally, the epitopes of the N protein were selected and analyzed by molecular docking analysis to evaluate their interaction with HLA molecules.

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Resumen corto

Effect of testosterone on oxidative stress in macrophages of *P. berghei* ANKA-infected mice.

Aguilar-Castro, J.[1]*, Salazar-Castañón, V.H.[1], Legorreta-Herrera, M.[1]

[1]Laboratorio de Inmunología Molecular, Facultad de Estudios Superiores Zaragoza, Batalla 5 de Mayo S/N, Col. Ejército de Oriente, Iztapalapa, CDMX, México. CP. 09230.
Email: jesus_aguilar_castro@yahoo.com.mx

Malaria, caused by the *Plasmodium* parasite, is the most lethal parasitic disease in the world. It is sexually dimorphic, with males developing more severe symptoms and higher mortality than females. A probable explanation is the differences in sex hormone concentrations and their effect on the immune response. In our research group we showed that administering testosterone increased the number of macrophages in both sexes. However, only in females did it decrease parasitaemia. It is likely that testosterone modifies the generation of oxidative stress in females since it is the main mechanism of parasite elimination. In this work we studied the effect of testosterone on oxidative stress in macrophages from *Plasmodium berghei* ANKA-infected mice. Macrophages were extracted from the peritoneum of *Plasmodium berghei* ANKA infected and uninfected CBA/Ca mice treated with testosterone or vehicle, cultured for 48 hours, and assessed for the activity of the antioxidant enzymes superoxide dismutase (SOD), glutathione peroxidase (GPx), catalase (CAT) and malondialdehyde (MDA), a marker of oxidative stress damage. The results were compared with those of macrophages stimulated in vitro with *Plasmodium berghei* ANKA antigen (AgPbA).

We showed that testosterone-treated macrophages from infected mice exposed to AgPbA had lower SOD activity and higher CAT activity than their controls, suggesting that hydrogen peroxide is preferentially produced in response to the parasite antigen. These findings show that testosterone modifies macrophage activity, which explains the sex differences in *Plasmodium* infections.

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Resumen corto

Determination of the oxidant-antioxidant process in ghosts of erythrocytes of neonates of women with pre-eclampsia

Aguilar-Dueñas, M. F.*[1,2], Fuentes-García, S.[1], Saucedo-Hernández, J.L.[1]; Salazar-González, B.U.[1,3]; Torres-Ramos, Y. D. [1]

[1] Laboratorio de bioquímica, departamento de inmunobioquímica, Instituto Nacional de Perinatología, CDMX, México. [2]Escuela Superior de Medicina, Instituto Politécnico Nacional, CDMX, México. [3]FES Cuautitlán, Universidad Nacional Autónoma de México, CDMX, México
fermexico.fa@gmail.com

Preeclampsia (PE) is a public health problem that is closely related to oxidative stress (OS), which is characterized by an increase in lipohydroperoxides (LHP) and malondialdehyde (MDA) in the plasma of women with PE. OS can affect the immune system by causing damage to immune cells and disrupting signaling pathways, leading to dysregulation of immune responses. The erythrocyte membrane is an excellent marker of oxidative stress since it contains several antioxidant defense systems, including superoxide dismutase, catalase, and glutathione peroxidase, which help to protect against oxidative damage. Our study aimed to evaluate the impact of PE on neonates by analyzing the oxidant-antioxidant process in ghosts of erythrocytes of newborns of women with PE. The study included 60 neonates, 30 in each group. The results showed that neonates of women with PE presented a significant increase in oxidative damage to lipids: Conjugated Dienes, LHP, and MDA, and an increase in the carbonylation of proteins. Also, the activity of antioxidant enzymes such as superoxide dismutase ($p<0.001$), catalase ($p<0.0001$) of newborns of mothers with PE was increased, while glutathione peroxidase was diminished ($p<0.03$). These findings suggest that the circulating lipids and proteins in neonates are affected by maternal OS in women with PE, the antioxidant system of cells is increased in response to the generation of reactive oxygen species (ROS), nevertheless, the enzyme glutathione peroxidase could be saturated meaning that there is a decrease in its activity. Further research is necessary to determine the long-term consequences of PE fetopathies on neonates.

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Resumen corto

Prophilactic effect of adoptive transfer of bone marrow-derived M2 macrophages in a murine model of dry eye disease.

Aguilar-Garduño, A.[1*], Cruz-Hernández, D.B.[1], Reyes-Hernández, J.L.[2], Rodríguez-Hernández, T.[1], González-Gonzalez, M.I.[2], Ramos-Montes, O.A.[1], Vázquez-Mendoza, A.[1]

[1]Laboratorio de Enfermedades Oculares Inflamatorias, UBIMED, Facultad de Estudios Superiores Iztacala UNAM, Tlalnepantla de Baz, Estado de México, México. [2]Laboratorio de Inmunología Experimental y Regulación de la Inflamación Hepatointestinal UBIMED, Facultad de Estudios Superiores Iztacala, UNAM, Tlalnepantla de Baz, Estado de México, México.
*Autor correspondencia: arturo.aguilar99@comunidad.unam.mx ;aliciavm@ired.unam.mx

Dry eye disease (DED) is an inflammatory disease affecting the ocular surface, where loss tear film stability and hyperosmolarity are the main hallmarks. High levels of inflammatory cytokines such as IL-1beta, IL17, TNF-alfa and macrophage migration inhibitory factor (MIF) are found in tear and serum samples. Also, infiltrating innate and adaptive cells (i.e. macrophages and T cells) promote chronicity in DED. The inflammatory response is central in triggering and maintaining injury in the eye tissues. Indeed, several DED therapies target diverse components of the immune response like leukocyte adhesion and proliferation. Furthermore, cell therapy has been proved to be highly effective in pre-clinical trials. Amongst others, macrophage manipulation and transfer has been explored in inflammatory diseases. In particular, M2 macrophages (macrophages exposed to Th2 cytokines, IL-4) transfer showed promising results in MS, diabetes and colitis models. However, whether this therapy can also display beneficial effects on eye diseasaes such as DED has not been reported yet. To test whether intraperitoneal M2 transfer ameliorates experimental DED. Six-to-nine week-old male BALB/c mice were induced DED and compared to M2 macrophage-given (4x106 cells) similarly induced individuals. Mice receiving M2 macrophages showed lessened DED signs, as gauged by Schirmer´s and ferning tests as compared to mice without cell transfer. M2 transfer also resulted in lower TNF-alfa levels. M2 prophilactic transfer attenuates signs in experimental DED.

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Resumen corto

Participation of MIF during tumor development of colitis-associated colorectal cancer in a mouse model

Alarcón-Campos, B.[1*], Andrade-Meza, U.A.[1], Ortiz-Robles, C.D.[1], Juárez-Avelar, I.[1], Rodríguez-Sosa, M.[1]

[1]Unidad de investigación en biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla de Baz, Estado de México, México
brendaalarconcampos@hotmail.com

Colorectal cancer (CRC) is caused by an uncontrolled growth in the inner lining of the colon or rectum. Inflammatory bowel diseases (IBD), such as colitis, increase the chances of developing colitis-associated colorectal cancer (CAC). Recently, it has been described that some inflammatory mediators such as macrophage migration inhibitory factor (MIF) could favor tumor growth and promote the development of CAC. CAC was induced by a chemical carcinogenesis model in WT and Mif -/- mice of the BALB/c strain. No differences were found in weight loss, polyp development, and damage (diarrhea and bleeding) on days 33 and 54; however, at day 75 we found significant differences in the number of tumors and damage for WT mice compared to Mif -/-. Mif -/- mice had fewer tumors compared to WT mice. These results suggest that MIF could play a key role in the development of CAC.

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Resumen corto

The autophagic proteín ATG16L1 modulates the inflammatory response during the infection with the neurotropic pathogen *Naegleria fowleri*

Alavez-Francisco, A.[1*], Carrasco-Yépez, M.M.[2], González-González, M.I.[1], Rojas-Hernández, S. [3], Reyes-Hernández, J.L.[1]

[1]Laboratorio de Inmunología Experimental y regulación de la inflamación Hepato-intestinal, UBIMED, UNAM FES Iztacala, Los reyes Iztacala, Tlalnepantla, 54090, Estado de México, México. [2]Grupo de Investigación CyMA, UIICSE, UNAM FES Iztacala, Los reyes Iztacala, Tlalnepantla, 54090, Estado de México, México. [3]Laboratorio de Inmunología Molecular, Instituto Politécnico Nacional, Escuela Superior de Medicina, Salvador Diaz Mirón Esq. Plan de San Luis S/N, Miguel Hidalgo, Casco de Santo Tomas, Ciudad de México, México. arelialavez8@gmail.com

Proteic complexes assambld by autophagy related proteins (ATGs) are the core machinery during the various stages of the autophagic flux. However, ATG proteins can also display autophagy-independent features. In particular, ATG proteins have emerged as relevant modulators in the immune response against pathogens invading diverse organs. Recent evidence has, for instance, attributed a highly relevant role for ATG16L1 protein in intestinal infections caused by *Salmonella* or by uropathogenic *Escherichia coli.* However, the involvement of ATG16L1 in neurotropic pathogens is not known. To describe the role of ATG16L,1 as immune-modulator, during the experimental infection with *Naegleria fowleri*. Six-to-eight week-old wild-type (WT) and ATG16L1 hypomorphic (ATG16L1^{HM}) mice were intranasally (i.n.) infected with 6000 trophozoites of *N. fowleri.* Survival and bodyweight changes were daily recorded. At the moment of death, brain tissues were collected and 5µm sections H&E stained for histopathological análisis. Also, cytokine levels were determined in blood samples obtained by tail snips as well as in secondary lymphoid organ culture supernatants. Flow cytometry was used to identify changes in immune cell populations present in secondary lymphoid organs such as cervical lymph nodes and spleen. Mice with impaired ability to express ATG16L1 protein turned out to be more susceptible to *N. fowleri* infection as evidenced for reduced survival and increased levels of inflammatory cytokines (TNFα and IL-1β). The autophagic protein seems to be a break for the inflammatory response triggered by the experimental infection with *N. fowleri*. DGAPA-PAPIIT-UNAM IN215323

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Resumen corto

Role of antigen abundance and affinity in CD4 T cell fate

Albarrán-Godínez, A.[1,2 *], Delgado-Zaldivar, D. [1,2], Suárez-Rojas, G. [1,2], Arias-Guerra, M.L.[1,3] ,Barroso-Zuppa, M. [1,3] , Rosetti, F. [1], Madera-Salcedo, I.K. [1], Crispín, J.C. [1]

[1]Departamento de Inmunología y Reumatología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, México.[2] Programa de Doctorado en Ciencias Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, México [3] Escuela de Medicina y Ciencias de la Salud, Instituto Tecnológico de Estudios Superiores de Monterrey Campus CDMX, Ciudad de México, México.adrianbiomed@gmail.com

Antigen presentation in non-inflammatory conditions induces tolerance through different mechanisms including apoptosis, anergy, and regulatory T cell differentiation. However, the factors that determine the different fates of CD4 T cells are mostly unknown. The main goal of this work was to analyze the role of antigen abundance and affinity in this process.

To determine the role of antigen abundance, we adoptively transferred OT-II cells into B6 mice and orally administered different doses of ovalbumin. We evaluated the cellular tolerance fates (apoptosis, anergy, and FoxP3 expression) at different time points. In complementary in vitro experiments, we analyzed the effect of varying the TCR affinity for the cognate peptide.

These experiments have revealed a complex process whereby low TCR affinity promotes the induction of anergy and FoxP3 expression in a non-mutually exclusive manner. We have observed that in the mucosal-associated lymphoid tissue, induction of oral tolerance is established by a successive process where CD4 T cells acquire FoxP3 expression in a short-lived manner and then progress into an anergic phenotype.

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Resumen corto

Hematopoietic niches are modified by heavy metals in childhood leukemia: Cadmium as an example of a regionally prevalent environmental pollutant

Alberto-Aguilar, D.R. [1*], Zamora-Herrera, G.R.[1] , Casique-Aguirre, D. [1], López-Blanco, G.A. [1], Ramírez-Ramírez, D. [1], Pelayo, R. [1,2]

[1] Centro de Investigación Biomédica de Oriente (CIBIOR)-IMSS, Puebla, México. [2] Unidad de Educación e Investigación, Centro Médico Nacional Siglo XXI, IMSS, CDMX, México.
dulze.alberto@gmail.com

Puebla, Tlaxcala, and Oaxaca report a high incidence and mortality rate (5.5, 5.4, and 5.2 per 100,000 children <18 years old, respectively) in pediatric population caused by acute lymphoblastic leukemia. Also, an environmental emergency zone due to contaminated soil and water in urbanized areas is reported in these States which causes constant exposure to a number of pollutants and toxic agents in the general population and children. Regionally prevalent pollutants include heavy metals, which can induce inflammation, signaling pathways activation and overproduction of reactive oxygen species.

The hematopoietic niche is a highly orchestrated space allowing the proper growth and maintenance of normal hematopoietic cells. Micro and macro environmental factors can modify it and favor tumor progression and maintenance of leukemic cells. The present work aim to demonstrate the damage effects of the environmental pollutant cadmium at the hematopoietic niche in a three-dimensional model with normal or leukemic stromal cells cocultured with hematopoietic precursors and leukemic blasts. Exposure with 2.5 uM Cadmium for 4 hours was able to modify the expression levels of key regulatory molecules like PD-L1, IL-7 and IL-1b in mesenchymal cells. Additionally, there was a substantial increase of the $CD45^{+}$ $CD19^{+}$ ROS^{hi} cell population, which may imply a global modification of the general state of the niche. Although additional studies are needed to elucidate the effects of these changes on leukemogenesis, overall these results suggest that cadmium is capable of altering both, stromal cells and the normal or leukemic hematopoietic cells.

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Resumen corto

Evaluation of the pUC-RNA-VMLP platform for synthetizing messenger RNA with or without modified nucleosides.

Alemán-García, Y.P. [1,2,3] *, Varona-Velázquez, A.G. [1], Luna-Pineda, V.M. [1,2]

[1]Laboratorio de Investigación en Inmunología y Proteómica, Hospital Infantil de México Federico Gómez, Ciudad de México, México. [2]Laboratorio de Investigación en COVID-19, Hospital Infantil de México Federico Gómez, Ciudad de México, México. [3]Posgrado en Ciencia en Inmunología, Escuela Nacional de Ciencias Biológicas, Ciudad de México, México. yopaale.qfb@gmail.com

The first vaccine was created by Dr. Edward Jenner, inoculating matter from a cowpox lesion. Since then, vaccines have been made with attenuated or inactivated microorganisms, but it doesn't work with all pathogens. This leads to the research of new technologies like viral vectors or antigenic subunits. Dr. Kariko studies messenger RNA vaccines, where this technology allows coding almost any antigenic protein in the receptor cells transiently, such as HIV and Zika proteins. COVID-19 leads to the first mRNA vaccine approval by WHO. We developed the platform, pUC-RNA-VMLP, which contains all the parts needed for a functional mRNA and allows us to insert different sequences due to multiple cloning site in the ORF. The *gfp*, *luc,* and *s*-SARS-CoV-2 sequences were cloned, and IVT generated mRNA with nucleosides without/with modification while capping with the vaccinia virus system. The mRNA evaluations were performed in HEK293T cells at different concentrations (250, 500, and 750 ng) and times (24, 48, and 72 h). GFP analysis was performed by EPI-fluorescence and luciferase microscopy with a luminometer and transilluminator, while RT-PCR determined spike-SARS-CoV-2. We observed the presence of fluorescence in the cells transfected with mRNA-*gfp*, which increases at 48h and remains stable up to 72h. Cells transfected with mRNA-*luc* present bioluminescence at 24h in a concentration-dependent manner. The mRNA-s-SARS-COV-2 transfected with 500 ng was evaluated by RT-PCR, where an amplicon of ~3,800 bp (ATG-TAA) was identified. In conclusion, our mRNA synthesized from the developed platform can enter the cells and be translated into proteins. Funding: Federal Funds HIMFG, HIM/2020/029, HIM/2020/060 and HIM/2021/007. CONACyT scholarship 931901.

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Resumen corto

Regulation of the lung immune microenvironment by the CD43 sialomucin during Tuberculosis

Alemán-Navarro, E. [1,4] *, López-Torres, M.O. [2], Flores-Alcántar, A.F.[1], Mata-Espinosa, D.A.[2], Barrios-Payán, J.A.[2], Parada-Colín, C.[3], Espitia-Pinzón, C.I. [3], Hernández-Pando, R.E. [2] , Rosenstein, Y. [1]

[1]Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México. [2]Departamento de Patología Experimental, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, CDMX, México. [3]Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [4]Posgrado en Ciencias Bioquímicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. estefania.aleman@ibt.unam.mx

Mycobacterium tuberculosis (Mtb) is the etiological agent of Tuberculosis (TB). Due to the lack of an effective vaccine, the lengthy and expensive TB treatments, and the emergence of multidrug-resistant Mtb strains, TB remains a leading global cause of death. The early interplay between Mtb and the host immune system defines a subtle balance between pro- and anti-inflammatory factors, determining whether a latency condition or an active disease is established after infection. CD43, a multifunctional glycoprotein abundantly expressed on immune cells, interacts with the Mtb capsular proteins Cpn60.2 and DnaK. We aimed to characterize the contribution of CD43 to the pathogenesis and outcome of TB, focusing on the pulmonary microenvironment during disease progression, with two mice strains with contrasting inflammatory immune responses, C57BL/6 and BALB/c. While in both strains CD43KO mice exhibited a higher lung bacterial load than WT mice, lung pathology, as assessed by histological and immunohistochemical evaluation of inflammation and cytokines signature, was significantly reduced in mice with an anti-inflammatory immune-biased profile. This data underscores a role for CD43 in defining a particular balance between inflammation, local immune response, and cytokines signature, differentially impacting the survival rate depending on the mice predominant immune response, promoting a more favorable outcome in an anti-inflammatory background. Overall, our results identify CD43 as an important regulatory molecule that impacts different aspects of the TB-associated pathology by controlling the inflammatory immune balance in the lung. Funding: CONACyT and PAPIIT/UNAM, Mexico.

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Resumen corto

(-)-Epicatechin regulates mast cell activation by FcεRI crosslinking

Alfaro-Doblado AR*[1], Soria-Castro R[1], Meneses-Preza YG[1], García-Pérez BE[1], Estrada-Parra S[1], Pérez-Tapia SM[2], Chacón-Salinas R[1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), CDMX, México. [2]Unidad de Desarrollo e Investigación en Bioprocesos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), CDMX, México. angelalfado@gmail.com

Mast cells are immune response cells that are involved in different biologic processes, among them stands out their role in allergic diseases. Due to the central role of mast cells on such a prevalent condition, it is of great importance to discover new compounds capable of regulate their activation.

Epicatechin (EC) is a flavonoid which is abundant in fruits and seeds. EC has been shown to have anti-inflammatory activity on different immune cells, so in this work we evaluated the activity of the EC on the IgE/antigen activation of the mast cells. For this purpose, we derived Bone Marrow Mast Cells (BMMC) of C57BL/6 mice, we treated this BMMC for a period of 18 h with EC and we evaluated if there was a decreased activity in their subsequent activation. The activation of the BMCC was evaluated through degranulation and cytokine release.

The results showed that the EC is capable of decrease mast cell IgE/antigen activation as refelected by cytokine production. However, mast cell degranulation was unaffected. These results showed that the EC has the capacity of attenuate the mast cell IgE/antigen activation.

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Resumen corto

CD5 ITIM domain plays a key role in Treg induction and function

Alvarado-Luis, B. [1], Saint-Martin, A. [1], Acevedo-Dominguez, N.A.[1], Hernández-Campos, Ó.[1], Raman Chander [3], Soldevila Gloria[1,2]

[1] Departamento de Inmunología Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, México [2] Laboratorio Nacional de Citometría de Flujo, Instituto de Investigaciones Biomédicas, UNAM, Ciudad de México, México [3] Department of Dermatology, University of Alabama at Birmingham, Birmingham, AL, United States.

CD5 is a negative regulator of TCR signaling whose expression levels on T cells correlate with TCR affinity/avidity, exhibiting higher expression within Tregs. Additionally to TCR signaling, CD28 and the yc chain mediated signals have been shown to interact with CD5 downstream effectors, modulating the generation of Tregs. The CD5 cytoplasmic tail contains multiple signaling motifs, including CK2BD, ITIM, and the C-terminal, which may differentially modulate TCR signaling. Notably, the absence of CD5 induces increased Treg selection and decreased iTreg generation. In this context, our group has reported that the ITIM domain acts as a negative regulator of TCR signaling, restraining tTreg development. However, the precise function of this domain in Treg differentiation *ex vivo* is currently unknown. To investigate the role of CD5-ITIM signaling during Treg induction, we generated a knock-in mouse in which we introduced the Y429A and Y441A mutations to block the signaling pathways regulated by this motif. FACS sorted naïve CD4+ T cells were cultured in the presence of anti-CD3/CD28 and TGF-β.. Although there were no differences in iTreg frequencies, the division index showed an increase of ~10% (8.7%±0.7, $p<0.05$) in CD5-ITIM KI iTreg compared to their WT counterparts, which was accompanied by an enhanced expression of CD25 (20.0%, $p<0.05$). Furthermore, sorted CD5-ITIM KI Tregs exhibited higher suppressor activity than WT Tregs. Our data indicate that the ITIM domain of CD5 may have a specific role in Treg induction and function. We are currently evaluating the molecular mechanisms involved.

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Resumen corto

Comparative analysis of macrophage extracellular traps under different stimuli

Alvarez-García, L.[1*], Rojas-Espinosa, O. [1], Islas-Trujillo, S.[1],
Rodas-Suárez, O. [2], Díaz -Contreras, R.S. [1],
De los Santos-González, L.A. [1] , Moreno-Altamirano, M.M.B.[1]

[1]Laboratorio de Inmunorregulación, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas (UST), Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2] Laboratorio de Microbiología General, Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas (UST), Instituto Politécnico Nacional, Ciudad de México, CDMX, México. linamaryalvarezgarcia@gmail.com

Extracellular traps (ETs) are structures composed of double-stranded DNA and several proteins, released by immune cells such as neutrophils and macrophages. ETs immobilize microorganisms and, in some instances have anti-microbial activity. Neutrophil extracellular traps (NETs) have extensively studied, whereas macrophage extracellular traps (METs) are still controversial. In this regard, the inducing mechanism and their relationship with the control of diseases are still not clear. The **aim** of this study was to investigate the capability of different types of macrophages to form METs in response to different stimuli (bacteria, fungi, phorbol myristate acetate (PMA), and viruses). RAW 264.7 (a murine macrophage cell line) and human monocyte-derived macrophages (MDMs) were activated with *Candida albicans*, *Staphylococcus aureus*, PMA, *Escherichia coli*, Zika, dengue and chikungunya virus, for 6 and 24 h, after which cells were stained with Hoechst and observed under an epifluorescence microscope, to assess the formation of METs. Result showed that RAW 264.7 cells were less capable to release METs than MDMs, the MDMs readily released METs when stimulated with *S.aureus*, *C. albicans* or some viruses, but not with *E. coli* or PMA, and that more than 6 h of stimulation were required for METs release. These results will allow us to analyze the mechanisms involved in METs release and their role in the control of infectious diseases. This project is supported by COFAA, SIP20230145. CONACyT (1281524) supports to LAG.

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Resumen corto

Association of *CY24A1* polymorphisms with soluble levels of calcidiol, calcitriol and disease risk in patients with rheumatoid arthritis.

Alvarez-Chavez, Y.A.[1,2]*, Campos-López, B.[1,2], Ruiz-Ballesteros, A.I.[1,2], Meza-Meza, M.R.[1,2], Rivera-Escoto, M.[1,2], Mora-García, P.E.[1,2], Pesqueda-Cendejas, K. [1,2], Vizmanos, B.[1,3], Parra-Rojas, I.[1, 4], Montoya-Buelna, M.[1,5], Cerpa-Cruz, S.[6], De la Cruz-Mosso, U.[1,2,3]

[1]Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, México. [2]Instituto de Neurociencias Traslacionales, Departamento de Neurociencias, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, México. [3]Cuerpo Académico UDG-454, Alimentación y Nutrición en el proceso Salud Enfermedad, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara Jalisco, México. [4]Laboratorio de Investigación en Obesidad y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, Chilpancingo de los Bravo 39087, Guerrero, México. [5]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, México. [6]Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara 44280, Jalisco, México. yoallialvarez12@gmail.com

Rheumatoid arthritis (RA) is a chronic multifactorial disease. Vitamin D in RA patients correlate negatively with disease activity. Single nucleotide variants (SNV) in the *CYP24A1* gene, such as rs4809959, have been associated with modulation of vitamin D levels. The aim of this study was to determine the association of the *CYP24A1* polymorphism (rs4809959) with serum vitamin D levels and clinical variables in patients with rheumatoid arthritis. The study was conducted in 117 patients with RA and 196 control subjects (CS), allelic discrimination was performed with TaqMan probes. Vitamin D serum levels (calcidiol and calcitriol) was analyzed trough ELISA commercial kits. According to, DAS 28 clinical activity criteria, 37% of RA patients were in remission, 22% in mild clinical activity, 24% in moderate clinical activity and 8% in severe clinical activity. RA patients had higher calcitriol (47.83 vs. 36.85 pg/mL; p<0.001), and calcitriol/calcidiol ratio (2.07 vs. 1.48 pg/ng; p<0.001) compared to CS. Regarding SNV rs4809959 in *CYP24A1,* RA patients showed a higher frequency of AA (46 vs. 35 %), AG (47 vs. 22 %) genotype and lower GG (7 vs. 22 %) genotype frequency compared to CS. Furthermore, GG genotype was associated with a 4.21-fold lower risk to RA (OR= 0.24 IC 95% 0.09-0.57). Also, G allele was associated with 1.75-fold lower risk to RA (OR=0.57 IC 95% 0.39-0.81). In conclusion, RA patients showed higher calcitriol and calcitriol/calcidiol ratio compared to CS. Regarding rs4809959 in CYP24A1, GG genotype as well as G allele were associated to lower risk of RA.

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Resumen corto

Effect of temperature on metabolism and immune system in *Procambarus clarkii.*

Álvarez-Lee, L.[1], Díaz, F.[1], Hernandez, P.[2], Sánchez-Ovando, J. P. [1], Pérez-Carrasco, L.[1] ,Denise Re, A.[1]*

[1] Centro de Investigación Científica y de Educación Superior de Ensenada (CICESE) Ensenada, Baja California, México. Laboratorio de Ecofisiología de Organismos Acuáticos. Departamento de Biotecnología Marina.[2] Universidad Autónoma de Occidente Unidad Regional Los Mochis Sinaloa. Laboratorio de Acuicultura, Sinaloa, México. denisre@cicese.mx

Temperature is a crucial environmental factor affecting all organisms' physiology, behavior, and ecology. The species' thermal tolerance is an essential physiological feature that influences the possibility of adapting to a new environment to survive when the conditions have changed due to climate change. Furthermore, a sufficient energy supply is necessary to cover the costs of basal maintenance, and immunocompetence is not in equilibrium. In this work, we evaluate the effect of temperature on the metabolism and hemocyte viability of swamp *crayfish Procambarus clarkii*. The organisms were acclimated to 20, 24, 28, and 32° C during four months. We measured the metabolism through intermittent respirometry and cell viability through apoptosis kit by cytometry. We found that metabolic performance has differences between acclimation temperatures, and the cell viability is different between populations of hemocytes under each condition. The results show that the cell death signal could be related to the chronic temperature effect, so the acclimation could affect the immunocompetence.

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Resumen corto

Neuroprotective capacity of Tregs stimulated with the dopaminergic agonist Pramipexole

Álvarez-Luquín, D.D. [1], Netzahualcoyotzi-Piedra, C. [2,3], Guevara-Salinas, A. [1], Pérez-Figueroa, G.E. [1]*, Castellanos-Barba, C, [4], Velasco, I. [3], Adalid-Peralta, L[1]

[1] Unidad Periférica para el Estudio de Neuroinflamación de Patologías Neurológicas del Instituto de Investigaciones Biomédicas en el Instituto Nacional de Neurología y Neurocirugía "Manuel Velasco Suárez", Ciudad de México, CDMX, México. [2] Laboratorio de Reprogramación Celular, Instituto Nacional de Neurología y Neurocirugía "Manuel Velasco Suárez", Ciudad de México, CDMX, México. [3]Laboratorio de Neurodesarrollo y Fisiología, Instituto de Fisiología Celular UNAM, Ciudad de México, CDMX, México. [4]Laboratorio Nacional de Citometría de Flujo, Instituto de Investigaciones Biomédicas UNAM, Ciudad de México, México. *E-mail: gerapfi3@gmail.com.

Parkinson's disease (PD), the second most common neurodegenerative disorder, is characterized by the death of dopaminergic neurons due to an accumulation of alpha-synuclein, but neuroinflammation is also known to be a key component of the disease. Little is known about the functions of immune regulatory cells, including T regulatory (Treg) cells, which regulate inflammation and maintain homeostasis, in the central nervous system. Tregs, which express all five dopamine receptors, have shown neuroprotective effect in murine models. This work is aimed to determine whether pramipexole could increase the neuroprotective capacity of regulatory cells.

CD4+, CD25hi, CD127- Tregs were purified from healthy donor PBMC by flow cytometry. The cells were stimulated with pramipexole (2 or 200 ng/mL) for 24 h and co-cultured for an additional 24 h with differentiated dopaminergic neurons from human embryonic stem cells. The neuroprotective effect of the immunoregulatory populations was assessed by 6-OHDA induced damage. The percentage of TH+ neurons was determined by microscopy. Pramipexole-stimulated Tregs increased the percentage of TH+ neurons after 6-OHDA damage. This suggests that the effect of dopaminergic treatment on Tregs could result in neuroprotection. In addition to palliating the lack of dopamine, this treatment could protect neurons from further damage. Funding: CONACyT Frontera 64382.

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Resumen corto

Determination of the expression of the hypoxia inducible factor 1 (HIF-1) and the interleukin-33 (IL-33) in pediatric medulloblastoma tumors

Anaya-Estrada, D. [1]*, Cabrera-Muñoz, M.L. [3], Eguía-Aguilar, P. [4], Rodríguez-Hernández, A.P. [1], Hernández-Cueto, D.D. [1], Luria-Pérez, R. [1], Baay-Guzmán, G.J. [1]

[1] Unidad de Investigación en Enfermedades Oncológicas, Hospital Infantil de México Federico Gómez. Ciudad de México, CDMX, México. [2] Servicio Patología Clínica y Experimental, Hospital Infantil de México Federico Gómez. Ciudad de México, CDMX, México. [3] Laboratorio de Biología Molecular, Servicio de Patología Clínica y Experimental, Hospital Infantil de México Federico Gómez. Ciudad de México, CDMX, México.

The Central Nervous System (CNS) tumors are the second cause of children cancer in Mexico, the medulloblastoma (MB) is the most common malignant brain tumor. The actual classification is divided in 4 molecular subgroups, WNT, SHH, Grupo 3 and Grupo 4. Nevertheless, is necessary yet the understanding of the tumoral microenvironment (TME). The hypoxia is one of the most important components of the TME, this can activate the transcription factor hypoxia inducible factor 1 (HIF-1), which is a bad prognosis factor, besides, Interleukin 33 (IL-33) is a nuclear protein with a dual role in cancer, in lung, breast, and colon cancer is related to a bad prognosis. In this work we determined the expression of the protein HIF-1α and IL-33 in pediatric patient tissues with medulloblastoma and evaluated their clinical implication by immunohistochemistry stains of the proteins HIF-1α and IL-33 in 7 tissue microarrays of pediatric patients with MB. The stains were digitalized and the percentage of positive cells in the cytoplasmatic and the nucleus to HIF-1 and IL-33 were quantified in 5 areas for patient of 200 μm^2, the results were correlated with clinic and demographic data of 48 patients. We found an overexpression of HIF-1α and IL-33 on the patients' tumors in comparison with the cerebellum normal tissues used as control. Also exist differences of the nuclear expression of HIF-1α between the different molecular subgroups, but these differences were not significative. These results suggest that the transcription factor HIF-1 and the interleukin IL-33 can have an important role in the medulloblastoma.

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Resumen corto

MIF as an Enhancer of Malignancy in Colitis-Associated Colorectal Cancer

Andrade-Meza, A. [1]*, Alarcón-Campos, B. [1], Juárez-Avelar, I. [1], Rodríguez-Sosa, M. [1]

[1]Unidad de Investigación en Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México. [2] Programa de Doctorado en Ciencias Biomédicas, UNAM.
*E-mail: jnksaam@gmail.com

Colorectal cancer (CRC) is the second leading cause of death by cancer worldwide. Inflammatory bowel diseases increase up to 20 % the risk to develop CCR. In line with this, immune response is a key factor during carcinogenesis. Macrophage inhibitory factor (MIF) is a proinflammatory cytokine with chemokine-like functions, overexpressed during cancer development which may attract immune cells to the microenvironment. In this work, we determine if MIF is responsible for modulating immune cell recruitment to the tumor. Using male BALB/c mice WT ($MIF^{+/+}$) and Knockout ($MIF^{-/-}$) we elucidate if MIF exacerbates tumor progression during a chemical CAC model with AOM/DSS. Briefly, mice weight, clinical signs and survival were monitored weekly. Mice were euthanized at the end of the model. Tumor tissue was obtained and washed. A sample was fixed for histology and the remaining tissue was separated in a single-cell suspension and immune cell populations were evaluated by flow cytometry. We found that $MIF^{-/-}$ exhibited less damage during CRC development with fewer tumors. Histology showed an enhanced cell transformation and Goblet cell depletion in WT mice. Fewer neutrophils, CD4+ T cells and myeloid-derived cells were infiltrated in tumor tissue of $MIF^{-/-}$ mice. So far, these results suggest that the absence of MIF resulted in fewer immune cells infiltrated in tumor tissue, suggesting that MIF could be responsible for enhancing tumor malignancy. This work was funded by the National Council of Science and Technology of Mexico (CONACYT), grant number (A1-S-10463) and the Support Program for Research Projects and Technological Innovation (PAPIIT)-UNAM, grant number (IN-217021).

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Resumen corto

Expression of sGRP78 and CXCR4 is associated with B-Cell Acute Lymphoblastic Leukemia in High-Risk pediatric patients

Angeles-Floriano, T. [1,2,3]*, Rivera-Torruco, G. [3,4], García-Maldonado, P. [1], Juárez, E. [5], González, Y. [5], Parra-Ortega, I. [6], Vilchis-Ordóñez, A. [6], López-Martínez, B. [6], Arriaga-Pizano, L. [7], Orozco-Ruíz, D. [8], Torres-Nava, J.R. [8], Licona-Limón, P. [9], López-Sosa, F. [10], Bremer, A. [10], Álvaez-Arellano, L. [11],Valle-Rios, R. [1,3]

[1]Unidad Universitaria de Investigación, División de Investigación, Facultad de Medicina, UNAM-Hospital Infantil de México Federico Gómez. [2]Programa de Maestría y Doctorado en Ciencias Médicas Odontológicas y de la Salud, UNAM. [3]Unidad de Investigación en Inmunología y Proteómica, HIMFG. [4]Departamento de Fisiología y Neurociencias, CINVESTAV. [5]Depto de Investigación en Microbiología, Instituto Nacional de Enfermedades Respiratorias. [6]Depto. de Laboratorio Clínico, HIMFG. [7]Unidad de Investigación Médica en Inmunoquímica, CMN Siglo XXI, IMSS. [8]Hospital Pediátrico de Moctezuma. [9]Depto. de Biología Celular y del Desarrollo, Instituto de Fisiología Celular, UNAM. [10]Depto. de Ortopedia, HIMFG. [11]CONACYT-HIMFG.
*E-mail: vallerios@unam.mx

GRP78 has been proposed to be an important regulator of stem cell survival, since its deficiency leads to increased cell death by decreasing the hematopoietic stem cell compartment. Recently, the localization of GRP78 in the plasma membrane (sGRP78) of tumor cells has been observed as a multifunctional receptor. Although it has been observed in many cancers its evaluation in hematological neoplasms has been little studied. Therefore, evaluating the presence of sGRP78 in B-ALL cells from pediatric patients at diagnosis is important. Samples of bone marrow (BM) aspirates were collected, as well as peripheral blood from patients with B-ALL at diagnosis. Using multiparametric flow cytometry, B-ALL patients were characterized through the following markers: CD45, GRP78, CD34, CD38, CD19, CD10, and CXCR4. Data were analyzed using FlowSOM and tSNE and a xenotransplantation assay using immunodeficient nude BALB/c mice was performed. Different cell clusters with elevated expression of sGRP78, CD10, CD19, and CXCR4 were observed in BM samples. This was confirmed in circulating cells from patients with high-risk ALL. Their migratory capacity towards BM and lymph nodes was observed, with a sustained expression of CXCR4. The evaluation of sGRP78 and CXCR4 together allows a better stratification of patients at diagnosis. The presence of circulating sGRP78+ CXCR4+ cells allows for a less invasive diagnosis. sGRP78 may be associated with a stem phenotype, as well as cell migration, increasing the risk of relapse in pediatric B-ALL patients and make it a potential therapeutic target in the treatment of leukemia. Funding: HIM 2016 057, HIM 2016 023.

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Resumen corto

Hif-1 regulates CD47 expression in lung cancer cells

Antonio-Ríos, G. [1]*, Sánchez-Godínez, J.Y. [1], Orozco-Morales, M. [2], Colín-González, A.L. [1], Barrios-Bernal, P. [1], Hernández-Pedro, N.Y.[1], Arrieta, O. [1,3]

[1]Laboratorio de Medicina Personalizada, Instituto Nacional de Cancerología, Ciudad de México, CDMX, México. [2]Laboratorio de Neuroinmunología, Instituto Nacional de Neurología y Neurocirugía, Ciudad de México, CDMX, México. [3]Unidad Funcional de Oncología Torácica, Instituto Nacional de Cancerología, Ciudad de México, CDMX, México.
*E-mail: gpe2909@ciencias.unam.mx

Uncontrolled tumor cell proliferation and abnormal blood vessel formation lead to the deprivation of oxygen in tumor tissue, inducing a hypoxic condition. Hypoxia induced the expression of hypoxia-inducible factor (HIF-1) which activates the transcription of genes that enable cancer cells to invade and metastasize, leading to patient mortality. CD47 is a protein on the cell surface that enables cancer cells to avoid destruction by macrophages. Here we try to evaluate if HIF-1 is a molecular mechanism that regulates CD47 expression and how this affected the phagocytosis of tumor cells. For that, we evaluate the expression of HIF-1α on normoxic and hypoxic conditions in four lung cancer cell lines: H522, A-549, HCC827 and H1975 through flow cytometry, western blot and immunofluorescence. Our results demonstrated that an increase of HIF-1α in hypoxic conditions can modify CD47 overexpression on the cell surface. We conclude that HIF-1α stimulates the synthesis of CD47 and down-regulation of HIF increased the phagocytosis of lung cancer cells by bone marrow-derived macrophages.

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Resumen corto

Impact of maternal obesity on neonatal immune response.

Arcadia-Paredes, E. [1,2]*, Camacho-Pacheco, R.T. [1,3], Soto-López, I. [1], Casorla-Cervantes, B.G. [1], Arreola-Ramírez, G. [1], Coronado-Zarco, A. [1], Mancilla-Herrera, I.[1]

[1]Departamento de Infectología e Inmunología Perinatal, Instituto Nacional de Perinatología (INPer), Ciudad de México, México. [2] Facultad de Química, UNAM, Ciudad de México, México. [3] Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. *E-mail: elizabetharcadia02@gmail.com

Obesity is a condition characterized by chronic low-grade inflammation, presenting high levels of inflammatory mediators and antibody polarization. This condition during pregnancy brings both maternal and neonatal complications, which can arise from the first months of life and transcend into adulthood. Little has been explored about the influence of this maternal condition on the offspring, so the aim of this work is to elucidate the impact of maternal obesity on the immune response of newborns. For this purpose, we performed an observational study analyzing, by flow cytometry, the cellular compartments of monocytes and lymphocytes, as well as the antibody concentrations of 37 umbilical cord samples from babies born to women with normal weight, overweight and pregestational obesity. We observed that the newborns presented similar developmental values at birth, as well as frequency of NK cells, monocytes, T and B lymphocytes. However, a lower activation phenotype was observed in monocytes and, both, T-helper and cytotoxic T lymphocytes as the degree of maternal obesity increased. On the other hand, the concentration of IgG2 and IgG4 antibodies is higher in the group of infants of mothers with obesity. In conclusion, our results suggest that maternal obesity has an impact on the activity and development of the immune system of the progeny that would help them to face the first antigenic challenges.

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Resumen corto

Non-activated T cells increase osteoclast formation and bone metastases from breast cancer in mice

Arellano, D.L. [1,2], Corral Avila, J.A. [1,2], Olvera, F. [3], Jiménez, S. [1], Juárez, P. [1], Fournier, P.G.J. [1]*

[1]Departamento de Innovación Biomédica, Centro de Investigación Científica y de Educación Superior de Ensenada, Ensenada, BC, México. [2]Posgrado en Ciencias de la Vida, Centro de Investigación Científica y de Educación Superior de Ensenada, Ensenada, BC, México. [3]Departamento de Biología Molecular y Bioprocesos, Instituto de Biotecnología Universidad Nacional Autonoma de México, Cuernavaca, MO, México.
*E-mail: fournier@cicese.edu.mx

Bone metastases are a frequent (>75%) complication of advanced breast cancer (BCa). BCa cells in bone are supported by cytokines released during the osteoclastic resorption and remain untreatable. T cells during immunotherapy could turn against BCa cells in bone but could also increase osteoclasts and bone metastases.

We compared bone metastases from 4T1 BCa cells between Balb/C and SCID or T cell-depleted mice. The absence of T cells decreased bone metastases (-72% and -38%, respectively), while orthotopic tumors were increased. Histology confirmed that the osteoclast number was decreased at the tumor-bone interface of mice lacking T cells. *Ex vivo* addition of non-activated T cells increased osteoclast formation, and flow cytometry confirmed that >85% of T cells in bone metastases were not expressing activation markers.

In sharp contrast, activated T cells inhibited osteoclast formation, which would be beneficial for patients. This anti-osteoclastic effect was not due to T cell cytotoxicity and reversed by the combined neutralization of IFNγ and IL-4. Thus, we sought to activate T cells of bone metastases. However, it was not possible to activate T cells in bone marrow cultures *ex vivo*. This could be due to an increase of myeloid-derived suppressor cells (MDSCs) in 4T1 bone metastases, including monocytic MDSCs that were PD-L1^{+} (>85%) and could suppress PD-1^{+} T cells (>70%) in bone.

Our results suggest that while T cells under the influence of the bone microenvironment promote BCa bone metastases, immunotherapy-activated T cells could suppress bone resorption and eliminate BCa cells in patients with bone metastases.

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Resumen corto

Targeted TSDR demethylation by CRISPR-TET1 enhances the suppressive capacity of induced T regulatory cells

Arroyo-Olarte, R.D. *, López Martínez, E.A.,
Flores Castelán, J.C., León Cabrera, S.

Laboratorio de Inmunidad tumoral (L16), Unidad de Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México.
*E-mail: rubendao@gmail.com

T regulatory cells (Tregs) are a T lymphocyte subpopulation that can suppress inflammatory immune responses. *In vitro*-induced Tregs (iTregs) hold great potential as a therapy against autoimmune and inflammation-driven diseases. Nevertheless, iTregs cannot sustain a prolonged suppressor phenotype due to the methylated state of the TSDR region of the FOXP3 gene, leading to the unstable expression of Foxp3, which is considered the master regulator of the Treg phenotype. In this work, CRISPR-TET1 was targeted to demethylate the TSDR in iTregs obtained from peripheral lymphocytes from wild-type or STAT6-/- mice. pdCas9-Sgmouse8-TSDR-TET1-mCherry (pSgM8) transfection increased Foxp3 mRNA levels while decreasing GATA mRNA, suggesting an interdependence between Treg and Th2 differentiation pathways. TSDR-targeted demethylation also increased the suppressive capacity of both wild-type and STAT6-deficient iTregs over CD4+ and CD8+ T lymphocyte proliferation. Moreover, pSgM8 (but not a control plasmid) transfection caused an additive increase compared to STAT6 deficiency alone on the suppressive capacity of iTregs. The targeted TSDR-demethylation via CRISPR-TET1 combined with STAT6 deactivation constitutes a valid protocol for generating iTregs with a more potent and stable suppressor phenotype.

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Resumen corto

Exosomes released by *Helicobacter pylori*-infected human mononuclear cells promote migration and invasion of AGS cells

Atrisco-Morales, J. [1], Ramírez-Ruano, M. [2], Juárez-Cruz, J.C. [3], Mendoza-Catalán, M.A. [4], Fernández-Tilapa, G. [1]*

[1] Laboratorio de Investigación Clínica y Laboratorio de Investigación en Biomoléculas, Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero, Chilpancingo, Guerrero, México. [2] CONACYT-Universidad Autónoma de Guerrero, Chilpancingo, Guerrero, México. [3] Laboratorio de Biología Celular del Cáncer, Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero, Chilpancingo, Guerrero, México. [4] Laboratorio de Biomedicina Molecular, Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero, Chilpancingo, Guerrero, México.
*E-mail: josefinaatrisco@uagro.mx

Between gastric epithelial cells and immune system cells, *Helicobacter pylori* (*H. pylori*) induces the secretion of cytokines and exosomes, which promote the development of chronic gastritis and gastric cancer. Exosomes participate in local and systemic intercellular communication; through the biomolecules they transport. In cancer cells, exosomes from the microenvironment promote cellular processes that characterize tumor progression. The aim of the study was to evaluate the effect of exosomes released by human peripheral blood mononuclear cells (PBMCs) infected with *H. pylori*, on the migration and invasion of tumor gastric epithelial cells (AGS). PBMCs were obtained by Ficoll density gradient from peripheral blood of two *H. pylori*-negative donors. PBMCs were infected with *H. pylori* strain 26695 at an MDI of 1:100, cultured in RPMI-1640 medium with 5% exosome-free FBS, at 37°C, 5% CO_2 for 24 h. The exosomes were isolated by ultracentrifugation from the supernatant of the PBMCs-*H. pylori* or PBMCs-Control. AGS cells cultured in DMEM-F12 medium with 0.5% exosomes-free FBS and were treated with 80 µg of exosomes released by PBMCs-*H. pylori* and PBMCs-Control. Untreated AGS cells were used as control. AGS cell migration was analyzed by wound closure (24h) and invasion in a Transwell chamber with Matrigel (48h). AGS cell invasion and migration were significantly increased in response to treatment with PBMCs-*H. pylori* exosomes compared to control exosomes. In conclusion, exosomes from *H. pylori* infected PBMCs promote the migration and invasion of AGS cells, and this suggest that in the tumor microenvironment, they contribute to the progression of gastric cancer.

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Resumen corto

Secretion of IL-17A, IL-21 and IL-25 is dependent on vacA genotype and cagA status of *Helicobacter pylori* in human mononuclear cells

Atrisco-Morales, J. [1]*, Román-Fernández, I.V. [2], Castañón-Sánchez, C.A. [3†], García-Arellano, S. [2], Muñoz Valle, J.F. [2], Fernández-Tilapa, G. [1]

[1]Laboratorio de Investigación Clínica y Laboratorio de investigación en Biomoléculas, Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero, Chilpancingo, Guerrero, México. [2]Instituto de Investigación en Ciencias Biomédicas, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [3]Laboratorio de Investigación Biomédica, Hospital Regional de Alta Especialidad de Oaxaca, San Bartolo Coyotepec 71256, Oaxaca, México.
*E-mail: josefinaatrisco@uagro.mx

Helicobacter pylori (*H. pylori*) infects the gastric mucosa and induces inflammation, development of chronic gastritis and gastric cancer (GC). *H. pylori* strains with *s1m1/cagA*+ genotype is associated with gastritis, duodenal ulcer, and GC. VacA and CagA cytotoxins induce the differentiation of specific CD4+ lymphocytes to Th1, Th2, Th17 and Treg subpopulations. In adaptive immunity anti-*H. pylori*, the Th1/Th17 response predominates. The aim of this study was to evaluate the effect of *H. pylori* genotype on the expression of Th17 cytokines in human peripheral blood mononuclear cells (PBMCs). PBMCs were obtained from peripheral blood of two *H. pylori*-negative donors. PBMCs cultured in RPMI-1640 medium with 5% exosome-free SFB were infected with strains Tx30 (*vacA s2m2/cagA*-), *ΔcagA* (*vacA s1m1/ΔcagA*), or 26695 (*vacA s1m1/cagA*+) of *H. pylori*, at an MDI of 1:100, and incubated in a 5% CO_2 at 37°C for 6, 12 and 48 h. The level of Th17 cytokines (IL-17A, IL-17F, IL-21, IL-22, IL-23, IL-25) was quantified using the Bio-Plex immunoassay in the culture supernatant. The level of IL-17A and IL-21 increased significantly at 12 and 48 h in PBMCs infected with the *ΔcagA* or 26695 strains, compared to PBMCs infected with the Tx30 strain. In PBMCs infected with Tx30 and 26695 the concentration of IL-22 experienced a significant increase at 6 and 12 h. The IL-25 level was significantly increased in 26695-infected PBMCs at 12 h. No significant differences were found in the level of IL-17F and IL-23. In conclusion, IL-17A and IL-21 expression is influenced by *vacA* genotype and *cagA* status, whereas IL-25 expression is only affected by *H. pylori* cagA status.

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Resumen corto

Expression, purification of the meVP2Spike protein in VLPs of human parvovirus B19 for prototypes of multiepitopic vaccines against SARS-CoV-2

Avalos-Carreón, G. [1,2]*, Ruiz-Cruz, A.A. [2,3], Moreno-Fierros, L. [2,3]

[1]Red de Apoyo a la Investigación, Facultad de Estudios Superiores Iztacala, Tlalnepantla de Baez, México. [2]Universidad Nacional Autónoma de México, CDMX, México. [3]Departamento de Inmunidad de mucosas, Unidad de Biomedicina Tlalnepantla de Baez, México.
*E-mail: getse.avalos@comunidad.unam.mx

The COVID-19 pandemic has highlighted the urgent need to develop effective and safe vaccines to combat the spread of the SARS-CoV-2 virus. Virus-like particle (VLP)-based vaccines are a promising strategy for generating robust immune and specific responses. Human parvovirus B19 (B19V) can produce highly immunogenic and safe VLPs. The meVP2Spike protein, a variant of the B19V capsule protein modified with epitopes from the receptor-binding domain (RBD) of the SARS-CoV-2 spike protein, has been shown to be capable of specific immune responses and neutralization of the SARS virus. -CoV-2 in vitro.

This study aims to assemble the meVP2Spike protein in VLPs to develop prototypes of multi-epitopic vaccines. The methodology employed includes the design of the VP2 Tag construct, the transformation of competent BL21 (DE3) bacteria by heat shock, the standardization of IPTG, temperature, amino acids and optical density, and the purification of meVP2Spike. The results indicate that the protein was expressed correctly at a temperature of 32°C, with IPTG [0.5 mM] and an optical density of 0.6, and was purified by affinity chromatography with Nickel columns. The successful expression of the meVP2Spike protein in B19V VLPs could represent a promising strategy to generate a safe and effective vaccine against the SARS-CoV-2 virus.

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Resumen corto

The SARS-CoV-2 E protein interacts with distinctive PDZ proteins in immune cells

Ávila-Flores, A. [1], Casado, S. [1], Liébana, R. [1], Checa, A.[1], Rosas-García, J. [2], Téllez-Araiza, M. [2], Sánchez-Cabezón, J.J.[1], Ochoa-Echeverría, A. [1], Santos-Mendoza, T. [2]*, Mérida, I. [1]

[1] Department of Immunology and Oncology, Spanish National Centre for Biotechnology (CNB-CSIC), Madrid, Spain. [2] Laboratory of Transcriptomics and Molecular Immunology, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas, Mexico City, Mexico.

PDZ proteins are central in the assembly of multiprotein complexes that regulate cell polarity. Viral pathogens express proteins harboring PDZ binding motifs (PBM) as a strategy to facilitate their dissemination.

SARS-CoVs harbour the protein E, a viroporin with a conserved PBM. SARS-CoV1 E interaction with PDZ proteins like PALS1 in epithelia promote disruption of cell junctions, which contribute to the pathogenicity of this virus. SARS-CoV-2 infects epithelium, but also components of the innate immunity, like monocytes, alveolar macrophages and dendritic cells. Viral targeting of PDZ proteins in immune cells is expected to result in impaired immune responses and virus dissemination.

Identification of targets of the SARS-CoV-2 E protein (2E) in immune cells might offer valuable clues to understand viral immunopathogenicity and to highlight the function of PDZ proteins in immune fitness.

In order to determine the 2E PDZ-dependent interactome in innate immune cells, the ORF encoding 2E was cloned in the pEZYeGFP vector, which allowed to express 2E fused to a GFP-tag at the N-terminal. GFP tagged proteins were expressed in THP-1 cells, a human monocyte cell line, and immunoprecipitated using the GFP-trap system. Associated proteins were analyzed by liquid chromatography coupled to Triple-TOF Mass Spectrometry.

The interactome of 2E in THP-1 cells provided 372 proteins. Only 8 of these proteins harbor PDZ domains. We found novel interactions of 2E protein with distinctive PDZ proteins whose function has been related with polarity and immune response. Our findings support the notion that viral targeting of PDZ proteins alters inflammatory response.

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Resumen corto

Preschoolers born preterm at risk of development delay have high percentages of lymphocytes and low percentages of neutrophils

Bahena-Delgado, A.I. [1], Hernandez-Chavez, M.C. [2], Martínez-Medina, S.[2], Canul-Euan, A.A. [2], Tolentino-Dolores, M.C. [3], Estrada-Gutierrez, G. [4], Gonzalez-Perez, G. [1]

[1]Physiology and Cellular Development Department, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City. [2]Developmental Neurobiology Department, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City. [3]Coordination of Nutrition and Bioprogramming, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City. [4]Research Division, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City.

Premature infants lose an important phase in their brain prenatal maturation and immune system development that increases their risk to develop neurological and immunological alterations later in life. Thus, there is a growing interest in evaluating if there is a correlation between infant neurodevelopment and the immune system state. The aim of the study was to analyze the neurodevelopment of preschoolers born preterm and the percentage and total counts of immune cells to evaluate if neurodevelopmental delay was associated with immune cells alterations. We recruited 36 preschoolers between 42-48 months and classified them in normal development (n=12), development lag (n=12), and risk of development delay (n=12) according with the Infant Development Evaluation Test second edition (EDI-2). Complete blood counts were used to analyze the percentages and total cell counts of leukocytes, lymphocytes, monocytes, eosinophils, and basophils. Our results showed that preschoolers at risk of development delay exhibited higher percentages of lymphocytes and basophils and lower percentages of neutrophils than preschoolers with normal development.

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Resumen corto

Evaluation of the profile of specific T cells against rotavirus induced by intestinal-type dendritic cells in an *in vitro* model

Balbuena-Sánchez, R.A. [1]*, Esquivel-Guadarrama, F.R. [1], López-Guerrero, D.L. [2]

[1] Facultad de Medicina, Universidad Autónoma del Estado de Morelos (UAEM), Cuernavaca, Morelos, México. [2] Facultad de Nutrición, Universidad Autónoma del Estado de Morelos (UAEM), Cuernavaca, Morelos, México.

Intestinal dendritic cells (DCs) are the main inducers of tolerogenic response in the intestine through the secretion of retinoic acid (RA). When DCs develop in an environment with high levels of RA, they increase the expression of the integrin CD103 and the enzyme Aldh1a2, markers that have been described in populations of DCs that promote the secretion of anti-inflammatory cytokines and a profile Treg in T cells. The detailed study of the DC response in situ and its effects on T cells it is difficult because they represent only between 2-5% of the total cells in the intestine. The aim of this work was to determine the response induced by DC with RA (DC-RA) on rotavirus-specific T cells. In this study, were obtained DC from mouse bone marrow precursors in the presence of GM-CSF and RA. The DC obtained under these conditions were activated and loaded with rotavirus antigens. On the other hand, CD4+ cells were obtained from spleens of immunized mice previously infected with rotavirus. Cocultures with DC-RA and T lymphocytes showed decreased production and proliferation of inflammatory cytokines compared to cocultures with DC without RA. Our results suggest that when DCs are differentiated in an environment rich in RA and loaded with rotavirus antigens induce a tolerogenic environment compared to DC without RA, promoted less T-cell proliferation and a decrease in proinflammatory cytokines.

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Resumen corto

Prolactin and 17β-estradiol modulates the innate immune response through epigenetics mechanisms in bovine macrophages challenged with *Staphylococcus aureus*

Barajas-Mendiola, M.A. [1*], López-Meza, J.E [1],

Ochoa-Zarzosa, A. [1]

[1]Centro Multidisciplinario de Estudios en Biotecnología, Facultad de Medicina Veterinaria y Zootecnia. Km 9.5 carretera Morelia-Zinapécuaro, Posta Veterinaria, C. P. 58893, Morelia, Michoacán, México.
*E-mail: 1919466e@umich.mx

Subclinical bovine mastitis is an inflammatory disease of the mammary gland of dairy cattle mainly caused by *Staphylococcus aureus* (*S. aureus*) that significantly affects the economy of dairy farming. The neuroendocrine system regulates critical immune system components, such as macrophages, through bidirectional communication by neurotransmitters, cytokines, and hormones involving epigenetic regulation. Therefore, changes in the levels of reproductive hormones, like bovine prolactin (bPRL) and 17β-estradiol (E2), compromise the innate immune response (IIR) of the mammary gland. In this work, we evaluate the effect of bPRL and E2 on the IIR of bovine macrophages challenged with *S. aureus*. We showed by RT-qPCR and flow cytometry that physiologic concentrations of the hormones (bPRL 5 ng/mL; E2 50 pg/mL) induced significant changes in the expression of pro and anti-inflammatory cytokines, chemokines, and antimicrobial peptides in bovine macrophages challenged with *S. aureus*. Notably, these effects are non-dependent on the TLR2 receptor. Additionally, miRNA expression was analyzed by qPCR. Results showed that miR-451, miR-155, miR-7863, and miR-146a expression was increased significantly in macrophages challenged with *S. aureus* but decreased substantially in the presence of the hormones. Interestingly, a contrary effect was observed in the expression of Let-7a-5p in the same conditions. Moreover, we determined that bPRL and E2 induced HDAC activity in macrophages, which was increased by the bacterium. Finally, we showed that bPRL and E2 favor the global acetylation of histone H3 in macrophages challenged or not with *S. aureus*. All these findings suggest that bPRL and E2 regulate IIR elements and epigenetic mechanisms in macrophages challenged with *S. aureus*.

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Resumen corto

Mitochondrial function on B cell response against non-bilayer phospholipid arrangements

Barrera-Aveleida, G.B.*, Sotelo-Rodríguez, A., Galarce-Sosa, E.I., Isidro-Magallán, J.E, Reséndiz-Mora, C.A, Wong-Baeza, C., Baeza-Ramírez, M.I.

Laboratorios de Biomembranas y de Enzimología, Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México.
*E-mail: aveleida@gmail.com

During immune response, mitochondria play a crucial role in B cell activation and differentiation. However, the involvement of mitochondria from this cell lineage against lipidic antigens is not known with certainty. Cell membrane lipids can present antigenic properties when they form stable non-bilayer phospholipid arrangements (NPA) induced by some drugs. Stable NPA induce the production of anti-NPA IgG antibodies, which are present in autoimmune diseases such as Systemic Lupus Erythematosus. In this work we analyzed by flow cytometry the B cell response, the mitochondrial dynamics and mitochondrial membrane potential in a murine model that resembles human lupus induced by liposomes bearing drug stabilized NPA. We found that B2 cells mainly respond through the germinal center pathway against this lipidic antigen and differentiate into plasma and memory B cells. The germinal center and the memory B cells presented fused mitochondria with increased mitochondrial membrane potential; therefore, these cells lead their metabolism to oxidative phosphorylation. A significant number of plasma cells with fissioned mitochondria and with decreased mitochondrial membrane potential was found; therefore, these cells metabolism reaches glycolysis. Our data suggest that there is a strong relationship between the *in vivo* B cells response against a lipidic antigen and mitochondrial functions.

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Resumen corto

Generation of a TGFβ3 knockout murine melanoma cell line using CRISPR-Cas9

Barroso-Zuppa, M. [1,2*], Delgado-Zaldivar, D. [2], de la Cruz, A. [2], Albarran-Godinez, A. [2], Rubio, R.M. [2], Madera-Salcedo, I.K. [2], Rosetti, F. [2], Crispín, J.C. [1,2]

[1]Escuela de Medicina y Ciencias de la Salud, Tecnológico de Monterrey, Ciudad de México, CDMX, México. [2]Departamento de Inmunología y Reumatología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, CDMX, México.
*E-mail: A01371162@tec.mx

Melanoma is the leading cause of skin cancer-related mortality worldwide. Despite recent advances in the field, the urgent need to find new therapeutic targets to improve the clinical outcomes of patients remains. Acting as an immunosuppressive cytokine, transforming growth factor beta (TGF-β), plays a key role within the tumor microenvironment by inhibiting $CD8^+$ T cell cytotoxicity, blocking tumor infiltration by T cells, and enhancing regulatory T cell differentiation. Although most information refers to TGF-1, the canonical isoform, recent data suggests that other TGF-β isoforms may play a role in tumor-associated immune modulation. In this work, we generated a B16-OVA melanoma cell line deficient in *Tgfb3*, the gene that encodes TGFβ3, using CRISPR-Cas9. Here, we present the generation of this novel tool that will allow us to identify the role of this TGF-β isoform in the immune response against melanoma.

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Resumen corto

Role of adipokines in the outcome of SARS-CoV-2 infection

Basilio-Aguilar, K.J. [1,2], Villaseñor-García, A.M [1,2*], Pérez-Fragoso, A.[1,3], Absalón-Aguilar, A. [1,3], Ortega-Mejía, I.I. [1,2], Bernal-Alferes, B. [1,2], Padierna-Olivos, J. [4], Domínguez-López, M.L. [1], Gómez-Martín, D. [3], Torres-Ruiz, J. [3], Romero-López, J.P. [1,2].

[1]Laboratorio de Inmunoquímica I, Posgrado en Ciencias Biológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Patogénesis Molecular, Red MEDICI, Carrera de Médico Cirujano, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México [3]Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, CDMX, México. [4]Laboratorios Especializados en Inmunología (LEI), Ciudad de México, CDMX, México.
*E-mail: alanvilllasenor@gmail.com

The coronavirus disease 2019 (COVID 19) has gained relevance due to its high mortality. Obesity participates as an independent risk factor for increased mortality. Adipokines produced in adipose tissue have been associated with inflammatory load and dysregulated immune responses that may influence the pathogenesis, and course of the disease by contributing to the development of cytokine storm and cytokine release syndrome. For that reason, it is important to correlate serum levels of adipokines in patients with SARS-Cov-2 infection with the clinical outcome of the disease. In this work we measured Adiponectin, Adipsin, RBP4, MCP-1, IL-1β, IP-10, IL-10, IL-8, Leptin, IL-6, IFN-γ, Resistin and TNF-α using the Capture Bead Analysis method. Cytokines such as resistin and MCP-1 presented particular patterns, with statistically significant differences observed when comparing severe non-obese patients against non-obese critical patients, severely obese patients versus obese critical patients and obese controls against obese critical patients. In addition, positive correlations were presented between IL-1β levels against IL-10. Also, we observed significant differences in the secretion patterns of IFN-γ, IL-1β and TNF-α, where a decrease in these molecules is observed as the severity of the disease increases, both in non-obese and obese patients. We found no significant differences on levels of the different adipokines between the obese and non-obese groups, but we found that cytokines such as IL-1β and IFN-γ increase in mild and severe disease, while decreasing in critical disease, which may be related to an exhaustion of the immune response to sustained inflammation.

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Resumen corto

Characterization of monocytes from patients with COVID-19 complicated or not with bacterial sepsis

Basilio-Gálvez, E. [1,2*], García-de la Rosa, M.T. [1,2], Juárez-Palacios, J.E. [1,2], Madera-Sandoval, R.L. [1], Rivero-Arredondo, V. [1], Prieto-Chávez, J.L. [1], Cabrera-Rivera, L. [1], Miranda-Cruz, P. [1], García- Rodríguez, J. [1], Vázquez-Estrada, J. [1], Molina-Serrano, E.D. [1], Salazar-Ríos, M.E. [1], Rodríguez-Hernández, D. [1], Ramírez-Hernández, A. [1], López-Macías, C.R. [1], Ferat-Osorio, E.A. [1], Rivas-Hernández, N. [2], Arriaga-Pizano, L.A. [1]

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades del Centro Médico Siglo XXI, Instituto Mexicano del Seguro Social, 06720 CDMX, Mexico. [2]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (IPN), Prolongación de Carpio y Plan de Ayala, Casco de Santo Tomás, 11340 CDMX, Mexico. *E-mail: edbgalvez@gmail.com

A prevalence of 1 to 30% of bacterial secondary infections and coinfections during COVID-19 hospitalization has been reported. This is directly related to higher mortality rates. In sepsis of bacterial origin, decreased HLA-DR expression in monocytes has been proposed as a potential biomarker of poor prognosis. It is uncertain if this can also be applied in the case of sepsis added to severe COVID-19. Our aim was to evaluate the HLA-DR expression in monocytes from hospitalized patients with COVID-19 complicated or not with bacterial sepsis. After signing the informed consent, peripheral blood samples were taken from patients with COVID-19 with(C19BISurvived/C19BIDeceased) or without bacterial sepsis(C19Survived/C19Deceased). A group of non-COVID-19, non-sepsis volunteers constituted the control group(C). Total monocytes(leucocytesFSCmedSSCmedCD45^{+}CD14^{+}CD16$^{-/+}$) and their subtypes: classical(CD14^{+}16^{-}), intermediate(CD14^{+}16^{+}) and non-classical(CD14^{lo}16^{+}), proportion and HLA-DR expression were evaluated with multiparametric flow cytometry at day 1(D1) and 7(D7) days of hospitalization. The total monocytes and their subtypes were the same among all the groups (p>0.05). In comparison to control group, at day 1 and day 7 of hospitalization, in COVID-19 patients, with or without coinfection, a diminished HLA-DR expression was observed in total monocytes(CvsC19DD1p<0.0001,CvsC19DD7p<0.0001, CvsC19SD1p=0.01,CvsC19BIDD1p=0.04,CvsC19BIDD7p=0.01), and their subtypes(Classic CvsCvsC19DD1p=0.0002,CvsC19DD7p=0.0009, CvsC19SD1p=0.0008, Intermediate CvsC19DD1p=0.0008,CvsC19DD7p=0.006, CvsC19SD1p<0.0001,CvsC19BIDD1p=0.04,CvsC19BIDD7p=0.01, Non-Classical CvsCvsC19DD1p=0.03,CvsC19DD7p=0.001,CvsC19SD1p=0.001, CvsC19BIDD1p=0.0001).This differences were sustained in classical monocytes when analyzing the expression of HLA-DR^{+} MFI index, observing a decrease in the expression of the marker(CvsCvsC19DD1p=0.009,CvsC19SD1p=0.004, CvsC19SD7p=0.0003,CvsCBIDD7p=0.02). These results suggest that COVID-19 patients with fatal outcome have decreased HLA-DR expression, as observed in sepsis, but further studies are required to define it as a potential biomarker.

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Resumen corto

Conjugated Bilirubin regulates human T cell functions in the presence of Hepatitis E Virus antigenic peptides during acute infection.

Batún-Alfaro, J.A. [1]*, Anaya-Covarrubias, J.Y. [2], Du-Pont, G. [1], Lamoyi, E. [1], Fierro, N.A. [1]

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad Universitaria, CDMX, México.

[2]Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, México.
*E-mail: juliobatun96@hotmail.com

Hepatitis E virus (HEV) is the leading cause of acute viral hepatitis worldwide. The progression of the disease is restricted by host immune response, that may be also affected by host-metabolic components. Such is the case of Bilirubin, a metabolic subproduct resulting from hepatocytes destruction during liver disease, and whose concentration is upregulated during acute viral hepatitis. Apart from antioxidative functions, immunoregulatory roles have been associated to this metabolite. We previously reported that conjugated bilirubin (CBR) has role during the acute Hepatitis A virus infection by modulating T cell function. However, the effect of CBR on immune response regulation during other viral hepatitis has not been described. Herein, the effect of CBR on HEV associated lymphocyte response was tested by using an antigenic re-stimulating model. Human lymphocytes were isolated from individuals with previous contact with HEV (IgG anti-HEV positives and HEV RNA negatives) and cultured *in vitro* with antigenic viral peptides and differential concentrations of CBR; cell function was evaluated by multiplex and flow cytometry. We found that CBR treatment *in vitro* at 2 mg/dL promotes a decrease in CD4+ T cell proliferation and reduces the secretion of cytokines linked with the cytotoxic response of CD8+ T cells. Likewise, acutely HEV-infected patients with CBR values above 2 mg/dL showed higher IFN-gamma levels in sera relative to patients with lower CBR levels in sera. Taken together, these findings suggest that CBR exerts an immunomodulatory role during HEV infection.

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Resumen corto

Effect of thermal stimulation on neuroimmunological pathways in a murine sepsis model

Bautista-Hernández, M.A. [1*], Argueta-Figueroa, L. [2], Castro-Gutiérrez, M.E.M. [1], Ávila-Curiel, B.X. [3], Moreno-Rodríguez, A. [4], Pérez-Cervera, Y. [5], Solórzano-Mata, C.J. [5] ,Torres-Rosas, R. [5].

[1] Programa de Doctorado en Biociencias, Facultad de Medicina y Cirugía, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México. [2] Consejo Nacional de Ciencia y Tecnología, Ciudad de México, CDMX, México. [3]Laboratorio de Medicina Complementaria Asociado al Centro de Estudios en Ciencias de la Salud y la Enfermedad, División de Posgrado, Facultad de Odontología, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México., México, [4] Facultad de Ciencias Químicas, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México. [5] Laboratorio de Inmunología Asociado al Centro de Estudios en Ciencias de la Salud y la Enfermedad, División de Posgrado, Facultad de Odontología, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México.
*E-mail: mbautista.alu@uabjo.mx

Neuronal networks represent physiological mechanisms selected by evolution to control inflammation, that can be exploited for the treatment of inflammatory and infectious disorders. Previously we reported that ST36 acupunctural point activation with electroacupuncture controls systemic inflammation in sepsis model by a catecholaminergic pathway. However, acupuncture includes several acupoint stimulation techniques, and those may activate different neuroimmunological pathways that can be exploited for the treatment of inflammatory and infectious disorders. To characterize the effect of thermal stimulation at ST36 (TE-ST36) on serum TNFα, survival rates, and neurotransmitters release, a sepsis model was induced in C57/BL6 mice using cecal ligation and puncture (CLP). The septic mice were subsequently treated with TE-ST36 (CLP+ST36), and serum samples were collected and analyzed for cytokines levels. The serum TNFα levels in the CLP+ST36 group were significantly lower ($p<0.0001$) compared with the group CLP without treatment, however, the survival rates were significantly lower ($p<0.05$). On the other hand. The serum levels of the three catecholamines and cortisol were significantly higher in the CLP+ST36 group ($p<0.0001$), In conclusion, in CLP mice model, the thermal stimulation activates neuroimmunological pathways that diminish the cytokines levels and survival rates.

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Resumen corto

Cry1Ac toxin and protoxin attaches to epithelial gut cells and change the permeability and junction protein expression in monolayers of Caco- 2 cells

Bautista-Jacobo, I.S. [1] , Ilhuicatzi-Alvarado, D. [1],
Hernandez-Almaraz, K.B. [2,] Schnoor, M. [2] Moreno-Fierros, L. [1]

[1] Laboratorio 9 UBIMED Facultad de Estudios Superiores Iztacala UNAM Av. de los Barrios 1, Hab Los Reyes Ixtacala Barrio de los Árboles/Barrio de los Héroes, 54090 Tlalnepantla de Baz, Méx. [2] Centro de Investigación y de Estudios Avanzados IPN Av Instituto Politécnico Nacional 2508, San Pedro Zacatenco, Gustavo A. Madero, 07360 Ciudad de México, CDMX

The *Bacillus turingiensis* Cry1Ac-proteins, had been used as bioinsecticides for over a decade, to control pests in human consumption crops, also had been considered innocuous for vertebrates. Nevertheless, our group has demonstrated that Cry1Ac proteins are mucosal and systemic immunogens able to activate macrophages using MAPK pathways, while the protoxin is also a promising adjuvant able to improve protection in different infection mouse models. Currently, transgenic crops that express Cry1Ac proteins are world wide able for human consumption and it had been reported that intragastric administration of Cry1Ac toxin provokes moderately allergy and lymphoid hyperplasia in large intestine in mice. Therefore, it is important to characterize its effects in human the cells, particularly in gut epithelial cells. Human Caco-2C2BBe1 cell-line, is used as an invitro model that mimics a gut human monolayer, it was used to determine the responses generated in colon epithelial cells, after the stimulation with Cry1Ac. We evaluated whether Cry1Acproteins were able to, attach to human cells surface, change the monolayer integrity,activate MAPK signalling and if this activation modifies the tight junction protein expression. The results indicates that Cry1Ac proteins has several binding proteins in intestines, some of the identified proteins are HSP, cadherin and alkaline-phosphatase, also its administration induce the activation of ERK, p38 and JNK. We also observed that permeability is enhanced after the treatments. the outcomes indicate Cry1Ac, toxin and protoxin proteins are not innocuous for vertebrate intestinal epithelial cells thus encouraging the need to perform further safety studies focused on intestinal effects. Apoyo PAPIT in202923

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Resumen corto

Bactofection of the Gene that Encodes the Interleukin-12 Elicits Antitumor Activity in a Murine Xenograft Model of Human Non-Hodgkin´s Lymphoma

Becerra-Báez, E.I. [1,2], Magaño-Bocanegra, K.J. [1,3*], Muñoz-López, P. [1,4], Flores-Martínez, L.F. [1], García-Nava, Y.E. [1,5], González-Franco, J. [1,6], Luria-Pérez, R. [1]

[1]Unit of Investigative Research on Oncological Diseases, Children's Hospital of Mexico Federico Gomez, Mexico City, Mexico. [2]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [3]Department of Molecular Biomedicine, Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico City, Mexico. [4]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, Mexico. [5]Faculty of Veterinary Medicine and Zootechnics, National Autonomous University of Mexico, Mexico City, Mexico. [6]Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, México. E-mail: kevin.magano@cinvestav.mx

The survival of patients with non-Hodgkin´s Lymphoma (NHL) has substantially improved with conventional treatments. However, the appearance of refractory disease makes finding new and most effective antitumor therapies for these patients necessary. In this study, we propose using interleukin-12 (IL-12) as an immunotherapeutic approach. Since side effects have been associated with the systemic administration of IL-12 in clinical trials, we use an attenuated *Salmonella enterica*, with tropism by the tumor microenvironment, as a delivery system of the plasmid that encodes the gene of IL-12; these bacteria will allow the transfer of the gene of IL-12 (Bactofection) in both tumors and immune response cells, favoring the synthesis of this cytokine in the tumor microenvironment that will improve the antitumor immune response. Thus, with the recombinant DNA technology, we construct a *Salmonella enterica* that carries a plasmid encoding for the single-chain murine IL-12 (scmIL-12). The scmIL-12 mRNA (measured by RT-PCR) and the presence of the recombinant scmIL-12 (documented by dob blot and Cytometric Bead Array) were detected using the extracts and the supernatant of transfected or bactofected cells (monkey kidney epithelial cells: Vero, and human NHL cells: Ramos). Indeed, this recombinant scmIL-12 induced the proliferation of the human peripheral blood mononuclear cells. The intravenous administration of the *salmonella enterica* carrying the gene of scmIL-12 elicited antitumor activity and extended survival in a murine xenograft model of human NHL; **in** these mice, the enhanced presence of murine IL-12 was detected. Our approach may represent an eventual alternative to treat relapsing or refractory NHL.

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Resumen corto

Development of gold-based biomimetic mycobacterial nanoparticles.

Becerra-Hernández, A. [1*], Ramírez-García, G. [1],
López-Marín, L.M. [1]

[1]Centro de Física Aplicada y Tecnología Avanzada (CFATA), Universidad Nacional Autónoma de México, Juriquilla, México.

E-mail: armbecc@gmail.com

Mycobacterium tuberculosis (Mtb) is again the major infectious killer worldwide, after the decline of SARS-CoV-2 deaths since 2022. Serodiagnosis is an attractive strategy for tuberculosis (TB) control since it can be used at resource-limited primary health care sites. Therefore, there is a need to develop new serodiagnostic platforms that are rapid, sensitive, low cost and user-friendly. Mycobacteria possess a specialized cell wall known as mycomembrane composed by different amphipathic glycolipids. However, this structure has been poorly explored as an antigen in novel methods for TB serodiagnosis due to its low-water solubility. In this study we designed biomimetic nanoparticles made of gold (AuNPs) and liposomes that incorporate glycolipids derived from mycobacteria. The aim was to exploit the antigenic potential of these molecules in conjunction with the optical properties of metal-based nanoparticles. Analysis using transmission electron microscopy (TEM) of the construct showed that the AuNPs had a semi-transparent coating attributed to the lipid bilayer decoration. Further studies, including dynamic light scattering (DLS) and zeta potential (ζ) analyses, confirmed the presence of a layer that influences both the hydrodynamic radius and the surface charge of AuNPs. This layer was attributed to the use of acid phosphoinositide antigens. To our knowledge, this is the first hybrid antigen-gold construct that mimic mycobacterial cell surfaces. Currently, the feasibility of this nanosystem to capture TB-associated antibodies for optical-based detection methods is under evaluation.

This work was supported by DGAPA (UNAM) and CONACyT through Grants IT200421 and CF2019-53395, respectively. The authors wish to thank Lourdes Palma Tirado from the Microscopy Unit at the Institute of Neurobiology, UNAM, and Luz María Avilés Arellano from CINVESTAV-Querétaro for their excellent technical assistance.

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Resumen corto

Absence of CD103 in tissue-resident memory T-cells and intratumoral CD226+ cells associated with high expression of the immune checkpoint CD155 in advanced lung adenocarcinoma

Benito-Lopez, J.J. [1,2*], Marroquin-Muciño, M. [1,3], Aguilar-Cazares, D. [1], Chavez-Dominguez, R. [1,2], Lopez-Gonzalez, J.S. [1].

[1] Laboratorio de Investigación en Cáncer Pulmonar, Departamento de Enfermedades Crónico-Degenerativas, Instituto Nacional de Enfermedades Respiratorias "Ismael Cosio Villegas", Mexico City, Mexico. [2] Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Mexico City, Mexico. [3] Laboratorio de Quimioterapia Experimental, Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico.

E-mail: jareb.benito.l@gmail.com,

Tumor cells express several evasion mechanisms to escape from immune elimination, such as the overexpression of some immune checkpoints or their ligands, and soluble immunosuppressive mediators. As a result, most tumor-infiltrating antigen-specific T cells display an exhausted phenotype. Recently, it has been described a particular subset of immune cells called tissue-resident memory (Trm) T-cells, which are located in barrer-epithelial tissues, and may play an important role in elimination of tumor cells. We analyzed the correlation among IL-6, the immune checkpoint CD155 and the infiltration of Trm cells in lung adenocarcinoma. We found a positive correlation between IL-6 and CD155 on data from the TCGA, and in biopsies from lung adenocarcinoma patients. In addition, in lung cancer cell lines, IL-6 induced CD155 mRNA expression, but this effect was not reflected at the protein level, suggesting that other factors of the TME are involved in CD155 overexpression. Moreover, the relationship between IL-6, the checkpoint CD155, and TILs in patient biopsies was assessed by IHC. We found Trm CD8+T-cells distributed in the basal region of bronchioles in adjacent non-tumor tissues and into intraepithelial areas of cancer tissue at early stage. In contrast, CD226+ TILs from advanced stages were distributed mainly in the tumor stroma and few or no presence of these cells were found in close interaction with tumor cells. In conclusion, IL-6-related CD155 overexpression may act as a mechanism to target Trm CD8+T-cells, through loss CD226 expression, contributing to the inhibition of these tumor antigen-specific T cells. Partial Funding: CONACyT 284775

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Resumen corto

Association of commensal bacteria and immunoglobulins with regulatory T lymphocytes in human colostrum

Bermejo-Haro, M. [1,2], Hernández-Peláez, G. [1], De la Merced-D., S. [1], Mendoza-Ortega, J. A. [1], Domínguez-Vanegas, C. [1], Molina-Hernández, A. [1], Nájera-Hernández, M.A. [1,2], Camacho-Pacheco, R.T. [1,2], Brito-Pérez, Y. [1,2], Becerril-Soriano, D. [1], Figueroa-Damián, R. [1], Rodríguez-Martínez, S. [2], Mancilla-Herrera, I. [1].

[1]Infectology and Immunology Department, National Institute of Perinatology (INPer), Mexico City Mexico. [2] Posgrado en Inmunología, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City Mexico. E-mail: inmuno.lposgrado@gmail.com

Breastfeeding allows the newborn´s immune system training through the vertical transference of biocomponents (antibodies, cells and commensal bacteria), which migrated from maternal mucosa to mammary gland. The first breast milk produced is colostrum, which is enriched with Treg lymphocytes (Treg) and potentially may transfer immunological memory, helping to shape the first antigenic neonatal challenges. In addition, maternal antibodies in milk model the infant microbiota's biodiversity, meanwhile, milk commensal bacteria modulate newborn immune system. However, it is unknown whether there is any association between this biocomponentes. By flow cytometry we identified memory Treg lymphocytes ($CD45^{++}CD3^{+}CD4^{+}CD25^{++}CD45RO^{+}CD127^{-}$) in human colostrum from 33 healthy donors, being the 24% +/- 13.16 of the total lymphocytes. Furthermore, immunoglobulins were quantified by immunoassays, IgA was the principal immunoglobulin in colostrum (2207.6 ng / mL), followed by IgG3 (1121.3 ng / mL), IgG1 (100.6 ng / mL), IgG4 (29.6 ng / mL), IgG2 (10.6 ng / mL) and IgM (2.6 ng / mL). In addition, DNA of commensal bacteria were quantified by qPCR. *Streptococcus* and *Staphylococcus* were the predominant isolated genre in colostrum (46.6% and 44.86% respectively), followed by *Bifidobacterium* (3.76%), *Enterococcus* (3.4%) and *Lactobacillus* (1.37%). Correlation tests and multivariate analysis determinate that the presence of Treg was positively associated with the concentration of *Bifidobacterium*, and both negatively does with the concentration of IgA. This study shows for the first time, in human colostrum, a Lymphocyte Treg-IgA-Bacteria axis which could help to maintain the newborn homeostasis.

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Resumen corto

Adipsin and Resistin levels are increased in the serum of Spondyloarthritis patients

Bernal-Alferes, B. [1,2], Romero-García, H.A. [1,2*],
Basilio-Aguilar, K.J. [1,2], Padierna-Olivos, J. [3], Ortega-Mejía, I. [1,2],
Casasola-Vargas, J..C. [4], Meza-Olguin, G. [4], Burgos-Vargas, R. [4],
Domínguez-López, M.L [2], Romero-López, J.P [1,2].

[1]Laboratorio de Patogénesis Molecular, Red MEDICI, Carrera de Médico Cirujano, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México. [2]Laboratorio de Inmunoquímica 1, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, IPN Ciudad de México, CDMX, México. [3]Laboratorios Especializados en Inmunología (LEI), Ciudad de México, CDMX, México. [4]Departamento de Reumatología, Hospital General de México "Dr. Eduardo Liceaga", Ciudad de México, CDMX, México.
E-mail: garoheadan@gmail.com

Spondyloarthritis (SpA) is an inflammatory disease characterized by new bone formation that can be preceded by fat deposition. Adipose tissue can produce inflammatory mediators known as adipokines. There is evidence of increased adipokine levels in obese patients and in inflammatory conditions. It has been suggested that these adipokines have a chronic effect on the pathophysiology of SpA and its response to treatment. Adipsin is secreted in response to elevated serum glucose levels and increased insulin secretion. Likewise, resistin is related to glucose metabolism, but, when injected in the joint of mice, can lead to an arthritis-like state. Under inflammatory conditions, resistin increases IL-6 and TNF-α through NF-κB pathways. The concentration of adipsin and resistin was measured in the plasma of patients with SpA and compared to healthy controls. Patients were classified according to clinical disease activity as measured by the ankylosing spondylitis activity score (ASDAS)-CRP. 10ml of blood was drawn per patient and centrifuged to separate plasma for adipokine and cytokine measurement using a cytokine bead array and to measure adipsin, resistin, RBP4, IL-6, and TNF-α concentration. We found elevated levels of adipsin ($p = 0.0007$), and resistin ($p = 0.0150$) in the serum of SpA patients compared to healthy controls. Patients were classified according to their ASDAS-CRP activity into moderate, high, and very high activity indexes, nevertheless, we did not find any significant differences between these groups. We concluded that patients with SpA have higher serum levels of adipsin and resistin.

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Resumen corto

Altered function of innate immune response mechanisms to an antigenic challenge with *Aeromonas hydrophila* and diazinon co-exposure in Nile tilapia (*Oreochromis niloticus*)

Bernal-González, K.G. [1], Covantes-Rosales, C.E. [2*], Toledo-Ibarra, G.A. [2], Barcelos-García, R.G. [2], Bueno-Durán, A.Y. [2], Diaz-Resendiz, K.J.G. [2], Mercado-Salgado, U. [2,4], Martínez-Pérez, V.E. [3], Girón-Pérez, M.I. [2]

[1] Maestría en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [2] Laboratorio Nacional para la Investigación en Inocuidad Alimentaria (LANIIA) Unidad Nayarit. Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [3] Licenciatura en Químico Fármaco Biólogo, Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [4]Doctorado en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Tepic, Nayarit, México

Pesticides are used for pest control, including vectors of human and animal diseases. Diazinon is an organophosphate pesticide (OPs) that induces alterations in the neuronal and immune systems. Teleost fish were the first vertebrates to exhibit innate and adaptive responses, the former being much more robust. Among the cellular mechanisms of innate immunity, there is phagocytosis, which is a primary defense mechanism against pathogens. On the other hand, the respiratory burst is an oxygen-dependent non-specific microbicide cellular defense mechanism present in phagocytic cells, which generate reactive oxygen species (ROS). Therefore, this study aimed to evaluate phagocytic alterations in Nile tilapia leukocytes exposed *in vivo* to 0.95 mg/L (1/8 LC_{50}) of diazinon for 24 hours and subsequently challenged with *Aeromonas hydrophila* antigens. For the phagocytosis assay, whole blood leukocytes ($2x10^6$) were used and incubated with fluorescent beads (1 µm). For ROS determination, whole blood leukocytes ($2x10^6$) were isolated and incubated with dihydrorhodamine 123 (DHR_{123}) and dihydroethidium (DHE), to assess H_2O_2 and O^{2-} production, respectively. Each assay was analyzed by flow cytometry (10,000 events). The present project will describe how pesticide-induced immunotoxicity and inflammation alter innate mechanisms and thus the ability to respond to pathogens, as well as the increase in susceptibility to disease mediated by OPs.

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Resumen corto

Impact of oral consumption of cry1ac toxin on the inflammatory response of the large intestine: a comparative approach with a colitis model.

Betanzos-Laguna, X.I. [1*], Ilhuicatzi-Alvarado, D. [1],
Moreno-Fierros, L. [1], Perez-López, A. [2]

[1]Laboratorio de inmunidad de mucosas, [2]UBIMED, Facultad de estudios superiores Iztacala, Universidad Nacional Autónoma de México, Estado de México, México.
E-mail: lagunaxim@gmail.com

The Cry1Ac toxin, derived from Bacillus thuringensis, is a widely used biopesticide expressed in genetically modified (GM) plants for human and animal consumption. Cry1Ac is immunogenic and able to activate immune cells like macrophages, which necessitates thorough evaluation of immunological effects after intra-gastric administration. The intestine contains the largest pool of immune cells in the body, essential for maintaining mucosal homeostasis and protective immunity, but may also contribute to inflammatory bowel disease (IBD). This study aimed to evaluate the potential of Cry1Ac to induce IBD and compared the effects with a DSS-3% induced ulcerative colitis model. Mice were intragastrically administered with different doses of TCry1Ac for 7 days, and IBD-associated parameters were recorded. TCry1Ac administration provoked changes in cytokines essential for intestinal homeostasis, including IL-6, IL-10, IL-1β, and TNF-α. Moreover, the lamina propria cells in the intestine exhibited changes in immune cells' expression, and histopathological evaluation revealed pro-inflammatory changes in the TCry1Ac 2µg group compared to the PBS group such as edema and lymphangiectasis. Flow cytometry identified the changes in intestine immune cells, based on the expressions of CD11b+, CCR2+, CX3CR1+, Ly6G, CD19, CD80, CD86, and CD3. This study demonstrated that Cry1Ac has the potential to induce alterations in intestinal homeostasis, providing important insights to identify dysregulated immune factors in IBDs.

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Resumen corto

Toll-like receptor 4 expression in human decidual stromal cells associated with pregnancy complications

Blanco-Muñoz, O. [1]*, Granados-Cuao, J. [2]*, Blanco-Mardinis, Y.[3]

[1]Programa de Medicina, Facultad de Salud, Universidad del Magdalena, Santa Marta, Colombia. [2]Programa Bacteriología y Laboratorio Clínico, Facultad de Ciencias Médicas y de la Salud, Universidad de Santander, Bucaramanga, Colombia. [3]Entidad Promotora de Salud - Sanitas, Departamento de Ginecología y Obstetricia, Santa Marta, Colombia. E-mail: oblanco@unimagdalena.edu.co; jer.granados@mail.udes.edu.co

The Preeclampsia (PE) affects 8% of pregnant women. The decidua is the maternal tissue that plays an important role in the immunological regulation of pregnancy and its main cellular component is the decidual cells. The expression of the Toll-4 type receptor and cytokines associated with the immunomodulatory behavior of DSC in PE were determined. DSCs were isolated and cultured from placental tissue, from patients with uncomplicated vaginal delivery (control n=6) and cesarean delivery with preeclampsia (PE n=6). The phenotypic characterization of the DSCs was carried out using flow cytometry. TLR4 mRNA expression was quantified by real-time RT-PCR. Cytokine determination was performed by means of ELISA from DSC cell culture supernatants. The expression of characteristic antigens was similar in the DSC studied. The DSCs expressed TLR4, with no significant difference (p=0.136). Control DSCs secreted a higher amount of IL-6 (mean= 3631.7pg/mL) compared to PE DSCs (760pg/mL). The secretion of IL-10 presented a significant difference (control= 4pg/mL, PE= 11.2pg/mL p=0.0108). The control and PE DSCs do not show significant differences in the expression of TLR4, suggesting a protective role at the placental level.

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Resumen corto

SARS-CoV-2 viral load assessment by a Cycle-Threshold Value coefficient is associated with adverse clinical outcomes and death

Borrego-Moreno, J.C. [1,3]*, Canizález Román, V.A. [2], Angulo Zamudio, U.A. [2], Sánchez Cuén, J.A. [2], Rivas-Santiago, B. [3] Enciso Moreno, J.A. [3], Castañeda-Delgado, J.E. [4]

[1]Hospital General de Zona IMSS Zacatecas. [2]Laboratorio de Biología Molecular de la Facultad de Medicina de la Universidad Autónoma de Sinaloa. [3]Unidad de Investigación Biomédica de Zacatecas, IMSS. [4]Cátedras CONACYT, Unidad de Investigación Biomédica de Zacatecas, IMSS. *E-mail: bogue6@hotmail.com

Despite vaccination, COVID-19 infection is still a major concern for medical attention worldwide. There is an urgent need for better tools to be used in the clinical setting. The technology based on real-time quantitative polymerase chain reaction (RT-qPCR) allows viral load to be calculated indirectly through the Ct value ("Cycle threshold"). We sought to determine risk factors associated with the viral load, identified by the threshold cycle value (Ct) in a longitudinal, analytical, retrospective study. We made a categorization of 3 groups based on viral load distribution. The statistical methods used were Chi2 for proportions, Kruskal-Wallis, Student's T test, Mann Whitney U and ANOVA for quantitative variables accordingly. A Kaplan Mayer survival analysis and a Cox regression were performed. Hypertension, DM and asthma show higher frequency in patients with higher viral load, 61.9%, 46.03%, 6.35% ($p < 0.005$) respectively. The incidence of sequelae was higher in high viral load 24.4% (0.014). From logistic regression, high viral load (RR 3.14 CI 1.466-6.761 p 0.003) was significantly associated with a higher risk of death. In the Cox regression, hospitalized COVID 19 cases with high viral loads had a 6 time higher hazard ratio of dying, compared to those with low viral loads (RR Cox 6.2 CI 4.23 – 9.12). A strong association was identified between high viral load and the risk of death in hospitalized COVID 19 patients, plus the sequelae and the viral load of SARS-CoV-2.

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Resumen corto

Expression of IL-21, IL-21R and HLA-DR in circulating T follicular helper and T peripheral helper cells of Systemic Lupus Erythematosus patients

Borunda-Calderón, I.M. [1,2*], Ortiz-Lazareno, P.C. [3], Oregón-Romero, E. [2], Salazar-Camarena, D.C. [4], Muñoz-Valle, J.F. [2], Espinoza-García, N. [2], Marín-Rosales, M. [5] , Palafox-Sánchez, C.A. [2]

[1]Doctorado en Ciencias Biomédicas con orientación en inmunología, Centro Universitario en Ciencias de la Salud (CUCS), Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Instituto de Investigación en Ciencias Biomédicas (IICB), CUCS, Universidad de Guadalajara, Guadalajara, Jalisco, México. [3]División de Inmunología, Centro de Investigación Biomédica de Occidente, Instituto Mexicano del Seguro Social, Secretaría de Salud Jalisco, Guadalajara, Jalisco, México. [4]Grupo de Inmunología Molecular, CUCS, Universidad de Guadalajara, Guadalajara, Jalisco, México. [5]Hospital General de Occidente, Secretaría de Salud Jalisco, Guadalajara, Jalisco, México.
E-mail: Itzel.borunda2324@alumnos.udg.mx

Systemic lupus erythematosus (SLE) is an autoimmune disease characterized by the production of autoantibodies that affect multiple organs. In the pathophysiology of SLE, interleukin 21 (IL-21) is an essential cytokine for T and B lymphocyte cooperation; it promotes the proliferation of autoreactive cells, germinal center response, plasmablast differentiation, and autoantibody production. T peripheral helper (Tph) (CD4+ PD1+ CXCR5-) and circulating T follicular helper (cTfh) (CD4+ PD1+ CXCR5+) cells are important producers of IL-21, and their frequency increase is observed in SLE patients compared to healthy controls. This increase is also associated with disease activity and a higher plasmablasts frequency. In this study we evaluated intracellular IL-21 expression, IL-21 receptor (IL-21R), and cellular activation (HLA-DR) of these cell subpopulations in SLE patients. Nineteen SLE patients and 5 healthy controls (HC) were recruited. Peripheral blood mononuclear cells were isolated from a blood sample and cell staining with antibodies (anti-CD3, anti-CD4, anti-PD1, anti-CXCR5, anti-IL21R and anti-HLA-DR) and intracellular staining (anti-IL21) was performed for analysis by flow cytometry. We found a significant increase in the frequency of Tph lymphocytes and an upward trend for cTfh in SLE. Also, we found a higher expression of IL-21R and HLA-DR in these subpopulations of SLE patients compared to HC, could be associated a higher activation of the cells. These results suggest that both Tph and cTfh cells could be important drivers of the autoreactive response in SLE patients.

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Resumen corto

α4β7⁺ Th cells play an important role in protection against the rotavirus infection in mice immunized intranasally with a VP6 peptide

Bravo-Vizuett, M. [1]*, Elguea- Arroyo, K. [1]*,
López-Guerrero, D.V. [2] , Esquivel-Guadarrama, F.R. [1]

[1] Laboratorio de Inmunología Viral, Facultad de Medicina, Universidad Autónoma del Estado de Morelos, Cuernavaca, México. Facultad de Nutrición, Universidad Autónoma del Estado de Morelos, Cuernavaca, México. E-mail: vizuettbravo54@gmail.com.

Studies in mice have shown that an intranasal (i.n.) immunization with the peptide 289-302 of the internal rotavirus (RV) protein VP6 ($VP6_{289-302}$), which represents a Th cell epitope, can induce a protective immune response against an RV infection in the small intestine, that depends on Th1-type cells. However, the mechanisms by which the epitope-specific Th cells primed in the nasal mucosa travel to the intestinal mucosa are unknown. This study aimed to determine whether after the i.n. immunization, the peptide-specific Th cells positive for the intestinal homing receptor α4β7 travel to the mesenteric lymph nodes (MLN), and if this receptor participates in the protection. BABL/c mice were immunized i.n. two times with the peptide $VP6_{289-302}$ in the presence of cholera toxin (CT), as control only CT was used. After the last immunization, the presence of peptide-specific memory Th cells expressing CD69 and α4β7 in MLNs was evaluated by flow cytometry in one group of mice. Other group of mice were challenged with a murine RV and treated with an anti-α4β7 blocking mAb or with a non-specific mAb as control, and the virus load in feces was compared. It was found that after the i.n. immunization, peptide-specific memory CD69⁺ α4β7⁺ Th cells were present in the MLN, and the anti- α4β7 mAb induced an increment of the virus load in comparison with the control. These results show that the i.n. immunization induces α4β7⁺ peptide-specific Th cells that travel to the intestinal mucosa to protect against the infection. Funding: SEP-CONACYT- A1-S-9434.

*This work has two main authors with “equal contribution”.

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Resumen corto

Effect of coadministration of dehydroepiandrosterone and testosterone on the number of T lymphocytes in *P. berghei* ANKA infected mice

Buendía-González, F.O. [1,2]*, Legorreta-Herrera, M. [1]

[1]Laboratorio de Inmunología molecular, Unidad de Investigación Química Computacional, Síntesis y Farmacología de Moléculas de Interés Biológico, Facultad de Estudios Superiores Zaragoza, UNAM, Ciudad de México. [2]Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México Coyoacán, Ciudad de México.
E-mail: fidelbuendia2@gmail.com

Malaria caused by the *Plasmodium* parasite is the most lethal parasitic disease. Males have a higher mortality rate than females. This sex difference is associated with sex hormone concentrations among which testosterone increases the severity of the disease while dehydroepiandrosterone (DHEA) is related to low parasitemia. One possible explanation is that testosterone has immunosuppressive effects on T lymphocytes while DHEA increases their activity. However, it is not known whether there is a relationship between the effects of DHEA and testosterone on the number of T lymphocytes in malaria. CBA/Ca mice infected with *P. berghei* ANKA were treated as follows: Group 1 “Control”, Group 2 “1 mg DHEA”, Group 3 “0.9 mg testosterone”, Group 4 DHEA + Testosterone. Parasitemia and hemoglobin concentration were evaluated during infection. Furthermore, the percentage of T lymphocytes in the spleen was quantified. The administration of DHEA and testosterone did not modify parasitemia or hemoglobin level. Males treated with DHEA + testosterone had higher numbers of $CD3^+$ T lymphocytes than testosterone treated groups.

The administration of DHEA alone or in combination with testosterone increased the number of $CD8^+$ T lymphocytes compared to the groups treated with vehicle or testosterone. This contributes to explain in part the greater severity of pathology in men since $CD8^+$ T lymphocytes are associated with complications such as cerebral malaria.

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Resumen corto

Phenotypic study of cancer-associated fibroblasts in patients at different stages of cervical cancer and their effect on macrophage polarization

Bueno-Urquiza, L.J. [1]*, Godínez-Rubí, J.M. [2], Villegas-Pineda, J.C. [2], Jave-Suarez, L.F. [4], Martínez-Barajas, M.G. [1], Ramírez de Arellano, A. [,2], Silva-Martínez, M.G. [4], Puebla-Mora, A.G.[2], Pereira-Suarez, A.L. [1,2]

[1]Instituto de Investigación en Ciencias Biomédicas, CUCS, Universidad de Guadalajara, Guadalajara Jalisco, México [2]Departamento de Microbiología y Patología, CUCS, Universidad de Guadalajara, Guadalajara Jalisco, México [3]División de Inmunología, Centro de Investigación Biomédica del Occidente, IMSS, Guadalajara Jalisco, México [4]Departamento de Anatomía Patológica, CMNO, IMSS, Guadalajara Jalisco, México. E-mail: lesly.buenou@gmail.com

The tumor microenvironment of cervical cancer (CC) is composed of cell populations that participate in tumor progression, including cancer-associated fibroblasts (CAFs) and tumor-associated macrophages (TAMs) that participate in metastasis and invasion. CAFs express vimentin, α-smooth muscle actin (α-SMA), fibroblast-specific protein 1 (FSP1/S100A4) and fibroblast activation protein (FAP) and secrete cytokines that regulate polarization to TAMs. This project aims to evaluate the protein expression of FAP, S100A4, α-SMA, and vimentin in CAFs from patients at different stages of CC, and their effect on macrophage polarization.

We evaluate the expression of proteins FAP, S100A4, αSMA, and vimentin of CAFs in tissues from patients with CC by automated immunohistochemistry. In addition, we used mesenchymal cells (MSCs) stimulated with HeLa and SiHa supernatants and measured the expression of the same proteins by immunofluorescence. Subsequently, THP-1 macrophages were stimulated with MSC-CAF cell supernatant and evaluation of the cytokine profile. Vimentin, α-SMA, and FAP showed higher expression in patients with CC, increasing in advanced stages. Concerning CAFs with proliferation, we found a high positive association between proliferation with FAP in late stages. Furthermore, we observed higher expression of FAP in MSCs stimulated with supernatants. Stimulated MSC-CAF produced G-CSF, GM-CSF, CCL2, TNFα, IL-10, IL-6, and TGF-β. However, THP-1 stimulated with MSC-CAF supernatants produced antiinflammatory cytokines such as IL-10, IL-13, and TGFβ1.

In conclusion, MSF-CAF supernatants polarize THP-1 macrophages to M2 phenotype. FAP protein was overexpressed in CC samples and MSC-CAF cells and this shows that FAP could be considered as a biomarker of CC progression.

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Resumen corto

The role of O-GlcNAcylation in carcinogenesis.

Caballero-Sánchez, M.D. [1]*, Hernández-Cruz, P.A. [1],
Fernández-Rojas, B. [1], Gallegos-Velasco, B.I. [1]

[1]Laboratory of Glycobiology, Genomics and Proteomics of Cancer Research Center, School of Medicine and Surgery-UABJO. Autonomous University "Benito Juárez" of Oaxaca, México.
E-mail: casaninstitucional@gmail.com

The pathogenesis is associated with both behavioral risk factors and molecular aspects, for example, post-translational modifications of nuclear and cytoplasmic proteins, such as O-GlcNAcylation (O-GlcNAc), intervening in cell signaling, nutrient flow or oxidative stress itself. of carcinogenesis. It is therefore important to understand the role of O-GlcNAcylation in carcinogenesis. In the present work, the activity of O-GlcNAc in MCF-7 cells was evaluated by cytochemistry, cytometry and MTT assay after stimulation with glucosamine.

The results showed that the concentration of glucosamine at 20 mM is expressed O-GlcNAc. The results suggest the relationship with the flow of nutrients and the expression of O-GlcNAc in MCF-7 cells.

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Resumen corto

Participation of the CD43 sialomucin in T-cell proliferation

Cabañas-Huerta, M. [1,2]*, Flores-Alcantara, A.. [1], Pedraza-Alva. G. [1], Rosenstein Y. [1], Melchy-Pérez, E. [1]

[1]Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México, [2]Licenciatura en ciencias, Centro de Investigación en Dinámica celular, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México.
E-mail: maría.cabanas@ibt.unam.mx

CD43 is a highly glycosylated transmembrane protein abundantly expressed in leukocytes. By interacting with its different ligands, CD43 regulates several functions, such as adhesion/repulsion, cell activation, locomotion, and cellular migration. Particularly, In T Cells, we have shown that the CD43 signaling pathway reinforces that of the TCR, lowering the threshold for activation. In this study, with T cells isolated from the lymph nodes of wild-type (WT) and CD43KO C57BL/6 mice, we aimed to investigate whether CD43 signals regulate T-cell proliferation of CD4+ and CD8+ populations and death signals in response to a CD3/CD28 or PMA/Ionomycin stimulus. We have observed that T Cells CD43KO show a lower rate of proliferation than T Cells CD43 WT in response to PMA/Ionomycin stimulation. This suggests that CD43 may be involved in signaling pathways that impact the T-cell proliferation decision-making process.

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Resumen corto

Characterization of the B cells humoral response in HIV exposed uninfected (HEU) infants

Camacho-Pacheco R.T. [1,2]*, Hernández-Pineda, J. [2],
Brito-Pérez, Y. [1,2], Bermejo-Haro, M.Y. [1,2],
Nájera-Hernández, M.A. [1,2], Plazola-Camacho, N. [1],
Figueroa D.R. [1], Soriano-Becerril, D. [1], Mancilla-Herrera, I. [1]

[1]Instituto Nacional de Perinatología (INPer). CDMX, México. [2]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. E-mail: rodrigo.tonalli@gmail.com

Despite the great worldwide success that has been reducing HIV vertical transmission, concern has arisen that *in utero* viral exposure alone causes significant alterations in the immune system of neonates. Consequently, these HIV exposed uninfected (HEU) newborns have higher rates of opportunistic infections, including capsulated bacteria such as *Haemophilus influenzae* and *Streptococcus pneumoniae*, or parasites such as *Cryptosporidium sp*, which require an antibody defense (IgG2 or IgE) for their resolution, suggesting deficiencies in humoral defense. While most circulating antibodies in infants are of maternal origin, which decrease as they degrade during the first months of life, in HEU infants this does not appear to occur, maintaining similar levels up to 12 months after birth with an increased immunoglobulin IgG1 and IgG3 profile like their HIV+ mothers. These results suggest that B lymphocytes of EHU infants are programmed to maintain a restricted antibody profile that interferes with their optimal respond to infections. The proposal of this work is to describe with flow cytometry applications the phenotypic behavior of B lymphocytes and the antibodies they produce in HEU infants during the first year of life. Our results show minor differences in the proportions of B lymphocyte subpopulations. However, less phenotypic differentiation, lower proliferative capacity and dependence between cell number and antibody production are observed. Moreover, these results are not related to the clinical status of the newborn or their mother. Therefore, it is suggested that *in utero* exposure to HIV alone generates a fetal programming that affects the development of humoral defense.

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Resumen corto

Immunotoxic effect of diazoxon on signal transduction in Nile tilapia (*Oreochromis niloticus*) leukocytes.

Camacho-Pérez, M.R. [1,2*], Díaz-Reséndiz, K.J.G. [1,2,3], Girón-Pérez, M.I. [1,2,3], Corona-Navarro, A. [3], Altamirano-Medina, T.P. [3], Haro-Pérez, A.U. [3]

[1] Universidad autónoma de Nayarit, Laboratorio Nacional de Investigación para la Inocuidad Alimentaria (LANIIA)-Unidad Nayarit. Tepic, Nayarit, México. [2] Maestría en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Xalisco 63780, Nayarit, México. [3] Licenciatura en Biomedicina Ambiental Traslacional, Universidad Autónoma de Nayarit. Tepic, Nayarit, México. E-mail: Milton.Camacho@uan.edu.mx

Leukocytes are cells of the immune response and are characterized by having an extra-neural cholinergic system; they possess all the necessary machinery to generate *de novo* acetylcholine (ACh), a molecule that could play an important role in the immune response regulation. However, the integrity of these cells can be altered by exposure to organophosphate pesticides (OPs) such as diazinon, which during its biotransformation produces a highly toxic metabolite, diazoxon (DZO), which is characterized as a potent inhibitor of the AChE enzyme. Thus, the leukocyte cholinergic system could be a target of OPs and play a role in the phenomenon of immunotoxicity. In this study, the *in vitro* effect of DZO on signaling molecules (JAK1, STAT3, cyclic AMP (cAMP), inositol triphosphate (IP3), and diacylglycerol (DAG)) was evaluated in Nile tilapia leukocytes. JAK1 and STAT3 were determined by flow cytometry using monoclonal antibodies ANTI-JAK1 (pY1022), ANTI-STAT3 (pY705); cAMP, and IP3 by ELISA; and DAG by enzymatic activity. Data suggest that DZO causes an increase in the phosphorylation levels of JAK1 and STAT3, but limits the response of these molecules to cellular stimuli (PMA + ionomycin). DZO also causes an increase in IP3 and DAG levels and induces a decrease in cAMP. These results suggest that DZO may cause dysregulation of cell proliferation and differentiation processes, as well as alteration of innate mechanisms such as phagocytosis.

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Resumen corto

The leukocyte expression of CD39 and CD73 are deregulated in patients with sepsis or SIRS

Camargo-Juárez, M.F. [1,2*], García-de la Rosa, M.T. [2,3], Cabrera-Rivera, G.L. [3], Juárez-Palacios, J.E. [2,3], Basilio-Gálvez, E. [2,3], Torres-Flores, A. [2,3], López-Macías, C. [2], Arriaga-Pizano, L.A. [2]

[1]Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad de México (CDMX), México. [2] Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI, CDMX, México. [3]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. E-mail: camajua25@ciencias.unam.mx

SIRS and sepsis are characterized by an imbalance in production cytokine and hyperactivation of the immune, endotelial and coagulation systems, it results in acute and severe systemic inflammatory process. Several mechanisms promote inflammation contention and resolution. One of them involves adenosine which is produced by ectoenzymes such as CD39 and CD73. Currently there is limited evidence of the importance of the expression of this ectoenzymes in the peripheral blood cells of the immune system in severe inflammatory pathologies. In this project, we evaluated in peripheral leucocytes (lymphocytes, neutrophils, monocytes) the CD39 and/or CD73 expression, in patients with Systemic Inflammatory Response Syndrome (SIRS), sepsis or healthy donors, using leukocytes immunophenotyping analyzed by multiparametric flow cytometry. A total of 12 patients with systemic inflammation (6 patients with SIRS and 6 with sepsis) were recruited. Four healthy volunteers were included for normal reference values. We do not observed differences in CD39 and CD73 expression in lymphocytes from SIRS vs septic patient, in patients with SIRS(compared to those with sepsis), despite monocytes have an increased expression of CD39(1092+84.65vs747.9+65.46 p=0.0107) mainly the classical ones(CD14+16-)(1065+87.95vs704.7+74.22p=0.0092).

Comparing patients with sepsis with those with SIRS, we observed a significant lower proportion of neutrophils expressing CD39(97.56+1.320vs89.93+4.361 p=0.0260), this was also observed for CD73 coexpression(1.20+0.13 vs0.79+0.33, p=0.0290)., in addition, CD73 expression was significantly increased in neutrophils from sepsis patients(474.5+7.10vs580.2+49.80, p=0.0411). This data suggest that the activity of CD39 and CD73 ectoenzymes will be compromised to different extend depending on the origin of systemic inflammation, these are mostly deregulated in sepsis.

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Resumen corto

Drug recognition by the invariant TCR of human NKT cells

Campos-Juárez, A.D. [1]*, Cazares-Olvera, D.V. [2], Gómez-Castro, C.Z. [3], Hernández-Jaimes, O.A. [2], Rodríguez-Cortés, O. [1], Castrejón-Flores, J.L. [2]

[1]Laboratorio de Inflamación y Obesidad, Escuela Superior de Medicina-Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Biología Molecular y Cultivo Celular, Unidad Profesional Interdisciplinaria de Biotecnología-Instituto Politécnico Nacional, Ciudad de México, CDMX, México [3]Laboratorio de Química Teórica y Computacional, Universidad Autónoma del Estado de Hidalgo, Hidalgo, México.
E-mail: acamposj2200@alumno.ipn.mx

Adverse drug reactions (ADRs) can cause type IV hypersensitivity (HS-IV), have a late onset and present different clinical entities that can be localized or systemic which involves different T cell populations. Conventional T cells recognize peptides presented by MHC molecules, but there are non-conventional T cells like NKT cells that can recognize glycolipids presented on CD1d and have effector functions such as cytokine secretion and cytotoxicity. Recently, studies have shown that the invariant TCR of MAIT cells can be activated by drugs presented on MR-1, and this study aims to determine if NKT cells can recognize drugs presented by CD1d. To test this, a virtual screening was performed using the crystal structure of the NKT cell TCR-invariant and the CD1d pocket (PDB: 4EN3). The screening was challenged against 3,953 molecules from the ZINC database, and the drugs with the highest probability of interaction with the CD1d pocket and the TCR were sulfamethoxazole and sulfadiazine.

An assay was then carried out by loading these drugs onto a CD1d dimer plated with PBMCs from healthy donors. The percentage of NKT cells was determined by flow cytometry, and it was observed that in 3 out of 5 donors, there was NKT TCR-specific recognition of the drug-CD1d complex. These results suggest that NKT cells can recognize drugs presented by CD1d, and could be involved in HS-IV. Further research is needed to determine the clinical implications of these findings and to develop strategies for predicting and preventing ADRs.

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Resumen corto

Looking for activator-drugs of TVγ9Vδ2 cells from healthy subjects

Campos-Juárez, A.D. [1]*, García-Núñez, A.A. [2], Gómez Castro C.Z. [3], Hernández-Jaimes, O.A. [2], Rodríguez-Cortés, O. [1], Castrejón-Flores, J.L. [2]

[1]Laboratorio de Inflamación y Obesidad, Escuela Superior de Medicina-Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Biología Molecular y Cultivo Celular, Unidad Profesional Interdisciplinaria de Biotecnología-Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Laboratorio de Química Teórica y Computacional, Universidad Autónoma del Estado de Hidalgo, Hidalgo, México.
E-mail: acamposj2200@alumno.ipn.mx

TVγ9Vδ2 cells are a population of non-conventional T cells found in peripheral blood. These cells have diverse innate effector roles in inflammation and especially in cytotoxicity, making them attractive targets for immunotherapy. Their activation has been extensively studied because they have unconventional mechanism for TCR activation, and the most described mechanism involves the intracellular accumulation of phosphoantigens (PAgs), such as HMBPP and IPP, in the B30.2 domain of BTN3A1 within an APC. In this study, we aimed to identify small and simple molecules like drugs that could activate TVγ9Vδ2 cells from healthy subjects. To achieve this, we performed a virtual screening workflow using a database of FDA-approved drugs with 2500 molecules and a co-crystal of the B30.2 domain of BTN3A1 with HMBPP (PDB 5ZXK). Our workflow included non-covalent molecular docking (with the binding free energy (BFE)), distance of interaction to mass center (DCM) and a geometric parameter called ligand-receptor contact distance (LRCD). Our results suggest that the five drugs with the highest probabilities capable of binding to the cytoplasmatic domain B30.2 in a similar way to HMBPP were antibiotics and smooth muscle relaxants, and then, could be potential activators of TVγ9Vδ2 cells. For all the results, we considered the most favorable BFE (-7 to -9.5 Kcal/mol), DCM (> 4 Å) and LRCD (0.6 to 0.85), and their interactions with the previously described key amino acids of the receptor. Activating these cells with small molecules like drugs could have a significant impact on the treatment of infections, autoimmunity and cancer.

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Resumen corto

Nutritional, biochemical, and clinical determinants of hyperuricemia in systemic lupus erythematosus patients: relationship with clinical and renal disease activity

Campos-López, B. [1]*, Meza-Meza, M.R. [1], Pesqueda-Cendejas, K. [1], Ruiz-Ballesteros, A.I. [1], Rivera-Escoto, M. [1], Vargas-Morales, J.M. [2], Parra-Rojas, I. [1,3], Mora-García, P.E. [1], Vizmanos, B. [1], Montoya-Buelna, M. [1,4], Cerpa-Cruz, S, [5], de la Cruz-Mosso, U. [1]

[1]Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [2]Facultad de Ciencias Químicas, Universidad Autónoma de San Luis Potosí, San Luis Potosí, Mexico. [3]Laboratorio de Investigación en Obesidad y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, Chilpancingo de los Bravo 39087, Guerrero, Mexico. [4]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [5]Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara 44280, Jalisco, Mexico.
E-mail: ulises_cdm@hotmail.com, ulises.mosso@academicos.udg.mx

Systemic lupus erythematosus (SLE) is the prototypical autoimmune disease considered an independent risk factor for cardiovascular disease mortality. Currently, uric acid is described as a novel biomarker associated with cardiometabolic outcomes. However, nutritional and serum determinants that influence hyperuricemia development in autoimmune diseases have not been fully elucidated. This study aimed to assess the nutritional, biochemical, and cardiometabolic determinants of hyperuricemia and its relationship with clinical variables in SLE patients. A cross-sectional study was conducted on 167 SLE patients and 195 control subjects (CS). Nutrient intake, anthropometry, biochemical, and cardiometabolic indexes were evaluated. In SLE patients an adequate protein (OR=0.4; p=0.04) and carbohydrate (OR=0.2; p=0.01) intakes were associated with a lower risk of hyperuricemia. SLE patients with hyperuricemia presented a higher risk of clinical (OR=2.2; p=0.03) and renal activity (OR=3.4; p<0.01), as well as triglycerides ≥150 mg/dL (OR=3.6; p<0.01), hs-CRP ≥1 mg/L (OR=3.1; p<0.01), Kannel score ≥3 (OR=2.5; p=0.02), BMI ≥25 kg/m^2 (OR=2.2; p=0.02). Oppositely, serum levels of HDL-C ≥40 mg/dL (OR=0.2; p<0.01) were associated with a lower risk of hyperuricemia. According to the pharmacotherapy administered, prednisone treatment was associated with a high risk of hyperuricemia (OR=4.7; p<0.001). In contrast, the hydroxychloroquine treatment was associated with a lower risk of hyperuricemia (OR=0.4; p=0.02). In conclusion, SLE patients with hyperuricemia presented a high risk of clinical and renal activity as well as worse cardiometabolic status. Notably, an adequate intake of protein, carbohydrates, healthy HDL-C serum levels, and hydroxychloroquine treatment could be determinants of lower risk of hyperuricemia.

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Resumen corto

Efficacy and Safety of the anti-SARS-CoV-2 therapeutic antibody IgG-A7

Carballo-Uicab, G. [1,2]*, González-González, E. [1,2], Gómez-Castellano, K. [1,2], Vallejo-Castillo, L. [1,2], Almagro, J.C. [1,2,4], Pérez-Tapia, S.M. [1,2,3]

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City 11340, Mexico. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos, LANSEIDI-FarBiotec-CONACyT, Mexico City 11340, Mexico. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), Mexico City 11340, Mexico. 4GlobalBio, Inc., 320 Concord Ave, Cambridge, MA 02138, USA. E-mail: gregorio.carballo@udibi.com.mx

All the Food and Drug Administration (FDA) and European Medicine Agency (EMA) emergency use authorized (EUA) antibodies to treat or prevent COVID19 are targeting the receptor-binding domain (RBD) of SARS-CoV-2. The first UEA antibodies were developed to treat the Wuhan variant but, their neutralization potency decreased or faded away completely as variants of concern (VOC) such as Delta or Omicron emerged. Therefore, development of new antibodies has been necessary to treat SARS-CoV-2 infection caused by VOCs. Using a semi-immune phage library, we discovered an RBD-neutralizing antibody called IgG-A7, which neutralized in vitro Wuhan, Delta and Ómicron with EC_{50} of 0.56, 0.06 and 2.93 nM, respectively. Here we present the preclinical development of IgG-A7 including efficacy and safety studies in animal models. At a dose of 5 mg/Kg IgG-A7 was able to counteract weight loss, decrease viral load, and increase survival of transgenic mice that expressed the human angiotensin converting enzyme 2 (hACE2) and were infected with Wuhan, Delta, or Omicron.

Moreover, we demonstrated that IgG-A7 does not react to other targets or human tissues through a tissue cross-reactivity (TCR) study, nor did it show to facilitate the entry of the virus into cells in vitro. Furthermore, IgG-A7 did not showed toxicity related to i.v. administration of 50, 100 and 200 mg/Kg at single or repeated doses (once a week for 3 weeks) in CD-1 mice. These results indicate that IgG-A7 is both efficacious and safe, paving the way for clinical testing in phase 1 studies.

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Resumen corto

Babesia bovis Enolase is expressed in intracellular merozoites and contains predicted B-cell epitopes that induce neutralizing antibodies

Cárdenas-Flores, A. [1,6*], Camacho-Nuez, M. [2], Ueti, M. [3], Hidalgo-Ruiz, M. [4], Rodríguez-Torres, A. [5], Hernández-Silva, D.J. [1], Gómez-Soto, J.G. [7], Asada, M. [8], Kawazu, S.I. [8], Mosqueda-Gualito, J.J. [1].

[1]Immunology and Vaccines Laboratory, Natural Sciences College, Autonomous University of Queretaro, Queretaro, Mexico [2] Autonomous University of Mexico City, Postgraduate Program in Genomic Sciences, Mexico City, Mexico. [3] Animal Diseases Research Unit, USDA-ARS, Pullman, Washington, US. [4] College of Veterinary Medicine, Autonomous University of Chiapas, Tuxtla Gutierrez, Chiapas, Mexico. [5] Animal Health and Environmental Microbiology, Natural Sciences College, Autonomous University of Queretaro, Queretaro, Mexico. [6] PhD Program in Natural Sciences, Natural Sciences College, Autonomous University of Queretaro, Queretaro, Mexico. [7] Natural Sciences College, Autonomous University of Queretaro. [8] National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan.
acardenas906@alumnos.uaq.mx

Bovine babesiosis is the most important tick-borne disease in cattle worldwide; *Babesia bovis* is the species that causes the most serious clinical signs and the highest mortality. The identification of new antigens is necessary for the development of new generation vaccines. Enolase, a “Moonlight” enzyme of glucose metabolism, has shown potential as a vaccine candidate in different pathogens. However, enolase has not been studied in *B. bovis*. In this study, two *B. bovis* isolates from two states in Mexico were amplified, cloned, and sequenced. A gene of 1,366 bp was identified and its transcription by RT-PCR was verified. A predicted 438 amino acid sequence of the enolase protein was obtained, with a predicted molecular weight of 47 kDa and used for the identification of two conserved peptides with predicted B-cell epitopes. Synthetic peptides were obtained, and these were used to immunize rabbits. Rabbits generated antibody titers of up to 1:256,000 for peptide 1 and 1:512,000 for peptide 2. These antibodies recognized intraerythrocytic merozoites by indirect immunofluorescence (IFI) and bound to a protein of the expected molecular weight in lysates of *B. bovis*-infected erythrocytes by western blot. A neutralization assay with intraerythrocytic parasites *in vitro* was performed. Antibodies against peptide 2 neutralized parasite growth by 72%, while antibodies against peptide 1 had no effect. With the results obtained, we propose that *B. bovis* enolase is a protein expressed by *B. bovis* merozoites and contains B-cell epitopes that induce the generation of neutralizing antibodies and can be included in future vaccines.

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Resumen corto

Mosquito pericardial cells upregulate *Cecropin* expression after an immune challenge

Cardoso-Jaime, V. [1,2,a], Maya-Maldonado, K. [1,2,b], Tsutsumi, V. [2], Hernández-Martínez, S. [1*]

[1]Centro de Investigaciones Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública. Av. Universidad 655, Santa María Ahuacatitlan, Cuernavaca, Morelos, México. C.P. 62100. [2]Departamento de Infectómica y Patogénesis Molecular, Centro de Investigación y de Estudios Avanzados, IPN. Av. Instituto Politécnico Nacional 2508, Gustavo A. Madero, Ciudad de México, México. C.P. 07360. [a]Current address: W. Harry Feinstone Department of Molecular Microbiology and Immunology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA. [b]Current address: Department of Biology, Johns Hopkins University, Baltimore, Maryland, USA. *shernandez@insp.mx

Most mosquito-transmitted pathogens grow or replicate in the midgut before invading the salivary glands. Pathogens are exposed to several immunological factors along the way. Recently, it was shown that hemocytes gather near the periostial region of the heart to efficiently phagocytose pathogens circulating in the hemolymph. Nerveless, not all pathogens can be phagocyted by hemocytes and eliminated by lysis. Interestingly, some studies have shown that pericardial cells (PCs) surrounding periostial regions, may produce humoral factors, such as lysozymes. Our current work provides evidence that *Anopheles albimanus* PCs are a major producer of *Cecropin 1* (*Cec1*). Furthermore, our findings reveal that after an immunological challenge, PCs upregulate *Cec1* expression.

We conclude that PCs are positioned in a strategic location that could allow releasing humoral components, such as cecropin, to lyse pathogens on the heart or circulating in the hemolymph, implying that PCs could play a significant role in the systemic immune response.

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Resumen corto

Bisacodyl and Puerarin, two putative FLT3-ITD inhibitors for Acute Myeloid Leukemia treatment

Carranza-Aranda, A.S. *[1,2], Santerre, A.[1], Jave-Suárez, L.F. [3], Herrera-Rodríguez, S.E. [2]

[1]Centro Universitario de Ciencias Biológicas y Agropecuarias, Zapopán, Jalisco, México. [2]Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco, Guadalajara, Jalisco, México. [3]Centro de Investigación Biomédica de Occidente, Guadalajara, Jalisco, México. ahtziricarranza19@gmail.com

Acute Myeloid Leukemia (AML) is the most common hematologic cancer in the adult population worldwide. The ITD (internal tandem duplication) mutation in the FMS-Tyrosine-Kinase-3 receptor (FLT3) is responsible for the high proliferative capacity of leukemic cells in 35% of AML patients. Thus, FLT3 is a therapeutic target. Two synthetic molecules: Gilteritinib and Quizartinib, bind native FLT3 (FLT3-WT) and have been approved for AML treatment; however, their efficiency is limited in FLT3-ITD patients. This study used molecular docking to assess the molecular interactions of two molecules of natural origin, Puerarin and Bisacodyl, with wild-type and mutated FLT3. Moreover, their cytotoxic effect was tested on two leukemic cell lines: HL-60 (FLT3-WT) and MV4-11 (FLT3-ITD). The 3D models of FLT3-WT and FLT3-ITD were elaborated by Protein Homology Modelling. The interactions of Gilteritinib, Quizartinib, Puerarin, and Bisacodyl with FLT3 models, were tested by molecular docking. Their cytotoxic and antiproliferative effects were evaluated by MTT assay and flow cytometry. ERRAT (95.61; 90.27) and VERYFY (93.60%; 92.28%) data indicate a high structural quality of FLT3-WT and FLT3-ITD models. Gilteritinib and Quizartinib presented higher affinity to FLT3-WT meanwhile, Puerarin and Bisacodyl presented higher affinity for FLT3-ITD (7.9Kcal/mol; -9.0Kcal/mol vs -9.3Kcal/mol; -10.2Kcal/mol). Puerarin and Bisacodyl showed higher cytotoxicity than Gilteritinib and Quizartinib against MV4-11 cells (FLT3-ITD), induced apoptosis, and decreased cell proliferation. Instead, there was no cytotoxicity against HL60. Thus, the *in-silico* and *in-vitro* approaches allowed the rational identification and evaluation of two bioactive molecules: Puerarin and Bisacodyl, candidates for repositioning against AML.

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Resumen corto

Prolactin promotes proliferation of germinal center B cells, formation of plasma cells, and elevated levels of IgG3 anti-dsDNA autoantibodies

Carreón-Talavera, R. [*1], Santana-Sánchez, P. [1], Fuentes-Pananá, E.M. [2], Legorreta-Haquet, M.V. [1], Chávez-Sánchez, L. [1], Gorocica-Rosete, P.S. [3], Chávez-Rueda, A.K. [1]

[1]UIM en Inmunología, Hospital de Pediatría, CMN Siglo XXI, Instituto Mexicano del Seguro Social, México City, México. [2]Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México Federico Gómez, México City, México. [3]Departamento de Investigación en Bioquímica, Instituto Nacional de Enfermedades Respiratorias "Ismael Cosió Villegas", México City, México.

Systemic lupus erythematosus (SLE) mainly affects females at reproductive age, which has been associated with hormones, such as prolactin (PRL). Different studies suggest that PRL exacerbates the clinical manifestations of SLE both in patients and in mouse models (e.g., the MRL/lpr strain), increasing the production of autoantibodies, which can be deposited as immune complexes and trigger inflammation and damage to different tissues. The objective of this work was to explore the potential mechanisms by which PRL increases the concentration of self-reactive antibodies in the MRL/lpr SLE model. To this end, we determined the role of PRL on the activation and proliferation of germinal center B cells (B-GCs) and their differentiation into antibody-secreting cells (ASCs). We show that the absolute number and percentage of B-GCs were significantly increased by PRL *in vivo* or upon *in vitro* treatment with anti-IgM and anti-CD40 antibodies and PRL. The augmented B-GC numbers correlated with enhanced proliferation, but we did not observe enhanced expression of CD80 and CD86 activation markers or the BCL6 transcription factor, arguing against a more effective differentiation. Nevertheless, we observed enhanced phosphorylation of STAT1, secretion of IL-6, expression of IRF4, numbers of ASCs, and levels of IgG3 antibodies directed against dsDNA. Altogether, these results support the hypothesis that a PRL-mediated expansion of B-GCs yields more self-reactive ASCs, potentially explaining the pathogenic immune complexes that steadily lead to tissue damage during SLE.

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Resumen corto

Serum pro-inflammatory biomarkers associated with improvement in quality of life in pulmonary tuberculosis

Carreto-Binaghi, L.E. [1], Sartillo-Mendoza, L.G. [2,3], Guzmán-Beltrán, S. [4], Torres, M. [1], Carranza, C.[1], González, Y.[4], Muñoz-Torrico, M. [5], Juárez, E. [4]*

[1]Laboratorio de Inmunobiología de la Tuberculosis, INER, CDMX, México. [2]Facultad de Medicina, BUAP Puebla, México. [3]Becario de la Dirección General de Calidad y Educación en Salud, Secretaría de Salud, CDMX, México. [4]Departamento de Investigación en Microbiología, INER, CDMX, México.[5]Servicio clínico de tuberculosis, INER, CDMX, México.

*ejuarez@iner.gob.mx

Tuberculosis (TB) patients who develop pulmonary dysfunction have a poor quality of life (QoL) associated with an excessive inflammatory response. In TB, multiple pro-inflammatory cytokines induce bactericidal mechanisms at the cost of generating a potent inflammatory microenvironment that may damage lung parenchyma. This study aims to determine the profile of pro-inflammatory markers associated with respiratory dysfunction and quality of life in patients with pulmonary tuberculosis. In this study, we measured serum levels of pro-inflammatory cytokines and lipids (PGE2, LTB4, IL-8, and TNF-α), pro-resolutory lipids (RvD1, Mar1, and LXA4), and one marker of tissue damage (free nucleosomes) in patients with pulmonary tuberculosis at the beginning (t1) and two months after treatment initiation (t2). The patients also completed the St. George's QoL questionnaire at both time points.

All metabolites were measured by ELISA. At t2, levels of all lipid mediators decreased except for PGE2. We also measured pro-resolutory/proinflammatory lipids ratios since these are more informative than absolute levels. The Mar1/PGE2 and RvD1/PGE2 ratios, indicators of inflammation resolution, decreased at t2. Despite an improvement in QoL, we observed no reduction in the levels of proinflammatory cytokines and nucleosomes. This suggests that at the end of the intensive phase of TB treatment (2 months), regardless of an improvement in QoL, patients seem to have a sustained inflammatory process that could influence the outcome. Biomarkers of inflammation could help clinicians to follow the course of the disease, monitor treatment success, and predict long-term pulmonary dysfunction.

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Resumen corto

MBOAT7 and TM6SF2 prevalence in fatty liver disease associated with metabolic dysfunction (MAFLD) in mexican population

Carsolio-Sosa, M.B. *[1,2], Hernández-Flores, K.G. [2], Domínguez-Alemán, C.A. [2], Priego-Parra, B.A. [2], Vivanco-Cid, H. [2]

[1]Facultad de Bioanálisis, Universidad Veracruzana, Región Veracruz, México. [2]Instituto de Investigaciones Médico-Biológicas, Universidad Veracruzana, Región Veracruz, México. carsoliosoa@gmail.com

The main characteristic of fatty liver disease associated with metabolic dysfunction (MAFLD) is over-storage of fat in liver cells. Over the past 20 years, cases of MAFLD have increased dramatically around the world; in Latin America there is the highest prevalence of MAFLD, being calculated at approximately 30.5%. In Mexico it is estimated that the prevalence could exceed 50% of the population due to the correlation with factors such as diabetes, hypertension and cardiovascular diseases. Therefore, the objective of this projects were to evaluate in a cohort of mexican patients with clinical diagnosis of MAFLD, the prevalence of the gene polymorphisms (SNPs) TM6SF2 and MBOAT7, which have been associated with predisposition of MAFLD in other populations, for this purpose, TM6SF2 (rs 58542926) and MBOAT7 (rs 641738) were genotyped using Taqman assays. Heterozygotes (CT) was found in 19% in healthy subjects, 29% in MAFLD and 90% in fibrosis for TM6SF2. Heterozygotes (CT) was found in 43% in healthy subjects, 25% MAFLD and 65% in fibrosis for MBOAT7. Finally, we observed a prevalence of homozygotes (TT) less than 5% in both SNPs. Our study is the first to evaluate the frequency of these polymorphisms in Mexico.

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Resumen corto

Effect of the prenatal administration of LPS on BALB/c mice: Cellular evaluation

Cásarez-Alvarado, S. *[1,3], Márquez-Velasco, R. [1], Basilio-Gálvez, E. [2,3], Domínguez-López, M.L.[3], García-Latorre, E.A. [3]

[1]Departamento de Inmunología, Instituto Nacional de Cardiología "Ignacio Chávez, Ciudad de México, CDMX, México. [2]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades del Centro Médico Siglo XXI, Instituto Mexicano del Seguro Social, CDMX, México [3]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México.
secazalv@gmail.com

Lipopolysaccharide (LPS) is a component of the outer membrane of Gram negative bacteria. LPS induces a strong inflammatory response, signaling via TLR4, which induces an exacerbated production of pro-inflammatory response associated to tissue damage. Administration of repeated low doses of endotoxin can induce tolerance, in which levels of pro-inflammatory cytokines decrease, protecting against subsequent lethal doses. There are few studies on the effect of prenatal exposure to this antigen. In this study, we evaluated changes in splenocytes and target organs of adult animals treated prenatally with LPS. Gestational BALB/c female mice were grouped into 3 groups: a) control, treated with saline solution, while 2) orally (O) and 3) intraperitoneally (IP) BALB/c mice were treated with LPS serotype O55:B5 (50 mg) from E. coli, the offspring (at 12 weeks) was challenged with a sublethal dose of LPS via IP, and 3h later sacrificed by cervical dislocation, the spleens were obtained and were perfused, Populations of T lymphocytes, B lymphocytes and monocytes were analyzed by flow cytometry. Intracellular levels of IL-1β, IL-2, IL-6, IL-10 and TNFα were quantified by ELISA. We found higher concentrations of IL-1β, IL-6 and IL-10 in both groups treated with LPS prenatally, we found a significative increase in classical of monocytes in IP and O groups vs C although not their cytokine production; In addition, higher percentage of $TCD8^{+}IL\text{-}10^{+}$ and $CD19^{+}IL\text{-}10^{+}$ was observed in these same groups. These results suggest that prenatal administration of LPS alters immune response in adult animals, changing their normal cytokine response.

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Resumen corto

Allergic sensitization in a mexican population with allergic conjunctivitis treated at a ophthalmologic referral institute

Castillo-Balcázar, E. *[1], Quintana-Mexiac, G. [1], Casanova-Méndez, I. [1], Velázquez-Soto, H. [1], Cruz-Aguilar, M. [1], Jiménez-Martínez, M.C. [1]

[1] Department of Immunology and Research Unit, Institute of Ophthalmology "Conde de Valenciana Foundation", Mexico City, Mexico. estefania.cast569@gmail.com

Exposure to aeroallergens is the main trigger of allergic conjunctivitis. Aeroallergens related to other allergic diseases have been studied; however, the prevalence of sensitization of the different groups of aeroallergens in the Mexican population with diagnosis of allergic rhinitis and allergic conjunctivitis is unknown. A population of patients with diagnosis of allergic rhinitis and allergic conjunctivitis who received medical attention at the Institute of Ophthalmology "Fundación Conde de Valenciana" was evaluated. Sensitivity to pollens, fungal, domestic and food allergens was determined by skin prick test and the overall prevalence of each group was estimated as well as the individual prevalence of 58 allergens. The sample examined was 1574 patients aged 2 to 87 years who were tested in the period from 2008 to 2022. A descriptive analysis was performed. It was observed that domestic allergens were the most prevalent group, followed by pollens, food and finally fungi. It was concluded that the Mexican population is more susceptible to domestic allergens such as dust mites.

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Resumen corto

Role of autophagy in the intracellular infection of epithelial cells by *Candida glabrata*

Castillo-Cruz, J. [1,2]*, Castrejón-Jiménez, N.S. [3], Hernández-González, J.C. [3], Palacios-Barreto, S. [2], López-Álvarez X.G [1], Baranda-Sandoval, Y. [1], García-Pérez, B.E. [2]

[1]Escuela Superior de Medicina, Instituto Politécnico Nacional, juancast0508@gmail.com; xuxulopez39@gmail.com; barandayamileth@gmail.com. [2]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Prolongación de Carpio y Plan de Ayala s/n, Ciudad de México 11340, México; samarapalacios.0205@hotmail.com; abrilestela@hotmail.com. [3]Área Académica de Medicina Veterinaria y Zootecnia, Instituto de Ciencias Agropecuarias-Universidad Autónoma del Estado de Hidalgo, Av. Universidad km. 1. Exhacienda de Aquetzalpa A.P. 32, Tulancingo 43600, Hidalgo, México; nayeli_castrejon@uaeh.edu.mx, juan_hernandez8281@uaeh.edu.mx

Autophagy is a lysosomal-dependent degradation of damaged organelles, misfolded proteins, and intracellular microorganisms by forming a double-membrane vesicle called an autophagosome. Autophagy can effectively kill bacteria such as *Streptococcus pyogenes* and *Mycobacterium tuberculosis*. Nevertheless, autophagy can serve as a niche for the intracellular replication of other bacteria, such as *Porphyromonas gingivalis*. *Candida glabrata* is a fungal organism resistant to drugs such as azoles, forms biofilms, has high resistance to oxidative stress, and has been reported to evade the immune response. This work aimed to determine the role of autophagy in lung epithelial cells infected by *C. glabrata*. Autophagy was stimulated with rapamycin before infection. Western blotting and immunofluorescence determined the changes in LC3I/LC3II expression. The results showed that *C. glabrata* replicated within the first hour of infection; however, the infection resolved within 24 hours. Induction of autophagy with rapamycin in macrophages and epithelial cells prior to infection contributes to early clearance of intracellular infection. Whereas the inhibition of autophagy contributes to the persistence of the infection, avoiding acidification by the lysosomes.

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Resumen corto

Genetic data mining and analysis of protein-protein interactions in Alzheimer's disease and Type 2 Diabetes Mellitus

Castillo-Velázquez, R. [1], Lara-Ramírez, E.E. [2].

[1]Universidad Autonoma de San Luis Potosi (UASLP). Unidad de Investigacion Biomedica de Zacatecas. [2]Centro de Biotecnología Genómica, Instituto Politecnico Nacional. E-mail: A189489@alumnos.uaslp.mx.

Alzheimer's disease (AD) and Type 2 Diabetes Mellitus (DM2) are chronicdegenerative pathologies with complex molecular processes that today are associated due to failures in insulin metabolism and processes of cognitive deterioration, in the present study. Systems biology tools used to find and identify the main biological processes, signaling pathways and proteins associated with the possible AD-T2DM binomial using information present in databases (RNA seq) and scientific publications (data mining). The collection of information on biomolecules in common between AD and DM2 was carried out through data mining from various specialized platforms (DisGeNET, Ensembl, OMIM, Protein Data Bank, The Human Protein Atlas, UniProt, Gene Expression Omnibus, Human Cell Atlas and PubMed) and the scientific literature present in NCBI (pubmed), RNA seq data were subsequently selected on the Gene Expression Omnibus platform for both AD and DM2 with the aim of analyzing them using the GEO2R platform and determining the differentially expressed genes for both. pathologies, with this information proteinprotein interaction (PPI) networks were formed using the STRING and EnrichR platforms, determining the gene ontology processes and the signaling pathways associated with the AD-DM2 binomial, likewise the detection of Hub elements was conducted relevant aspects of protein-protein interaction networks. A total of 1551 common genes for AD and DM2 were identified. Protein-protein interaction (PPI) networks based on experimental data showed that "cellular response to cytokine stimulation (GO:0071345)", followed by "cytokine-mediated signaling pathway (GO:0019221)" are two of the elements that mainly relate DM2 to AD. In the present study we found biological information linking AD and DM2. PPI prediction shows deregulated biological processes and shared signaling pathways for both pathologies, highlighting inflammatory deregulation for the AD-DM2 association.

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Resumen corto

Catecholaminergic neuroimmunological system and pain control in the dental pulp: a cohort study

Castro-Gutiérrez, M.E.M. [1*], Argueta-Figueroa, L. [2], Bautista-Hernández, M.A. [1], Fuentes-Mascorro, G. [3], Moreno-Rodríguez, A. [4], Solórzano-Mata, C.J. [5], Torres-Rosas, R. [5]

[1]Programa de Doctorado en Biociencias, Facultad de Medicina y Cirugía, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México. [2]Consejo Nacional de Ciencia y Tecnología, Ciudad de México, CDMX, México. [3]Laboratorio de Investigación en Reproducción Animal (LIRA), Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México. [4]Facultad de Ciencias Químicas, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México. [5]Laboratorio de Inmunología Asociado al Centro de Estudios en Ciencias de la Salud y la Enfermedad, División de Posgrado, Facultad de Odontología, Universidad Autónoma "Benito Juárez" de Oaxaca, Oaxaca de Juárez, Oaxaca, México. marcecastrog@hotmail.com

Acupuncture treatment modulates inflammation and pain by activating several neuroimmunological communication pathways, including a catecholamine-dependent pathway. Also, diverse authors have reported that the sympathetic nervous system innervates the dental pulp. Therefore, this study aimed to determine if acupuncture provides an analgesic effect on the dental pulp and the relationship with neuroimmunological control elements in this tissue. A prospective cohort study was performed with patients scheduled for tooth extraction for orthodontic reasons, which were treated with complementary management of electroacupuncture during the extraction process. The success of dental anesthesia was determined using electrical tests. On the other hand, the presence of the α2 adrenergic receptor in cells of immune lineage in dental pulp was determined by fluorescence microscopy. The results showed that complementary therapy with electroacupuncture exhibited a success rate of 72.5%. In addition, cells with immune lineage (CD45+) in dental pulp expressed α2 adrenergic receptors. Consequently, we hypothesized that the catecholaminergic neuroimmune pathway in dental pulp is present in this tissue. The activation by electroacupuncture of this modulatory pathway may be related to successful pulp anesthesia and pain control during tooth extraction.

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Resumen corto

Influence of cells with immunosuppressive capacity on T cell activation of neonates born by cesarean section or vaginal delivery

Cedillo-Baños, A. *[1], Rodríguez-Jorge, O. [1], Santana-Calderón, M.A. [1]

[1]Centro de Investigación en Dinámica Celular, Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México.
alejandra.cedilloban@uaem.edu.mx

Newborns are a highly susceptible population to infectious diseases, leading to high morbidity and mortality rates. Neonatal T cells are different from adult cells, with a high tolerogenic and Th2-mediated response. In addition, in the neonatal period, an enrichment in T_{regs} and immature $CD71^+$ erythroid cells provide an immunosuppressive environment. The form of birth can also influence the neonatal immune system, as a predisposition to childhood asthma and, later in life, chronic inflammatory conditions have been associated with cesarean section delivered persons.

In this work, we evaluated the effect of the form of birth, and the influence of immunosuppressive T_{reg} and $CD71^+$ erythroid cells, on cytokine expression of $CD4^+$ and $CD8^+$ T cells in response to stimulation with antibodies against CD3/CD28 using flow cytometry.

Overall, we found a higher stimulation of cells from cesarean-section-delivered babies. We also found that depletion of $CD71^+$ immature erythroid cells lead to higher activation of T cells, suggesting a major role of these cells in the immunosuppressive environment of neonatal T cells.

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Resumen corto

Overexpression of molecular biomarkers in circulating tumor cells decreases overall and event free survival in DLBCL patients

Cerón-Maldonado, R. *[1,2], Martínez-Tovar, A. [2], Ramos-Peñafiel, C.O. [3], De la Cruz-Rosas, A. [2], García-Laguna, A.I. [2], Mendoza-Salas, I. [2], Soto-Cruz, M.I. [4], Gutiérrez-Kobeh, L. [5], Montaño-Figueroa, E.H. [3], Jiménez-Morales, S. [6], Martínez-Murillo, C. [3] , Olarte-Carrillo, I. [2]

[1]Posgrado en Ciencias Biológicas, Biomedicina, UNAM, CDMX, México; [2]Departamento de Biología Molecular, Servicio de Hematología, Hospital General de México, "Dr. Eduardo Liceaga", CDMX, México; [3]Departamento de Hematología, Hospital General de México, "Dr. Eduardo Liceaga", CDMX, México; [4]Laboratorio de Oncología Molecular, Unidad de Investigación en Diferenciación Celular y Cáncer, FES Zaragoza, UNAM; [5]Laboratorio de Inmunofisiología Celular, Unidad de Investigación UNAM-INC, Facultad de Medicina, UNAM, [6]Laboratory of Cancer Genomics, National Institute of Genomic Medicine, Mexico City, Mexico. cmrafael.bh@gmail.com

Diffuse large B-cell lymphoma (DLBCL) is a heterogeneous malignant lymphoid neoplasm and is the most common subtype of non-Hodgkin lymphoma in adults. More than half of patients with DLBCL can achieve remission with standard R-CHOP regimes; however, approximately 40% of patients are still failing this standard therapy, which remains as an important cause of progression and mortality of this disease. It is necessary to have diagnostic and monitoring tools that allow us to improve the accuracy of prognosis in these patients. Circulating tumor cells (CTCs) identification through circulant molecular biomarkers is one of the novel strategies that have been used in other types of cancer, and we aim to use this tool to analyze the potential role in DLBCL. We analyzed 138 blood samples of patients with DLBCL, of which CTCs were isolated by density gradient for subsequent detection and quantitation of molecular biomarkers using RT-qPCR with TaqMan probes. Survival analysis was performed using Kaplan–Meier curves. We found overexpression of *BCL2*, *BCL6* and *VEGFR1* genes, as well as the presence of CK19, *EpCAM*, and *TWIST1* genes. CK19 and EpCAM expression were associated with a minor OS (85.7% vs 98.1%, p = 0.002). The overexpression of BCL2, BCL6, *VEGFR1* and TWIST1 was related to a minor EFS (p = 0.001). This study showed that in liquid biopsies analyzed, the presence of CTCs can be confirmed through molecular biomarkers, and it has an impact on OS and EFs, making this detection useful in the follow-up and prognosis of patients with DLBCL.

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Resumen corto

Immunomodulatory effect of tamoxifen on B cells and NK cells in an experimental model of murine malaria

Cervantes-Candelas, L.A. Legorreta-Herrera, M.

Laboratorio de Inmunología Molecular, Faculta de Estudios Superiores Zaragoza, UNAM, Batalla 5 de Mayo S/N Col. Ejército de Ote. Iztapalapa, 09230, México, Ciudad de México Tel: 56230736.
cervantescandelasluis@gmail.com

Malaria is the most important parasitic disease, in 2022 it caused the death of 619,000 people and 247,000,000 new cases. This disease presents sexual dimorphism, in which women present greater protection than men. This phenomenon could be related to the higher concentration of estrogens in women and the possible positive immunoregulatory effects of these hormones. T lymphocytes and NK cells have been documented to promote parasite clearance by secreting cytokines that promote phagocytosis and maturation of B cells to plasmatic cells, which synthesize antibodies against the parasite. Furthermore, the immune cell has estrogen receptors, so, in this work we administered tamoxifen, an estrogen receptor blocker, and evaluated its effect on parasitaemia, as well as the number of T and B lymphocytes and NK cells in the spleen of mice infected with *P. berghei* ANKA (PbA).

Male and female mice were treated with tamoxifen or vehicle for 28 days prior to infection. Untreated mice were used as a control group. They were then infected with $1x10^3$ erythrocytes parasitized with PbA. On day 8 post infection, the animals were sacrificed, and the spleen was removed. The number of cytotoxic T cells, B cells and NK cells were stained with fluorochrome-coupled antibodies and cell numbers was quantified by flow cytometry.

Tamoxifen increased the parasitemia of male and female mice. It's possible that this finding is due at least in part to the decrease in the number of B cells caused by tamoxifen in both sexes. This suggests that estrogens intervene in both sexes to increase the number of B cells and promote their maturation. Interestingly, tamoxifen increased NK cell numbers only in females, suggesting that estrogen dimorphically regulates NK cell apoptosis.

These results demonstrate the immunoregulatory role of estrogens in malaria, which helps to explain at least in part the sexual dimorphism in the disease.

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Resumen corto

Functional characterization of an anti-TNF-a with potential therapeutic applications

Cervantes-Contreras, A. [1,2], Comparan-Alarcón, S. [1,2], Godínez-Palma, S. [1,2], Gómez-Castellano, K. [1,2], Elizarraras-Rodríguez, L. [1,2], Vázquez-Leyva, S. [1,2], Pérez-Tapia, S.M. [1,2,3] and Almagro, J.C. [1,2,4]

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos, LANSEIDI-FarBiotec-CONACyT CDMX, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), CDMX, México. [4]GlobalBio, Inc., Cambridge, MA, USA.
alfonso.cervantes@udibi.com.mx

Tumor Necrosis Factor-alpha (TNF-α) is a pro-inflammatory cytokine involved in the dysregulation of TNF causing numerous pathologies, including rheumatoid arthritis, psoriatic arthritis, severe plaque psoriasis, juvenile idiopathic arthritis, ankylosing spondylitis, Crohn´s Disease and ulcerative colitis. Diverse biological treatments with the capacity to neutralize TNF-α have been developed and approved, being therapeutic antibodies one of the most successful. We previously isolated an anti-TNF-α antibody called IgG1-B11 from ALTHEA Gold Libraries™ (MAbs. 11(3): 27, 2019) that displayed ideal characteristics to be considered as the lead for development of anti-TNF-α antibody-based drugs. Here, we evaluated their biological activity through binding to TNF-α, competition with adalimumab and infliximab, blockade of TNF-a binding to receptors (TNFR1 & TNFR2) and its neutralizing activity in L929 cells. IgG1-B11 is able to compete for the TNF-α binding site with the FDA-cleared drug adalimumab but not infliximab, suggesting that it may share some binding sites with adalimumab. Additionally, it has shown the ability to block the binding of TNFR1, the latter mainly involved in the response to inflammatory processes, so it will be a candidate with great therapeutic potential for treatment of pathologies such as arthritis, a disease that is on the rise in our country.

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Resumen corto

Revealing the mechanisms involved in the cellular uptake and activation by GK-1 peptide

Cervantes-Torres, J. [1,2†], Hernández-Aceves, J.A. [1†], Ramírez, G. [1], Gajón, J.[3], Vazquez, R. [4], Moctezuma, D. [1], Bonifaz, L. [3], Sciutto, E. [1], Fragoso, G. [1*]

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, México City, México. [2]Departamento de Microbiología e Inmunología, Facultad de Medicina, Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, México City, México. [3]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, CMN Siglo XXI, Instituto Mexicano del Seguro Social; Mexico City, Mexico [4]Departamento de Biología Molecular y Biotecnología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, México City, México.
*gladis@unam.com.mx [†]These authors contributed equally to this study.

The bio-distribution and cell interaction of immunomodulatory molecules are crucial to understand and to design the most powerful strategy to potentiate their functions. Compelling evidence obtained in our research group has demonstrated that the immunomodulatory peptide GK-1 delays the growth of the breast tumor and substantially reduces its metastatic capacity with an effective reversion of the intratumoral immunosuppression. This study was designed to identify mechanisms that underlie these effects. Fluorescent labeled GK-1 (GK-1-HF488) added to culture dendritic cells showed that GK-1 was inside dendritic cells as soon as 15 min after contact. It is taken up in a dose dependent manner, more efficiently at 37°C than at 4°C, indicating that the uptake occurred via an energy independent pathway, but also by energy dependent processes through a clathrin-mediated endocytosis. Theoretical and experimental evidence using HEK-293-TLR4 cells show that GK-1 can activate the TLR4-dependent pathway interacting with the same LPS-binding site.

Overall, herein it is demonstrated that GK-1 can enter to the cells by a passive diffusion and activate the transmembrane Toll like receptor 4, mechanisms that can be involved in distinct intracellular functions, that are presently being explored.

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Resumen corto

Role of sialomucin CD43 in the expression of GLUT-1

Chipres-Naranjo, L.E. *[1], Flores-Alcantar, A. [1], Melchy-Perez, E. [1], Sotomayor-Vivas, C. [1,2] Rodríguez-Jorge, O. [3], Rosenstein, Y. [1]

[1]Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México, [2]Licenciatura en Ciencias Genómicas, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México, [3] Centro de Investigación en Dinámica celular, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México. Luis.chipres@ibt.unam.mx

The sialomucin CD43 is a transmembrane protein abundantly expressed in T cells. It has been implicated in regulating T-cell homing and activation. We hypothesized that, because of its long and rigid structure, CD43 could be one of the first molecules to provide the cell with information about the environmental cues necessary for the complete activation of T cells. Specifically, we asked whether CD43 participates in the metabolic adaptation that T cells undergo during the activation process, where they depend on aerobic glycolysis to produce ATP and metabolic intermediates. We evaluated GLUT-1 dynamics in Jurkat cells activated by TCR/CD43 by measuring GLUT-1 expression level by flow cytometry, the localization of the protein by immunofluorescence, and the amount of mRNA by qPCR. We found that GLUT-1 levels do not differ in terms of total protein levels, but that cellular localization could vary during different activation times. To further understand the potential mechanisms regulating the cellular localization of GLUT-1, data from public RNA-seq databases evaluating the participation of vesicular will be discussed.

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Resumen corto

Global 5mC-RNA disruption reduces the vectorial competence to DENV2 of heat wave-exposed *Aedes aegypti*

Claudio-Piedras, F. [1]*, Recio-Tótoro, B. [1,2,] Vargas, V. [1,3],
Lanz-Mendoza, H. [1], Cime-Castillo, J. [1]*

[1] National Institute of Public Health, Center for Research on Infectious Diseases, Cuernavaca, Mexico. [2] Biotechnology Institute, National Autonomous University of Mexico, Cuernavaca, Mexico.[3] Institute of Biomedical Research, Department of Immunology, National Autonomous University of Mexico, Mexico City, Mexico.
fabiola.claudio@insp.edu.mx

Heat waves are an increasingly frequent environmental event associated with climate change. Abnormally high heat wave temperatures can affect several ectotherm vector traits that are determinants of pathogen transmission. The potential increase in vector competence of *Aedes aegypti* for DENV2 during climate change and how mosquitoes might acclimate to the high temperatures of heat waves are crucial questions for global public health. Here, the hypothesis that RNA methylation in mosquitoes participates in the acclimatization to heat waves, and how it influences vector competence to DENV2 is explored. Heat wave-treated and DENV-infected mosquitoes presented lower survivorship, and lower antiviral transcriptional response without modifications in the infection prevalence for DENV2. In contrast, inhibition of RNA methylation in heat wave-treated mosquitoes increases survivorship and the antiviral transcriptional response, while reducing the infection prevalence from 78% to 37%. These results indicate that the RNA methylation background in mosquitoes favors vector competence for DENV2 during a heat wave exposure, and points towards possible interventions to counter measure the effect of climate change in DENV transmission. This work was made possible thanks to a grant awarded by the Consejo Nacional de Ciencia y Tecnología (CONACyT) to FC-P, who is a postdoctoral researcher at the National Institute of Public Health.

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Resumen corto

Overexpression of CCR6 in pediatric medulloblastoma tumors via of the hypoxia inducible factor 1 (HIF-1)

Cocoletzi-Bautista, J.E. *[1], Anaya-Estrada, D. [1], Rodríguez-Hernández, A.P. [1], Cabrera-Muñoz, M.L. [2], Eguía-Aguilar, P. [3], Cid-Sánchez, D.R. [1], Hernández-Cueto, D. [1], Luria-Perez, R. [1] y Baay-Guzmán, G.J. [1]

[1]Unidad de Investigación en Enfermedades Oncológicas, Hospital Infantil de México Federico Gómez., Ciudad de México, México. [2]Servicio de Patología Clínica y Experimental, Hospital Infantil de México Federico Gómez., Ciudad de México, México. [3]Laboratorio de Biología Moleular, Servicio de Patología Clínica y Experimental, Hospital Infantil de México Federico Gómez., Ciudad de México, México. E-mail: jonathan.cocoletzi.ba@gmail.com

Central Nervous System (CNS) tumors are the second cause of childhood cancer in Mexico, and medulloblastoma (MB) is the most common among them. Despite the efforts to understand the mechanism involved in this disease, many questions remain unsolved, such as the role of the chemokines and their receptors. In this context, the dual role of pro-inflammatory or immunosuppressor of the receptor CCR6 and their ligand CCL20 in tumorigenesis has been documented. However, their role in the MB remains unknown. Several studies have documented that CCL20 is regulated by the hypoxia-inducible factor 1 (HIF-1), a transcription factor associated with a bad tumoral prognosis. In this study, we evaluate the expression of CCR6 and HIF-1α in pediatric biopsies of MB and their possible transcriptional regulation. For that purpose, we construct a tissue microarray (TMA) with 60 pediatric tumors with MB to analyze the expression of CCR6 and HIF-1α by immunohistochemistry staining. Indeed, the transcription regulation of the CCR6 promoter by HIF-1α was analyzed by luciferase reporter plasmid. Our results showed overexpression of CCR6 and HIF-1α in the MB tissues, and the binding of the HIF-1 to the putative binding sites in the CCR6 promoter was documented. These data suggest that the transcription factor HIF-1 can regulate CCR6 and that both participate in the pathogeny of pediatric MB.

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Resumen corto

Effect of short-chain fatty acid administration on the efficacy of monovalent Rotavirus vaccine in a murine model

Colliard-Flores, C.P. [1], Esquivel-Guadarrama, F.R. [2], López-Guerrero, D.V. [3]

[1] Instituto de Investigación en Ciencias Básicas y Aplicadas, UAEM, Cuernavaca, Morelos, México. [2]Facultad de Medicina, UAEM, Cuernavaca, Morelos, México. [3] Facultad de Nutrición, UAEM, Cuernavaca, Morelos, México.
Correo: vannylpzgro@gmail.com

Rotavirus (RV) is the main cause of gastroenteritis in children, and although there are two vaccines to prevent the disease, their efficacy is variable. Short-chain fatty acids (SCFAs), produced by the fermentation of dietary fiber in the gut, are immunomodulators with beneficial effects on the immune system, especially in mucosa. We propose that administering SCFAs before and during vaccination can improve the protective immune response induced, although their involvement in both infection resolution and acquired immunity generation through vaccination is unknown.

Evaluation of the protection induced by the monovalent vaccine (Rotarix) in mice supplemented with SCFAs before and during vaccination and challenged with murine rotavirus (EDIM).

BALB/c mice were supplemented with SCFAs for 9 days prior to and 3 weeks after vaccination with Rotarix. They were challenged with RV EDIM 21 days post-vaccination, and the viral load, presence of RV-specific intestinal IgA in feces, and IgG antibodies in the serum of vaccinated mice before and 21 days after challenge were measured by ELISA.

An increase in the production of RV-specific IgA and a decrease in the viral load excreted in the feces were observed in mice vaccinated and supplemented with SCFAs. There was also an increase in total serum IgG 21 days post-infection, despite it being an oral, non-systemic vaccine.

These results demonstrate that the antibodies produced are protective by increasing the production of RV-specific IgA and reducing the viral load in mice supplemented with SCFAs and vaccinated against rotavirus.

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Resumen corto

Characterization of the function of TIF1γ in the control of T regulatory cells

Contreras-Castillo, E. [1], Zambrano-Romero, J.D. [1],
Ramos-Balderas, J.L. [1] y Licona-Limón, P. [1]

[1]Instituto de Fisología Celular, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.

TGF-β can regulate T cell differentiation and effector phenotypes. In particular, it can induce the differentiation and function of regulatory T cells (Tregs) in vitro and in vivo. TGF-β signaling depends on phosphorylation of Smad2 and Smad3, which interact with the common Smad: Smad4. This Smad2/3/4 complex was considered the main signal transduction element in the pathway. However, the transcriptional intermediary factor 1 γ (TIF1γ) was recently shown to interact with Smad2/3, leading to a distinctive gene expression profile and cell fate. The objective of this work is to elucidate the role of TIF1γ in the differentiation, cell function, and stability of Tregs. Using different conditional mouse models we demonstrated that under homeostatic conditions, TIF1γ is dispensable for Treg generation. However, it is required for the maintenance of suppressive functions and stability under inflammatory conditions, both in vivo and in vitro models. We also identified the molecular mechanism by which TIF1γ regulates Treg function, modulates the expression of different suppressive markers, and maintains Foxp3 expression under inflammatory conditions. In conclusion, TIF1γ is required for proper differentiation Treg lymphocytes and their acquisition of a suppressor phenotype.

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Resumen corto

Standardization of an experimental murine model for two anti-VEGF antibodies evaluation in diabetic retinopathy

Contreras-Zetina, J.C. *[1], López-Sánchez, P. [1], Pérez-Cano, H.J. [2], Somilleda-Ventura, S.A. [3]

[1]Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, CDMX, México. [2]Facultad de Química, Universidad Nacional Autónoma de México, CDMX, México. [3]Centro de Investigación Biomédica, Fundación Hospital Nuestra Señora de la Luz I.A.P., CDMX, México. jcontrerasz1400@alumno.ipn.mx

Diabetic retinopathy (DR) is a leading cause of sight-loss among the working age population, and it is expected to affect over 190 million patients by 2030. The objective of this study is to characterize a diabetic retinopathy murine model and determine whether it is useful for the evaluation of anti-VEGF antibodies and the pathways involved in their effectiveness. A total of 18 male Wistar rats were divided into six groups (n=3 per group): non-diabetic, non-diabetic + aflibercept and non-diabetic + ranibizumab; diabetic, diabetic + aflibercept, diabetic + ranibizumab. Diabetes was induced by single intraperitoneal doses of streptozotocin (STZ) (65 mg/kg). Non-diabetic rats were administered vehicle alone. Treatment groups received 2 µl of 40 mg/ml aflibercept or 2 µl of 10 mg/ml ranibizumab intravitreally at the eleventh day of the experiment. Thirty days after antibody administration, indirect ophthalmoscopy was performed. Food intake, water intake and diuresis were measure with metabolic cages. Statistical significance was determined with ANOVA followed by Tukey's test; P values <0.05 were considered significant. We found significant difference (P <0.0001) in glycemia levels, food intake, water intake and diuresis between diabetic and non-diabetic rats. Moreover, diabetic rats displayed clinical signs of diabetic retinopathy, namely microaneurysms, hard exudates and hemorrhages. Additionally, groups treated with anti-VEGF antibodies showed diminished clinical severity when compared with non-treated groups.

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Resumen corto

IL-18 as a potential biomarker of the highly frequent hepatitis E virus in blood donors

Copado-Villagrana, E.D. [1], Pizuorno, A. [2], García-Suárez, A. [3], Abarca-Magaña, J.C. [3], Mazas, C. [3], Du Pont, G. [3], Fierro, N.A. [3]

[1]Hospital General de Zona No.2, Instituto Mexicano del Seguro Social, Nogales, México. [2]Health Science Center, The University of Texas, Houston, USA. [3]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad Universitaria, CDMX, México.

Efforts in HEV research have driven to the implementation of HEV screening in human blood in diverse developed countries; however, studies in middle and low-income regions are still limited. Furthermore, no specific biomarkers of exposure to this virus have yet identified. Mexico´s situation is unique, with the circulation of three different HEV strains. However, HEV is not routinely screened in blood banks, and biochemical markers for liver disease are not tested in blood banks in the country.

This cross-sectional, single-center study included 691 serum samples of blood donors obtained in 2019. Anti-HEV IgG and IgM immunoglobulins were detected in sera; the viral genome was screened in samples. A statistical comparison of risk factors for infection, demographic and clinical features was performed; IL-18 and IFN-γ values were tested in sera.

Of the 691 samples, 9.4% were positive for anti-HEV antibodies and viral RNA detection was confirmed in one of the pools positive for anti-HEV. From the analysis of risk factors, age and having pets were statistically significant for anti-HEV antibodies detection. In addition, seropositive samples showed significantly higher IL-18 concentrations relative to samples from seronegative donors. Interestingly, IL-18 values were similar when HEV seropositive samples were compared to samples from clinically acute previously confirmed HEV patients.

Our findings alert the need to follow up on HEV in blood banks in Mexico and underscore that IL-18 could represent a biomarker of HEV exposure.

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Resumen corto

Comparative study of inflammatory markers expression in cutaneous tuberculosis and mycetoma by immunohistochemistry in human skin biopsies

Coronado-Rodríguez, F. [1*], Mejía-Torres, M. [1],
Salinas-Carmona, M.C. [1]

[1]Departamento de inmunología, Hospital Universitario "Dr. José Eleuterio González", Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México.
fernanda.cr@live.com.mx

The differential diagnoses in chronic dermatoses that present with granulomatous inflammation are complex. Tuberculosis and mycetoma are both infectuous diseases, caused by intracellular pathogenic bacteria, and they are among the most frequent nosological diseases associated with dermatoses. The clinical consequences associated with each of the infections previously mentioned and their specific treatments are different, thus a correct and early diagnosis is necessary. Particularly in infections by actinomycetes, the severity of the tissue´s destruction and the scarce therapeutic repertoire require early identification of the infectious agent. Usually, both infections require the use of invasive methods such as biopsy for their study and histopathological interpretation. From the immunological point of view, it is necessary to understand the inflammatory mechanisms that make these infections two different entities. In the present paper a comparative analysis of the expression of IL-6, TGF-β, VEGF and eNOS proteins was performed by immunohistochemistry in skin biopsies obtained from patients with a definitive diagnosis of cutaneous tuberculosis or mycetoma. The primary objective was to evaluate the presence of a differential and specific patterns of inflammatory markers for each infection. The secondary objective was to evaluate the tissue distribution of the evaluated marks and their spatial association with inflammation with granulomatous characteristics. The results indicate that the expression pattern of the evaluated marks is specific for each type of infection evaluated. On the other hand, the tissue distribution of the marks is either extensive or localized, providing information about the inflammatory process as something focused on a specific location.

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Resumen corto

Antibodies directed against epitopes in the receptor binding domain of SARS-CoV-2 can bind to multiple variants of concern in protein-protein docking assays

Corona-Guerrero, I. *, Mosqueda, J.

[1]Laboratorio de Investigación en Inmunología y Vacunas, Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Querétaro, Qro. México. ivan.corona@uaq.mx

After the initial outbreak at the end of 2019, WHO declared the coronavirus disease 2019 (COVID-19) as a global scale pandemic in March 2020. This pandemic has caused more than 6 million deaths worldwide as well as severe economic loss and mental health issues at a global scale.

The causative agent of COVID-19 is the SARS-CoV-2, a betacoronavirus with a single-stranded, positively oriented RNA genome. The SARS-CoV-2 genome characteristics and the lack of a proofreading viral RNA-polymerase enable the rapid mutation of the virus and, thus, the developing of novel variants.

The SARS-CoV-2 variants of concern (VOC) have developed various immune evasion mechanisms, including mutations on the Spike (S) protein. These mutations have risen concern about the effectivity of vaccines against new variants of concern.

In this work, protein-protein molecular docking assays were carried out to test the affinity of anti-Receptor Binding Domain (RBD) monoclonal antibodies with RBDs of different VOCs.

The results of the docking assays indicated a high binding affinity between each antibody and the original antigen compared to the RBD of different VOC. We observed high binding energies to the delta VOC with antibodies neutralizing the Wuhan (-175.4 J/mole), alfa and beta, (-301.2, -341, and -417.5 J/mole) and delta VOCs (-622 J/mole). Although binding energy it's not the same, these antibodies recognize antigenic peptides of the RBD and can be considered as neutralizing antibodies. These results indicate a favorable landscape for recombinant and chimeric vaccines against SARS-CoV-2 based on the S-protein RBD. Founded by: AMECXID-SRE and UAQ.

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Resumen corto

Thymic Atrophy in *Plasmodium berghei ANKA* and *Plasmodium yoelii 17XL* Infection

Corral-Ruiz, G.M. [a,b*], Pérez-Vega, M.J. [a,b], Galán-Salinas, A. [a,b], Mancilla-Herrera, I. [c], Barrios-Payán, J. [d], Fabila-Castillo, L. [a], Hernández-Pando, R. [d], Sánchez-Torres, L.E. [a,]

[a] Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico. [b] Posgrado en Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico. [c] Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología, Mexico City, Mexico. [d] Sección de Patología Experimental, Departamento de Patología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Mexico City, Mexico.
gcorral@outlook.com

The thymus is a primary lymphoid organ that supports a highly coordinated and regulated sequence of events that allow the selection, proliferation, and maturation of T cells. However, the immunological functions of the thymus can be compromised upon exposure to different infections, affecting thymocyte populations. This work was focused on characterizing and contrasting the events related to thymic atrophy in different immunological scenarios by comparing two distinct lethal malaria infections in C57BL/6 mice that represent the most severe complications, cerebral malaria (*P. berghei ANKA*), and anemia (*P. yoelii 17XL*). Our results showed that in both models, infected mice die on the same day but with different parasitemia and clinical score and that the development of thymic atrophy unfolds at a different time during infection. In both cases, we found a reduction in thymic weight and cellularity involving different thymocyte stages, mainly $CD4^+CD8^+$ thymocytes, as well as an increased presence of apoptotic cells, leading to thymic anatomical architecture disorganization and cortex reduction. Thymus atrophy showed no association with the elevated serum cytokines levels detected in both malaria models (IFN-γ, TNF-α, IL-6, CXCL9, CXCL10, CCL2, and CCL4), but it did with those of corticosterone. In these malaria models, thymic atrophy is due to the specific host-parasite interaction, and it seems to be related to a corticosterone-induced effect derived from the activation of the hypothalamic-pituitary-adrenal axis, but it is not related to the parasitemia level.

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Resumen corto

CCR3 and CCR10 receptors as targets for the modulation of neutrophil activation

Correa-Becerril, D.A. [1], Juarez-Macias, B. [1], Cabellos-Avelar, T. [1], Torres-Ruiz, J. [2,3], Sosa-Hernandez, V.A. [4], Cervantes-Diaz, R. [4], Perez-Fragoso, A. [2], Romero-Ramirez, S. [4], Gomez-Martin, D. [2], Maravillas-Montero, J.L. [4], Raffatellu, M. [5], and Perez-Lopez, A. [1].

[1] UBIMED, Facultad de Estudios Superiores Iztacala, UNAM. [2] Department of Immunology and Rheumatology, Instituto Nacional de Ciencias Medicas y Nutricion Salvador Zubiran. [3] Emergency Medicine Department, Instituto Nacional de Ciencias Medicas y Nutricion Salvador Zubiran. [4] Red de Apoyo a la Investigacion, Universidad Nacional Autonoma de Mexico and Instituto Nacional de Ciencias Medicas y Nutricion Salvador Zubiran. [5] Division of Host-Microbe Systems & Therapeutics, Department of Pediatrics, University of California San Diego.

Neutrophils represent one of the host's first lines of defense against invading pathogens, however, aberrant activation causes host damage. Aberrant neutrophil activation plays a central role during severe COVID-19. Therefore, modulation of effector functions or neutrophil migration constitutes an opportunity for pharmacological intervention. We aimed to determine if the blockade of CCR3 and CCR10 receptors using specific antagonists modulates the activation of neutrophils. First, we determined the expression of CCR3 and CCR10 in neutrophils from COVID-19 patients. Peripheral blood neutrophils from critically ill patients with COVID-19 express CCR3 and CCR10; which correlates with clinical parameters of severe disease such as inflammation and procoagulant state. Then, we evaluated the ability of CCR3 and CCR10 antagonists to reduce neutrophil activation by measuring the formation of NETs *in vitro*. Our result indicated that blocking CCR3, but not CCR10, reduces the production of NETs. Thus, we determined whether the administration of CCR3 antagonist, SB328437, could modulate neutrophil recruitment *in vivo*, using the LPS-induced acute respiratory distress syndrome model in C57/BL6 mice. We found a reduction of total cells in BALF and neutrophil presence in mice treated with SB328437 in comparison with the mock treated group. All these data together showed that CCR3 and CCR10 receptors are expressed on the surface of neutrophils isolated from patients with COVID-19 and their activation correlates with disease severity. However, only CCR3 blockade reverses the effect of CCL28 on NET formation and reduces neutrophil recruitment to the lung in the LPS-induced distress model.

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Resumen corto

Protective role of SARS-CoV-2-neutralizing antibodies against the development of severe COVID-19. Retrospective cohort study

Cortés-Vieyra, R. *[1], Martínez-Sepúlveda, J.D. [2], Perez-Duran, F. [1], Calderón-Rico, F. [1], Ortega-Flores, R. [1], Gutierrez-Castellanos, S. [3], Nuñez-Anita, R.E. [1]

[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Michoacana de San Nicolás de Hidalgo, Morelia, Michoacán, México. [2]Programa Institucional de Licenciatura en Biotecnología, Universidad Michoacana de San Nicolás de Hidalgo, Morelia, Michoacán, México. [3]Centro de Investigación Biomédica de Michoacán, División de Investigación Clínica, Instituto Mexicano del Seguro Social (IMSS), Morelia, Michoacán, México.

ricarda.cortes@umich.mx ; qfbrena@hotmail.com

Most people with SARS-CoV-2 infection produce neutralizing Ab (NAb) whose main function is the binding to the receptor binding-domain (RBD) of the S protein, in order to avoid infection. However, there is still controversy about the protective role of NAb generated by SARS-CoV-2 infection against the development of severe COVID-19. On the other hand, it has been reported that high levels of NAb within the first weeks after vaccination against COVID-19 correlate well with the efficacy of the vaccines. Nevertheless, the decay of the NAb titer months after vaccination predicts that a significant loss in protection against SARS-CoV-2 infection will occur. The objective of this study was to determine the protective role of NAb in the development of severe COVID-19 in vaccinated (after months) and unvaccinated subjects. The cohorts of patients included pre-pandemic subjects (n=16) and three groups of SARS-CoV-2 positive patients with COVID-19 moderate (n=16; 100% vaccinated), severe (n=13; 69.2% not vaccinated) and with death outcome (n=16; 75% not vaccinated). Serum samples from SARS-CoV-2 patients were obtained during the winter of 2021-2022 from HGZ-83-IMSS, Michoacán. We observed through a surrogate neutralization assay that severe patients showed a higher percentage of inhibition of RBD-ACE2 (converting enzyme 2) interaction compared to patients with moderate COVID-19 ($p>0.0001$). While the patients with death presented a lower percentage compared to severe COVID-19 patients ($p=0.0289$). In conclusion, NAb were not the primary correlate of protection during infection, months after vaccination, whereas NAb produced solely by infection protected patients with severe disease against fatal disease outcome. Funding: CONACyT A1-S-43236; INFR: 2015-255010; Fomento a la infraestructura científica 2021-317189. Scholarship C-VR: EPM 2022(2) CONACYT.

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Resumen corto

Integrative Bioinformatics Meta-Analysis of Gene Expression Profiles in Depression Patients: Unraveling Molecular Mechanisms and Novel Therapeutic Targets

Covarrubias-Martínez, E. [1], Rojas-Gutiérrez, S.E. [1], Elizondo-Solis, C.V. [1], Macías-Segura, N. [1]

[1]Laboratorio de Inmunología de Sistemas, Departamento y Servicio de Inmunología, Facultad de Medicina y Hospital Universitario, Universidad Autónoma de Nuevo León.

Major depressive disorder (MDD) is a highly prevalent psychiatric condition with complex etiology and heterogeneous clinical manifestations. Despite advances in the understanding of MDD, the molecular mechanisms underpinning the disorder remain largely elusive. In this study, we performed a comprehensive meta-analysis of gene expression profiles in depression patients to elucidate the molecular pathways involved in the pathogenesis and identify potential therapeutic targets. We systematically reviewed and integrated publicly available transcriptomic datasets from peripheral blood, utilizing rigorous inclusion criteria to ensure data quality and consistency. Differentially expressed genes (DEGs) between depression patients and healthy controls were identified using robust statistical methods. Functional enrichment analysis was carried out to elucidate the biological pathways and molecular functions associated with these DEGs. The meta-analysis revealed 100 significant down-regulated genes in patients with MDD, whereas we identify 3 up-regulated genes in MDD, both compared with MOOD patients and healthy subjects. The String interaction analysis identified across multiple independent studies, highlighting alterations in neuroplasticity, inflammation, neurotransmission, and stress response pathways. Notably, several novel candidate genes that can be used as molecular markers associated with MDD and potential therapeutic targets emerged from this integrative analysis. Also, our work contributes to a deeper understanding of the molecular landscape of depression and may pave the way for the development of novel, targeted treatments, and molecular markers for early diagnosis for MDD.

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Resumen corto

Kaempferol effect on MPO and ROS release in *E. histolytica* and hamster neutrophils interaction

Cruz-Baquero, C.A. *[1], Levaro-Loquio, D.[2], Santos-Ruiz, P.A. [1], Pérez-Vielma, N.M. [3], Arciniega- Martínez, I.M. [4], Reséndiz-Albor, A.A. [4], Pacheco-Yépez, J. [2]

[1] Programa Bacteriología y laboratorio clínico, Facultad de Ciencias de la Salud, Universidad Colegio Mayor de Cundinamarca, Bogotá, Colombia. [2] Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, México.[3] Sección de Estudios de Posgrado e Investigación, Centro Interdisciplinario de Ciencias de la Salud CICS, Santo Tomás, Instituto Politécnico Nacional, Ciudad de México, México.[4] Laboratorio de Inmunidad de Mucosas, Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, México. candreacruz@unicolmayor.edu.co

Entamoeba histolytica (E. histolytica) is the protozoan parasite that causes amoebiasis. The most used drug against the amoeba is metronidazole, but other compounds, such as the flavonoid kaempferol, have been reported to damage E. histolytica trophozoites. It is known that the first cells of the immune system to interact with trophozoites are neutrophils, however these cells in susceptible models do not attack amoebae. Neutrophil´s myelopexidase (MPO) is a cationic enzyme that in vitro damage amoebae through the action of hypochlorous acid (HClO). Currently, the effect of kaempferol on MPO and reactive oxygen species (ROS) production as neutrophil damage mechanisms in amoeba and neutrophils interaction has not been evaluated. Therefore, in the present work, the viability, MPO activity and ROS production in hamster neutrophil interactions with trophozoites in presence of kaempferol was analyzed. Our results show that kaempferol significantly diminish the amoeba viability vs the metronidazole and control without treatment also kaempferol diminish the MPO activity and reduce ROS production in hamster neutrophil and trophozoites interactions. Kaempferol has antioxidant activity controlling MPO activity and ROS secretion by hamster neutrophils in trophozoites and neutrophil interaction. The antioxidant activity of the flavonoid kaempferol reduces oxidative stress, which could generate in vivo in the amoebic liver abscess in a susceptible hamster model a lower damage on host cells.

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Resumen corto

Neutrophil FcγRIIIB and FcγRII are regulated between neonatal and adult age: links to superoxide production and phagocytic activity.

Cruz-Cardenas, J.A. [1], López Arredondo, A. [1], Brunck, M.E.G. [1,2]

[1]Escuela de Ingeniería y Ciencias, Tecnológico de Monterrey, Nuevo León, México.
[2]The Institute for Obesity Research, Tecnológico de Monterrey, Nuevo León, México.
*E-mail: a00829644@tec.mx

Neutrophils are the most abundant immune cells in human peripheral blood, and the first line of cellular defense against infections. While immune functions decline with increasing age, neonates are also immunologically immature, suggesting variations between adult and neonatal neutrophils. Fcγ receptors on neutrophil surfaces bind IgG-bound immune complexes which rapidly triggers phagocytosis and reactive oxygen species (ROS) production. Here, we collected umbilical cord blood and adult peripheral blood, enriched neutrophils using a density gradient, and applied a 4-colour + viability marker flow cytometry panel to evaluate CD16b and CD32 relative expression. We simultaneously measured pHrodo *E. coli* BioParticles phagocytosis, and ROS production using flow cytometric assays on these samples. Results evidenced a variable expression of CD11b, CD15, CD16b, and CD32 surface markers between adult and neonatal neutrophils. In addition, phagocytosis capacity was decreased in neonatal neutrophils. Further experiments are ongoing to correlate Fcγ receptor expression and antimicrobial activity in human neonatal and adult neutrophils..

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Resumen corto

Identification of OGT/OGA enzymes in extracellular vesicles from SCC-152 cell cultures

Cruz-Cruz, M. [1,2*], Jiménez-Castillo, V. [1,2,3], Illescas-Barbosa, D. [2], Solórzano-Mata, C.J. [2,3], Martínez-Cruz, M. [1], Pérez-Campos, E. [1] Pérez-Santiago, A. [1]

[1]National Technology of Mexico/IT.Oaxaca, Oaxaca, Mexico. [2]Faculty of Medicine and Surgery, Universidad Autónoma Benito Juárez de Oaxaca, Oaxaca, Mexico. [3]Faculty of Dentistry, Universidad Autónoma Benito Juárez de Oaxaca, Oaxaca, Mexico. *E-mail: cucm93@gmail.com

Oral squamous cell carcinoma (OSCC) is a malignant neoplasm of epithelial origin that is characterized by its high degree of aggressiveness and poor prognosis. Intercellular communication through extracellular vesicles (EVs) has been reported in the progression and metastasis of different cancers. On the other hand, glycosylation is the enzymatic process by which carbohydrates are added to proteins or lipids, the glycosylation pattern can be modified in various physiological or pathological situations. O-GlcNAcylation is a post-translational modification that is carried out through the OGT and OGA enzymes. O-GlcNAcylation has been shown to be modified in OSCC tissues. Our objective was to identify the presence of OGT/OGA enzymes in VE of culture supernatant of SSC-152 cells. VE extraction was performed by size exclusion chromatography. The expression of the OGT and OGA enzymes was measured by immunocytochemistry and western blot. The enzymes are expressed in the nucleus and cytoplasm, they are present in the content of the EVs with highly significant differences (p=0.006). Our results show that EVs carry information to transform and modify the content of other cells and promote O-GlcNacylation.

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Resumen corto

Pentoxifylline and Stattic enhance cytotoxic action of Docetaxel in DU145 cells of metastatic prostate cancer: Involvement of NF-κB and STAT3 pathways

Cruz-Lozano, J.R. [1,2]*, Ortiz-Lazareno, P.C. [1,2], Vázquez-Ibarra, K.C. [2], Ortiz-Tamayo, B.G.[2], Palafox-Mariscal, L.A. [1,2], Villaseñor-García, M.M. [1,2], Bravo-Cuellar, A. [1,2]

[1]División de Inmunología, Centro de Investigación Biomédica de Occidente (CIBO), Instituto Mexicano del Seguro Social (IMSS), Guadalajara, Jalisco, México. [2]Programa de Doctorado en Ciencias Biomédicas Orientación Inmunología, Centro Universitario de Ciencias de la Salud (CUCS), Universidad de Guadalajara, Guadalajara, Jalisco, México.
*E-mail: jroberto.cruz@alumnos.udg.mx

In Mexico, Prostate cancer (PCa) is the most common type of cancer found in males and is also the leading cause of death from cancer in this population. As reported in other malignancies, the transcription factors STAT3 and NF-κB show aberrant activation contributing to oncogenesis and immunosuppression and mediate a chemoresistance phenotype towards Docetaxel (Dtx), the drug of choice in patients with advanced PCa. Therefore, there is interest in investigating whether simultaneous blockade of the pathways with Stattic (Stt) and Pentoxifylline (Ptx) could help to increase apoptosis by themselves or in combination with Dtx. Here we evaluated the effects of the drugs alone or their combination at different doses and times in PCa DU145 cells. Subsequently, the induction of apoptosis and the activation of caspases that carry out this mechanism were assessed by flow cytometry; the role of mitochondria in this process was determined by evaluating the loss of their membrane potential (ΔΨm) by spectrophotometry. We also investigated affectation in proliferation, which was measured using bromodeoxyuridine incorporation. Flow cytometry was also used to assess cell cycle modifications by the treatments. We found that Ptx+Stt sensitizes DU145 cells to Dtx cytotoxicity. These observations are related to a substantial loss of ΔΨm and increased activation of caspase -9, which suggests that the intrinsic pathway of apoptosis is favored. As well this combination of drugs has antiproliferative effects and causes cell arrest at the G1 phase. Our findings demonstrate the potential of STAT3 and NF-kB pathways as therapeutic targets in metastatic prostate cancer.

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Resumen corto

Evaluation of secretory IgA levels in the mucosa, at different stages and regions of the gastrointestinal tract

Cuevas González, D.S.C. [1]*, Pérez Ramírez, I.F. [1], Rodríguez Torres, A. [2], García Gutiérrez, D.G. [1], Lira de León, K.I. [1], Nava Morales, G.M. [3], Bertadillo Jilote, A.D. [1]

[1]Departamento de Química Clínica y Diagnóstico Molecular, Universidad Autónoma de Querétaro, Santiago de Querétaro, Querétaro, México. [2]Laboratorio de Neurobiología Molecular, Universidad Autónoma de Querétaro, Santiago de Querétaro, Querétaro, México. [3]Laboratorio de Microbiología Molecular, Universidad Autónoma de Querétaro, Santiago de Querétaro, Querétaro, México.
*E-mail: sofia.cuevasg@hotmail.com

IgA is an immunoglobulin secreted in mucous membranes that neutralizes pathogens and balances the body's microbiota. Alterations in structure and concentration of secretory IgA are related to gastrointestinal disorders, so evaluating IgA supports the diagnosis of these conditions. *Gallus gallus* present similarities with the human immune system, avoiding the difficult collection of intestinal samples and providing approximations to know secretory IgA levels. In this work we are going to quantify secretory IgA in different stages of *G. gallus* intestinal mucosa, improving the separation of proteins to evaluate the potential diagnostic by ELISA´s method. Intestinal *G. gallus* tracts were obtained on days 7, 14 and 30 of development. The mucosa was sectioned and collected, generating pools. Centrifugation of total proteins were evaluated and quantified by Bradford´s method. Finally, secretory IgA will be measured with a commercial ELISA. In preliminary results we optimized the separation and quantification of total proteins, starting from: 0.02 g of sample, 20 min, 4°C, with and without protease inhibitor and at 3500, 5000 or 7000 rpm; obtaining similar concentrations. Samples without inhibitor degraded approximately 50% after a month of storage at -20°C. The highest amount of total proteins was obtained in the duodenum (13,021.48 µg/mL), followed by jejunum (10,277.04 µg/mL) and ileum (9836.29 µg/mL). With the use of protease inhibitor, we found a significant difference of protein concentration but not with different speed centrifugation. The concentration of total proteins in the duodenum > jejunum > ileum. I express my gratitude to CONACYT for the scholarship 1143728 and the synod committee for all the help.

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Resumen corto

Acute phase proteins in the evolution of SARS-Cov-2 infection

Damian-Morales, G. [1]*, López-Santiago, R. [1], Bonilla-Delgado, J. [2], Acosta-Altamirano, G.[2], Sierra-Martínez, M. [2], Cortés-Malagón, E.M. [3], Nieto-Velázquez, N.G. [3]

[1]Laboratorio de Inmunología Celular, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Unidad de Investigación, Hospital Regional de Alta Especialidad de Ixtapaluca, Ixtapaluca, México. [3]División de Investigación, Hospital Juárez de México, Ciudad de México, CDMX, México. *E-mail: goretinieto@gmail.com|

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the cause of coronavirus disease 2019 (COVID-19), has become a global health emergency. The virus infection keeps patient in a state of hyperinflammation that ultimately leads to multiple organ failure and later death. In this work, it has been proposed a panel to detect acute phase inflammatory biomarkers to prognosis clinical outcomes on patients infected by SARS-CoV-2. In this study, 62 samples from patients classified according to disease severity and 10 healthy donors were analyzed by flow cytometry. Patients who went to intensive care and those who died had high levels of IL-6 and IL-10 in serum. As well as C-reactive protein, procalcitonin, cortisol and VEGF compared with patients who had a mild disease. Markers of renal and cardiac failure were also detected in patients who died. The concentration of inflammatory markers is directly related to each other. These results suggest that acute phase inflammatory molecules detected in serum are potential biomarkers to decide the treatment that patients will receive. Therefore, the quantification of these proteins could be used as a routine test when patients' admission.

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Resumen corto

Effect of autophagy on the production of proinflammatory cytokines induced by S protein of the SARS-CoV-2

Dávalos-Zavala, J. [1]*, Baltierra-Uribe, S.L. [1], Vidales-Hurtado, M.A. [3], Martínez-Ortiz, M.J. [4], Sarmiento-Silva, R.E. [2], García-Pérez, B.E. [1]

[1]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Departamento de Microbiología e Inmunología, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Centro de Investigación en Ciencia Aplicada y Tecnología Avanzada, Instituto Politécnico Nacional, Santiago de Querétaro, Querétaro, México. [4]Departamento de Termodinámica del Equilibrio entre Fases, Escuela Superior de Ingeniería Química e Industrias Extractivas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México.
*E-mail: jdavalosz2100@alumno.ipn.mx

COVID-19 is a disease caused by the SARS-CoV-2 virus which is characterized by hyperinflammation denoted by the secretion of proinflammatory Cytokines. The role of autophagy as a negative regulator of the production of interleukins has recently been studied. In this work, the effect of autophagy in the production of IL-1β and IL-6 in epithelial cells and human macrophages stimulated with the S protein of the SARS-CoV-2 virus was studied. The cells were treated with nicotine to induce the expression of the ACE2 receptor, which was evidenced by immunofluorescence. Next, the cells were stimulated with the S1 subunit or the RBD domain of the S protein of the SARS-CoV-2 virus or a combination of these treatments with LPS. Autophagy activation was stimulated with rapamycin and inhibited with hydroxychloroquine. Interleukins production was assessed by ELISA and autophagy activation status by fluorescent labeling of autophagosomes. It was shown that nicotine turned out to be an inducer of ACE2 expression in both cells. IL-1β was produced only in macrophages, noting that S1 subunit or the RBD domain alone have an effect on the production of this interleukin but the combination with LPS potentiates it. By activating autophagy, IL-1B decreased considerably. For IL-6 the same trend was demonstrated in which the combination with LPS has a much more marked production effect than S1 or RBD alone. Autophagy activation reduced IL-6 production in macrophages and one of the two epithelial cell lines. Further study of autophagy is necessary to better understand its role in this model.

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Resumen corto

Effect of different methods of conservation on the human milk composition

Dávila Caraballo, G.J. [1], Serrato-Márquez, E. [1], Grimaldo-Rivas, M.D. [1], Garza-Villalobos, M. [2], Ortega-Alonzo, S.E. [3], Chuck-Hernández, C.E. [4], Vega Cantú, Y.I. [1], Urrutia-Baca, V.H. [4]*

[1]Escuela de Ingeniería y Ciencias, Tecnológico de Monterrey, Monterrey, NL, México. [2]Milk & Milk Mexico, Monterrey, NL, México. [3]Hospital Zambrano Hellion, TecSalud, Tecnológico de Monterrey, Monterrey, NL, México. [4]Institute for Obesity Research, Tecnológico de Monterrey, Monterrey, NL, Mexico. *E-mail: victor.urrutiaba@tec.mx

Human milk (HM) is the ideal food required by infants since it contains immunological factors and others, which provide health benefits. In Mexico, only 31% of children under six months of age receive exclusive breastfeeding which represents an important problem due to complications during delivery and health disease, this has allowed the generation of HM banks where conservation methods are applied, but, little is known about the effect on the constituents of HM. The aim was to evaluate the changes in the HM composition in function of three conservation methods: freezing at -20ºC and -80ºC and lyophilization. HM Pool was made from 15 donors following the ethical guidelines. HM pool was divided, one for each conservation method. Then, the quantification of Th1, Th2, and Th17 cytokines was performed by flow cytometry, secretory immunoglobulin A (sIgA) by enzyme-linked immunosorbent assay (ELISA) and quantification of seven human milk oligosaccharides (HMOs) by ultra-performance liquid chromatography coupled to mass spectrometry (UPLC-MS/MS). No statistical difference was observed in pH, density, humidity, cytokines (IL-2, IL-4, IL-6, IL-10, TNF, IFN- and IL-17A), HMOs (3-SL,6-SL, LNT, and LNnT) and total sIgA between the three preservation methods. In contrast, a lower concentration of total protein, free aminoacids, HMOS (3-FL, 2-FL, and LNFPI), and lactose was observed in freezing at -20ºC compared to freezing at -20ºC and lyophilization ($p<0.05$). Our results show that the MH components can be affected depending on the conservation methods. Therefore, we recommend comprehensively evaluating other emerging methods. Funding: Tecnológico de Monterrey I008-IOR001-C6-T1-E

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Resumen corto

Role of ARHGEF28 on NK cell effector functions

De la Cruz Rico, A.E. [1,2]*, Garcés-Alanís, M. [3], Vázquez-Prado, J. [4], Alarcón-Riquelme, M.E. [5], Madera-Salcedo, I.K. [1], Crispín, J.C. [1], Rosetti, F.[1]

[1]Departamento de Inmunología y Reumatología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, CDMX, México. [2]Plan de Estudios combinados en Medicina PECEM, Facultad de medicina, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Facultad de Ciencias Médicas y Biológicas "Dr. Ignacio Chávez", Universidad Michoacana de San Nicolás de Hidalgo, Morelia, Michoacán. [4]Departamento de Farmacología CINVESTAV-IPN, Ciudad de México, CDMX, México. [5]GENYO, Centro Pfizer-Universidad de Granada-Junta de Andalucía de Genómica e Investigación oncológica, Granada, España; Institute for Environmental Medicine, Karolinska Institute, Stockholm, Sweden. *E-mail: fanby13@gmail.com

Lupus nephritis (LN) is the most frequent severe manifestation in systemic lupus erythematosus (SLE). Deposition of immune complexes (IC) in glomeruli triggers inflammation through activation of complement and FcγRs. Interestingly, there is a subgroup of patients that present abundant IC deposition without associated inflammation (type V LN). It is unclear why these patients fail to develop a local inflammatory response. In order to identify potential biologically relevant molecules regulating the inflammation triggered by deposited IC, a genome-wide association study (GWAS) was performed comparing SLE patients with inflammatory vs. non-inflammatory nephritis. This analysis revealed a non-synonymous mutation in the *ARHGEF28* locus associated to type V nephritis. *ARHGEF28* encodes a guanine exchange factor, crucial for the regulation of integrin-dependent focal adhesion formation in fibroblasts. Interestingly, NK cells are the hematopoietic cells that express the higher amount of this protein and its role in these cells are not known. In this work, we evaluated the effects of the mutation in ARHGEF28 activation, as well as its role on NK cell functions that could be relevant for the pathogenesis of lupus nephritis. Using an NK cell line, YTS cells, we found that ARHGEF28 is important for migration and conjugate formation. These results suggest that ARHGEF28 could be modulating the kidney inflammatory responses to ICs through altering NK cell recruitment to the kidney. Funding: Proyecto CONACyT SALUD A1-S-34557 2018. Fellowship: CONACyT 1045788, De la Cruz Rico AE.

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Resumen corto

Relationship of IL-10 with transferrin in hemodialysis patients

De la Cruz-Ahumada, C.J. [1], Topete-Reyes, J.F. [2], Mena-Ramírez, J.P. [2], Guzmán-Flores, J.M. [1], Guzmán-González, J.I. [1], Ramírez-De los Santos, S. [3]*

[1]Laboratorio de Investigación en Biociencias, Centro Universitario de los Altos, Universidad de Guadalajara, Jalisco, México. [2]Instituto Mexicano del Seguro Social, Jalisco, México. [3]Departamento de Psicología Básica, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Jalisco, México.
*E-mail: saul.ramirez@cucs.udg.mx

Hemodialysis patients have a chronic inflammatory state that may contribute to the alterations in iron homeostasis often observed in them, characteristic of anemia of inflammation, a condition highly prevalent throughout the course of chronic kidney disease (CKD), increasing morbidity and mortality, and increasing the rate of progression of CKD. Therefore, an understanding of the impact inflammatory cytokines on transferrin will unravel the multifactorial interaction net of factors implicated in pathogenesis of anemia of chronic disease. In this work, we determined serum levels of IL-10 and transferrin by enzyme-linked immunosorbent assay (ELISA) to identify the relationship between these inflammatory biomarkers in patients undergoing hemodialysis. In our study group, we found that serum IL-10 levels were moderately positively correlated with serum transferrin levels ($r=.62$, $p<.001$), possibly due to inflammatory mechanisms underlying the pathophysiology of anemia, since transferrin concentration is influenced by nutritional status and varies in parallel with serum albumin concentration, as well as by cytokine production, and it is important to consider this when assessing iron therapy in these patients.

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Resumen corto

Multipotent and immunoregulation functions of mesenchymal stem cells (MSC) expressing damage-associated molecular patterns (DAMPs)

De la Peña-Sifuentes, A. [1]*, González-Salas, M.J. [1], Villa-Cedillo, S.A. [1], Martínez-Pérez, A.G. [1], Loera-Arias, M.J. [1], Saucedo-Cárdenas, O. [1], Montes de Oca-Luna, R. [1], Mecott-Rivera, G.A. [2], Pérez-Trujillo, J.J. [1]

[1] Departamento de Histología, Facultad de Medicina, Universidad Autónoma de Nuevo León. Monterrey, Nuevo León, México. [2] Departamento de Cirugía Plástica y Reconstructiva, Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León. Monterrey, Nuevo León, México.
*E-mail: andrea.sifuentes99@hotmail.com

Mesenchymal stem cells (MSC) have multipotent differentiation and immunoregulatory functions, being attributed their advantages in regenerative medicine. MSCs tolerate chemotherapeutic drugs and are therefore used as delivery vectors; however, these drugs are capable of inducing the cell expression of damage-associated molecular patterns (DAMPS) that alter cellular functions. We set out to assess multipotent and regulatory differentiation exposed to mitoxantrone. MSCs were isolated from human lipoaspirates by enzymatic method. The DAMPs were alterations in the levels of ATP and HMGB-1, and translocation of ecto-CALR, as well as reduction of proliferation markers, but cells retained their intracellular esterases functions. Sodium phenylbutyrate was used as a stress reducer. It was detected that at 72h, mitoxantrone induces an upregulation of the stress genes CHOP, ATF4 and ATF6 and a downregulation of GRP78, that can be reversed with the addition of sodium phenylbutyrate. The osteogenic and adipogenic differentiation was evaluated by alizarin red and oily red staining, respectively, and we detected that these were affected by mitoxantrone, and that sodium phenylbutyrate could only partially restore adipogenic capacity. In chondrogenic differentiation, evaluated by alcian blue, no alterations by mitoxantrone were detected. Up to date, no significant trends were detected in the cytokine profile in the coculture of MSC-splenocytes.

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Resumen corto

The immune microenvironment in melanoma is associated with disease control and response to Checkpoint Blockade Immunotherapy.

De León-Rodríguez, S.G. [1,2]*, Aguilar-Flores, C. [3], Mantilla, A.[4], Gerson-Cwilich, R. [5], Martínez-Herrera, J.F. [5,6], Rodríguez-Soto, B. [7], Gutiérrez-Quiroz, C. [8], Pérez-Koldenkova, V. [9], Fuentes-Pananá, E. [10], Bonifaz, L. [1,11]

[1] UMAE Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, CMN SXXI, IMSS, CDMX, México. [2] Posgrado en Ciencias Biológicas, UNAM, CDMX, México [3] UMAE Hospital de Pediatría, CMN SXXI, IMSS, CDMX, México [4] Servicio de Patología, Hospital de Oncología CMN SXXI, CDMX, México [5] Cancer Center, Medical Center American British Cowdray, CDMX, México [6] Latin American Network for Cancer Research, Lima, Perú [7] International Cancer Center, Campus Santa Fe, CDMX, México [8] UMAE Hospital de Especialidades, CMN General Manuel Ávila Camacho, Puebla, México [9] LNMA-IMSS, CMN SXXI, IMSS, CDMX, [10]México Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México Federico Gómez, CDMX, México. [11] Coordinación de Investigación en Salud, CMN SXXI, IMSS, CDMX, México *E-mail: sara.g.deleonr@gmail.com

Melanoma is the deadliest type of skin cancer with a growing incidence in Latin-American countries. Caucasic Melanoma is highly immunogenic and benefits from the use of checkpoint blockade immunotherapy (CBI). In contrast Acral melanoma, the most common melanoma in the Hispanic population, lacks UV mutation signatures, suggesting low immunogenicity in addition to the fact that there are few studies of the composition of the immune stroma that supports the benefit of the CBI. In the present work, we evaluated the presence of conventional dendritic cells type 1 (cDC1) and tissue-resident CD8 lymphocytes in the stroma of melanoma patients by multiplexed immunofluorescence and artificial intelligence image analysis. We found that both acral and cutaneous melanoma are infiltrated with similar levels of CD8 and cDC1 lymphocytes that express the PD-1-PD-L1 axis. Remarkably we found two populations of tissue-resident CD8 T cells: one that expresses the progenitor marker TCF7 (TCF7+) and another that doesn't (TCF7-). Both populations express different exhaustion features, retain effector functions such as IFN-γ and Ki-67 expression, and are related to disease control. Importantly in an independent cohort of patients, we observed that both populations of TRM cells and DCs were highly present in patients responding to CBI.

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Resumen corto

Immunophenotypic characterization of the cellular infiltrate associated with etiological factors in patients with atopic dermatitis

De los Santos-Carmona, S.V. [1,2]*, Hernández-Ricok, B. [1], Ortega Rocha, E.M. [1], Rincón-Pérez, C. [3], Pérez-Koldenkova, V. [4], Bonifaz-Alfonzo, L.C. [1]

[1]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, CMN Siglo XXI, Ciudad de México, CDMX, México. [2]Programa de Maestría en Ciencias Bioquímicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Servicio de Dermatología, Unidad de Especialidades Médicas, SEDENA, Ciudad de México, CDMX, México. [4]Laboratorio Nacional de Microscopía Avanzada, CMN Siglo XXI, Ciudad de México, CDMX, México. *E-mail: sofiadelossantosc@gmail.com

Atopic Dermatitis (AD) is one of the main causes of dermatological consultation and affects 2-10% of the adult population in Mexico. Its etiology is multifactorial, involving disruption of the epidermal barrier, genetic and environmental factors, neurological implications and altered immune cell infiltration. Characterizing the immune infiltrate and its association with other related factors can open a better understanding of the disease and improve personalized treatment. In this work, we evaluated by immunofluorescence the presence of different subtypes of T CD4+ cells, CD8+, mast cells and cytokine production; also, the presence of structural epidermal proteins such as filaggrin and involucrin, differentiation markers and tight junctions, as well we identified the presence of nerve endings, neuropeptides and its receptors in moderate to severe subacute and chronic AD lesions of 55 patients. We found a difference in the production of cytokines, with higher expression of IL-22, IL-13 and IL-17, also a bigger percentage of Th2 and Th22 CD4+ cells. For barrier proteins, there is a decrease in filaggrin expression, and we observed that the expression of receptors is bigger than the actual expression of neuropeptides. Considering this data, we can design a molecular signature of AD and to elucidate how these components relate to each other and affect the patient's progression.

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Resumen corto

Associated clinical factors in patients diagnosed with COVID-19 at the Civil Hospital of Guadalajara from January to August 2022

Del Moral-Trinidad, L.E. [1], Hernández-Flores, T.J. [2], Carrera-Escobedo, M.J. [1], Martínez Esparza, R.C. [1], Ruíz-Carrillo, J.D. [3], Torres-Báez, C. [1], Iñiguez-Gutiérrez, L. [1]*

[1]Hospital Civil de Guadalajara, Guadalajara, Jalisco, México. [2]Centro Universidatio de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [3]Clínica de Medicina Familiar 1° ISSSTE, Guadalajara, Jalisco, México. *E-mail: lilianainiguez11@gmail.com

Greater susceptibility and poor prognosis due to COVID-19 predominates in people who suffer from chronic comorbidities, are over 60 years old, are sedentary or even in individuals with low educational and socioeconomic status. Our aim is to describe the factors associated with the clinical characteristics of patients diagnosed at the Civil Hospital of Guadalajara from January to August 2022. Patients >18 years with suspected COVID-19 who agreed to participate in the study were included. Diagnosis was made by qPCR test. The telephone survey included questions related to sociodemographic and clinical characteristics. We included the following validated scales: the Latin American and Caribbean Food Security Scale, the Mexican Association of Market Intelligence Agencies and Opinion AMAI Rule, and the Brief Physical Activity Assessment Tool. Descriptive statistics were performed for all variables, associations were calculated with Spearman correlations, with a confidence level of 95% and a value of $p<0.05$ as significant. Qualitative variables were reported in percentages and quantitative variables in mean and standard deviation. A total of 142 individuals aged 40±16 years were included, 59.2% were women and 12% were over 60 years old. The most common comorbidities were: overweight (n=35), hypertension (n=24), obesity (n=17) and diabetes mellitus (n=17). Lower food security and socioeconomic status were associated with longer duration of the symptoms (r=0.344 and r=0.277, respectively) and severity of the infection (0.242 r=0.242 and r=0.299, respectively). In conclusion, our data show that it is a priority to develop preventive measures to complement the evaluation of vulnerable population.

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Resumen corto

Cry1Ac as an lectin binding protein adjuvant in mammals.

Del Palacio-Ortega, M.A.*, Ilhuicatzi-Alvarado, D.,
Moreno-Fierros, L.

Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. *E-mail: mauriciodelpalacio@gmail.com

Cry1Ac is a protein with insecticidal properties that is produced by the bacterium *Bacillus thuringiensis.* Upon ingestion by target insects, Cry1Ac is solubilized and cleaved by alkaline conditions and intestinal enzymes to become the active toxin that kills the insect. Recent studies have shown that Cry1Ac also has immunostimulatory properties in mammals, activating different types of cells such as macrophages and lymphocytes, and increasing antibody levels in serum and regionalized compartments such as respiratory and gut tissue. Cry1Ac appears to be a potent adjuvant and immunostimulatory molecule with promising results. Our study demonstrated that Cry1Ac binds to human and murine immunoglobulins, suggesting a direct effect on B lymphocytes in these species, as confirmed by western blot analysis. Additionally, Cry1Ac toxin binds in a lectin fashion to an N-acetylgalactosamine moiety in insects and mammals, as shown by pulldown assays with lymphocyte membrane extracts. Cry1Ac also stimulate expression of CD25, CD69, and IFN-gamma in T and B lymphocytes suggesting MAPKs pathway activation is involved, given the large number of possible receptors identified, implies in a dependent and/or independent of BCR/TCR stimulation by the binding of these glycoproteins. These findings provide important insights into the immunological effects of Cry1Ac and suggest potential applications for its use as an immunostimulatory molecule.

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Resumen corto

Uncovering the Role of TGF-β3 in Treg Differentiation

Delgado-Zaldivar, D. [1,2]*, Albarrán Godínez, A. [1,2], Barroso-Zuppa, M. [2,3], Ramirez-Velez, C. [2], Flores-Patiño, J.J. [4], Rosetti, F. [2], Madera-Salcedo, I.K. [2], Crispín, J.C. [2,3]

[1]Universidad Nacional Autónoma de México (UNAM), Posgrado en Ciencias Biomédicas, Cto. de los Posgrados S/N, C.U., Coyoacán, 04510 Ciudad de México, CDMX. [2]Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán (INCMNSZ), Departamento de Reumatología e Inmunología, Laboratorio de inmunopatología. Vasco de Quiroga 15, Tlalpan,14080, Ciudad de México, CDMX, México. [3]Tecnológico de Monterrey, Tlalpan, Ciudad de México, CDMX, México. [4]Universidad de Celaya (UDEC), Celaya, Guanajuato México C.P. 38080.
*E-mail: diegochpt@gmail.com

Regulatory T cells (Tregs) are a specialized subset of immune cells that play a crucial role in maintaining immune homeostasis and preventing autoimmunity. During Treg development, TGF-β promotes the differentiation, expansion, and function of Tregs. There are three isoforms of TGF-β (TGF-β1, TGF-β2, and TGF-β3). Less is known about the function of TGF-β2 and TGF-β3 in this process because TGF-β1 is the predominant isoform. However, studies have shown that all three isoforms have non-redundant functions in a variety of biological processes. For example, we have observed a high expression of TGF-β3 in barrier tissues and that this cytokine is necessary for oral tolerance induction.

In order to evaluate the role of TGF-β3 in Treg generation *in vitro*, CD4 naïve T cells were differentiated into Tregs in the presence of this cytokine, or with TGF-β1 as a control. Interestingly, we found no difference in the proportion of naive cells differentiating into Tregs using anti-CD3 and anti-CD28 antibodies. However, we observed a strikingly higher number of Tregs, as well as higher expression of FoxP3 when we differentiate OT-II cells with peripheric lymph node (pLN) DCs and a peptide derived from ovalbumin (OVAp) with TGF-β3. These results suggest that TGF-β3 isoform promotes the function of regulatory DC in barrier tissues.

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Resumen corto

Helios expression in intraepithelial lymphocytes

Delgado-Zaldivar, D. [1,2]*, Rubio, R.M.[2,3], Albarrán-Godínez, A.[1,2], Barroso-Zuppa, M. [2,3], Ramirez-Velez, C.[2], Rosetti, F.[2], Madera-Salcedo, I.K. [2], Crispín, J.C.[2,3].

[1].Universidad Nacional Autónoma de México (UNAM), Posgrado en Ciencias Biomédicas, Cto. de los Posgrados S/N, C.U., Coyoacán, 04510 Ciudad de México, CDMX. [2].Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán (INCMNSZ), Departamento de Reumatología e Inmunología, Laboratorio de inmunopatología. Vasco de Quiroga 15, Tlalpan,14080, Ciudad de México, CDMX, México. [3]. Tecnológico de Monterrey, Tlalpan, Ciudad de México, CDMX, México. diegochpt@gmail.com

Helios is a zinc finger transcription factor that plays a critical role in regulating gene expression during immune cell development. It is a member of the Ikaros family of proteins and is expressed in a variety of immune cells, including regulatory T cells (Tregs). Helios is important for the differentiation and function of these immune cells and has been shown to contribute to immune tolerance. Furthermore, recent studies have demonstrated that Helios is highly expressed in unconventional T cells, such as γδ T cells, which are enriched in barrier tissues like the intraepithelial cell compartment in the gut. Using FACS, we evaluated the expression of Helios in these lymphocytes and found that the proportion of γδ T cells expressing Helios was greater in this location than in secondary lymphoid tissues. Additionally, we observed that virtually all T CD8αα lymphocytes express Helios in a constitutive manner. To investigate the importance of Helios in unconventional T cells, we generated a colony of mice deficient in Helios in CD8α+ cells (Cd8aCre.Heliosfl/fl) while preserving Helios expression in Tregs. We observed a defect in the migration of T CD8αα and γδ Tαα to the small intestine when transferred into a RAG-/- recipient. These observations suggest that Helios expression by unconventional T cells may play an important role in the maintenance of immune homeostasis in barrier tissues.

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Resumen corto

CD13/APN influences Complement receptor 3 (CR3) activation and membrane expression in human macrophages via an inside-out signaling pathway.

Díaz-Alvarez, L. [1,2]*, Martínez-Sánchez, M.E. [3], Gray, E. [4], Pérez-Figueroa, E. [5], Ortega, E. [1]

[1]Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Instituto Nacional de Enfermedades Respiratorias "Dr. Ismael Cosío Villegas", Ciudad de México, CDMX México; [4]London Centre for Nanotechnology, University College London, London, United Kingdom. [1]Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [5]Unidad Periférica para el Estudio de la Neuroinflamación en Patologías Neurológicas del Instituto de Investigaciones Biomédicas de la UNAM en el Instituto Nacional de Neurología y Neurocirugía, Ciudad de México, CDMX, México.
*E-mail: laura.diaz-alvarez@ciencias.unam.mx

The myeloid immune receptors CD11b/CD18, also known as complement receptor 3 (CR3), and CD13, a moonlighting protein, have overlapping activities such as adhesion, migration, phagocytosis of opsonized particles, and respiratory burst induction. Because of their common functions, shared physical location, and the ability of some receptors to activate integrins, we hypothesized that CD13 could activate CR3 via an inside-out signaling mechanism and potentially affect its membrane expression. Our research demonstrated that crosslinking CD13 on human macrophages not only activates CR3, but also influences its membrane expression. Inhibitors of Src, Plcγ, Syk, and actin polymerization had an impact on both phenomena. After just 10 minutes at 37°C, cells with crosslinked CD13 began secreting IFNs type 1 and 2, IL-12p70, and IL-17a. We integrated our findings with a bioinformatic analysis to confirm the relationship between these receptors and suggest the signaling cascade linking them. Our research expands the list of CD13 features by demonstrating the activation of a different receptor via inside-out signaling. This opens up the possibility of exploring the combined contributions of CD13 and CR3 in contexts where either receptor plays a recognized role, such as the progression of some leukemias.

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Resumen corto

BNT162b2 vaccination after SARS-CoV-2 infection changes the dynamics of total and neutralizing antibodies against SARS-CoV-2: a 6-month prospective cohort study

Díaz-Pérez, S.A. [1], Hernandez-Bello, J. [1], Sierra-García de Quevedo [2], Morales-Nuñez, J.J. [1], Santoscoy-Ascencio, G. [2], Gutiérrez-Brito, J.A. [1], Muñoz-Valle, J.F. [1]

[1]Instituto de Investigación en ciencias biomédicas, Centro Universitario de ciencias de la Salud (CUCS), Universidad de Guadalajara, Guadalajara, Jalisco, Mexico. [2]Unidad de Patología Clinica (UPC), Guadalajara, Jalisco, Mexico. *E-mail: saul.diaz2330@alumnos.udg.mx

This study aimed to analyze the dynamics, duration, and production of total and neutralizing antibodies induced by the BNT162b2 vaccine and the possible effect of gender and prior SARS-CoV-2 infection on the generation of these. Total antibodies were quantified by chemiluminescent microparticle immunoassay (CMIA), and neutralizing antibodies were quantified with the cPass SARS-CoV-2 kit. Individuals with a history of COVID-19 produced twice as many antibodies than vaccinated individuals without prior SARS-CoV-2 infection, with an exponential increase in just six days. In those without COVID-19 history, similar antibody production was reached 45 days after vaccination. Although total antibodies decline considerably in the first two months, the neutralizing antibodies, and their inhibitory capacity (>96%) persist up to 6 months after the first dose. We suggest that the decline in total antibodies should not be considered an indicator of loss of protective immunity because most antibodies decay two months after the second dose, but neutralizing antibodies remain constant for at least six months; therefore, these last antibodies could be better indicators to estimate the time-dependent vaccine efficacy.

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Resumen corto

Immunotoxic effects caused by classic and emerging pesticides used for vector-borne disease control.

Díaz-Resendiz, K.J.G. [1,2,3*], Camacho-Pérez, M.R. [1], Moreno-Torres, F.S. [1], Corona-Navarrete, A. [1,2], Haro-Pérez, A.A. [1,2], Benítez-Trinidad, A.B. [1,2,3], Ventura-Ramón, G.H. [1,2,3], Covantes-Rosales, C.E. [1,2,3], Girón-Pérez, M.I. [1,2,3], Toledo-Ibarra, G.A. [1,2,3], Bueno-Durán, A.T. [1,2,3], Girón-Pérez, D.G. [1,2,3]

[1]Laboratorio de Inmunotoxicología. Secretaría de Investigación y Posgrado. Universidad Autónoma de Nayarit. Ciudad de la Cultura S/N, Centro. Tepic, Nayarit, México. C.P. 63000. [2]Laboratorio Nacional de Investigación para la Inocuidad Alimentaria (LANIIA)-Unidad Nayarit, Universidad Autónoma de Nayarit, Calle Tres S/N. Colonia. Cd. Industrial. Tepic, Nayarit, México. C.P. 63173. [3]Licenciatura en Biomedicina Ambiental Traslacional. Universidad Autónoma de Nayarit. Calle Tres S/N, Colonia Cd. Industrial. Tepic, Nayarit, México. C.P. 63173.
*E-mail: karina.diaz@uan.edu.mx.

For several years, pesticides have been reported to have toxic effects not only on the nervous system of non-target organisms but also on the immune system. In this regard, pesticides can disrupt neuroimmune communication, leading to immunotoxic effects. The pesticides temephos, spinosad, and *Bacillus thuringiensis* var. *Israelensis* (Bti) are used to control the Anopheles mosquito (vector) and thereby prevent the spread of vector-borne diseases (VBDs) spreading, such as dengue, chikungunya, and Zika; however, the inappropriate use and mishandling of these substances during their application cause toxic effects on the health of non-target organisms, such as birds, aquatic organisms, and humans. the aim of this work was to evaluate senescence induction and leukocyte death through *in vivo* exposure to temephos, spinosad, and Bti in guppy fish (*Poecilia reticulata*). Organisms were exposed to the three pesticides at concentrations applied by the SSA in mosquito control spraying campaigns [10 mg/L temephos 0.5 mg/L spinosad and 3.74 mg/L Bti], for 24 h y 72 h. Spleens were extracted, then, senescence and cell death were determined by flow cytometry through β-galactosidase enzyme activity and by Annexin V-FITC kit, respectively. The results indicated that temephos and spinosad exposure at 24 and 72 h induced leukocytes senescence and apoptosis, while Bti only induced apoptosis and senescence at 24 h of exposure. These results demonstrate that the most commonly used pesticides for the control of dengue vector control are not harmless to non-target organisms.

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Resumen corto

Defining exhausted T cell subsets during experimental cutaneous infection with *Leishmania* (L.) *mexicana*

Diupotex, M. *, Zamora-Chimal, J., Ingeborg, B.

[1]Unidad de Investigación en Medicina Experimental, Facultad de Medicina, Universidad Nacional Autónoma de México, Avenida Universidad 3000, C.P. 04510, Ciudad de México, México. *E-mail: diupotex@ciencias.unam.mx

Cutaneous leishmaniasis (CL) is the most prevalent form of leishmaniasis caused by vector-borne protozoan parasites. *Leishmania mexicana* is the main etiological agent of CL in Mexico, causing several clinical manifestations ranging from self-healing localized infection to chronic diffuse leishmaniasis (DCL) characterized by disfiguring nodular lesions. The functional impairment of T cells during DCL has been linked to the acquisition of an “exhausted” phenotype, defined by PD-1 up-regulation. Recent studies revealed that exhausted T (Tex) cells comprise heterogeneous subsets, including progenitor cells that sustain long-term immunity and terminally-differentiated cells. In this study, we used flow cytometry to define the phenotypic and functional profiles of Tex subsets in C57BL/6 mice infected with stationary-phase promastigotes of *L. mexicana*. Using CXCR5 and TIM-3 markers, we identified two subpopulations of Tex cells (PD-1$^+$) within both CD4$^+$ and CD8$^+$ T-cell compartments in draining lymph nodes. Our longitudinal analysis showed that CXCR5$^+$TIM-3$^-$ cells progressively augmented as the infection progressed, whereas CXCR5$^-$TIM-3$^+$ cells decreased after 60 days post-infection. Furthermore, we observed a high infiltration of CXCR5$^-$TIM-3$^+$ cells within the footpad lesions in the chronic phase. CXCR5$^+$TIM-3$^-$ cells expressed higher levels of CCR7, and lower levels of CX3CR1, PD-1 and CD39 compared to their counterpart subset. Consistently, we observed that the frequency of Ki-67 and IFN-γ expressing cells was higher in the CXCR5$^+$TIM-3$^-$ subset, whereas CXCR5$^-$TIM-3$^+$ cells exhibited heightened expression of CD107a. In conclusion, we identified for the first time a less differentiated Tex subset in CL, which represents a promising target to boost the current treatment of DCL.

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Resumen corto

Galectin 7 as potential diagnostic biomarker in dengue virus

Domínguez-Alemán, C.A. [1], Escalera-Flores, S.H. [1,2]*,
Ugarte-Álvarez, O. [3], Hernández-Flores, K.G. [1], Vivanco-Cid, H. [1]

[1]Instituto de Investigaciones Médico-Biológicas, Universidad Veracruzana, Región Veracruz, Veracruz 91700, México. [2]Facultad de Bioanálisis, Universidad Veracruzana, Región Veracruz, Veracruz 91700. [3]Facultad de Medicina, Universidad Veracruzana, Región Veracruz, Veracruz 91700, México. *E-mail: salma.hef@gmail.com

The arboviral disease caused by Dengue, Chikungunya and Zika virus are acute febrile diseases of tropical and subtropical areas. Currently, Mexico has become a highly endemic country for these viruses, its presence affects millions of people causing clinical manifestations that can be complicated in some cases, so it is represents a public health problem. In this context, it is difficult to make differential diagnosis the arboviral disease because their symptoms are similar and exists cross reactivity in antibodies tests. Galectin 7 is a cancer prognosis biomarker, participated in regulation of apoptosis, cell proliferation, cell to cell adhesion and cell migration. In this study, we evaluated galectin 7 like a biomarker to differentiate arboviral disease. We found higher concentration galectin 7 in dengue and zika patients compared with healthy subjects. Dengue patients demonstrated higher concentration galectin 7 versus zika patients and this difference was remarkable in critical phase (4-6 day). Additionally, we compare by ROC curve Dengue patients, we found that galectin-7 could differentiate Dengue patients from non infected patients, zika patients and chikungunya patients. Analysis of signs and symptoms detected difference in concentration galectin-7 in dengue patients with headache and gyngivorrhagia. Our further investigations indicated galectin 7 is a probable biomarker of dengue infection because permits differentiated dengue to zika and chikungunya infections.

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Resumen corto

Recombinant p40 protein from *L. rhamnosus GR1* increases occludin and claudin-1 expression on CaCo-2 and HaCaT cells

Domínguez-Díaz, C.[1,2*], Avila-Arrezola, K.E.[2], Rodríguez-González, J.A.[3], Del-Toro-Arreola, S.[4], Delgado-Rizo, V.[4] , Fafutis-Morris, M.[2,4]

[1]Doctorado en Ciencias Biomédicas, Con Orientaciones en Inmunología y Neurociencias, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Centro de Investigación en Inmunología y Dermatología (CIINDE), Zapopan, Jalisco, México. [3]Biotecnología Industrial, Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco A.C., Zapopan, Jalisco, México. [4]Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. carolina.dominguezd@alumnos.udg.mx

Epithelial barriers are the main defense line against the entry of external stimuli due to tight junctions, protein complexes that regulate the paracellular space to macromolecules, cells, and microorganisms. Bacterial metabolites and proinflammatory cytokines alter their permeability by causing changes in the expression of proteins forming these complexes. Postbiotics, molecules derived from probiotics, improve barrier function through the activation of survival pathways in epithelial cells. p40 is muramidase secreted by *Lacticaseibacillus rhamnosus* GG, it protects the intestinal barrier against oxidative stimuli through the activation of EGFR. In this work, the recombinant p40 protein from *L. rhamnosus* GR1 was cloned, expressed, and purified to evaluate its effect on epithelial barriers subjected to inflammatory stimuli. We studied its lytic biological activity with a qualitative test and performed cell culture of colonic CaCo-2 cells and HaCaT keratinocytes with LPS and TNF-α to observe its effect on tight junctions, as well as the EGFR activation by Western blot. We found a mutation in residue 368 that does not cause changes in our p40 structure. In addition, it presents biological activity even after being subjected to different storage conditions. Finally, we realized that, although the stimuli did not cause changes in the tight junctions' expression, p40 increases occludin and claudin-1 expression on CaCo-2 cells and occludin in HaCaT, though only on the former cells it increases EGFR activation. This suggests that our recombinant p40 protein improves epithelial barrier function through different signaling pathways in colonic and epidermic cells.

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Resumen corto

Association of the CTLA4 +49A>G polymorphism with plaque psoriasis susceptibility in a mestizo Mexican population and CTLA4 serum level determination

Domínguez-Díaz, C.[1,2*], Hernandez-Nicols, B.F.[2,3], Fajardo-Álvarez, B.L.[2,3], Santana-Osuna, E.I.[2,3], Wheber-Hidalgo, K.A.[3], Flores-Sánchez, P.F.[2,3], Hernández-Bello, J.[4], García-Arellano, S.[4], Muñoz-Valle, J.F.[4], Fafutis-Morris, M.[2,3], Alvarado-Navarro, A.[2,3].

[1]Doctorado en Ciencias Biomédicas, con Orientaciones en Inmunología y Neurociencias, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Centro de Investigación en Inmunología y Dermatología (CIINDE), Zapopan, Jalisco, México. [3]Instituto Dermatológico de Jalisco, "Dr. José Barba Rubio", Zapopan, Jalisco, México. [4]Instituto de Investigación en Ciencias Biomédicas Universidad de Guadalajara, Guadalajara, Jalisco, México. carolina.dominguezd@alumnos.udg.mx

Psoriasis is a chronic inflammatory skin disease. It is characterized by keratinocyte hyperproliferation and the presence of defined erythematous-scaly plaques with irregular borders. It is a multifactorial disease, with a 2 – 3% general prevalence worldwide. CTLA-4 is a protein from the immunoglobulin superfamily that is expressed on T lymphocytes and transmits an inhibitory signal by binding to B7, promoting immunoregulation. The SNP +49A>G of the CTLA4 gene causes a threonine for alanine substitution in the leader peptide of the protein. This SNP has been studied in autoimmune diseases in different populations; a risk association was found between this polymorphism and psoriasis susceptibility. In this work we analyzed the association between the CTLA4 +49A>G polymorphism with plaque psoriasis susceptibility in a mestizo population from western Mexico and quantified sCTLA4 serum levels. 100 patients with a diagnosis of plaque psoriasis and 100 control subjects were included. Peripheral blood DNA extraction was performed, which was processed by PCR-RFLPs and serum by ELISA. We found our control group is in Hardy-Weinberg equilibrium. In addition, we observed a higher frequency of the AA genotype in patients and AG in controls. When comparing the genotypic and allelic frequencies, we found statistically significant differences. However, we did not find a risk association (OR 0.45, p=0.049; OR 0.61 p=0.019, respectively). The sCTLA4 serum concentration in patients was lower than in the control group. Nevertheless, when comparing by genotype, no significant differences were found (p>0.05). In conclusion, we found no association between the polymorphism with psoriasis susceptibility was found.

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Resumen corto

Evaluation of the effect of valproic acid on mast cell activation with LPS from *Porphyromonas gingivalis*

Dominguez-Flores, A.[1*], Soria-Castro, R.[1], López-Santiago, R.[1], Cancino-Diaz, M.[1], Pérez-Tapia, S.M.[1,2], Flores-Mejía, R.[3], Estrada-Parra, S.[1], Flores-Borja, F.[4] y Chacón-Salinas, R.[1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2] Unidad de Desarrollo e Investigación en Bioprocesos (UDIBI) de la Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3] Laboratorio de Inflamación y Obesidad, Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [4] Centre for Immunobiology and Regenerative Medicine, Barts & The London School of Medicine and Dentistry, Queen Mary University of London, London, United Kingdom.
adominguezf0700@alumno.ipn.mx

Periodontitis is a disease initiated by a microbial dysbiosis promoted by *Porphyromonas gingivalis* (*P. gingivalis*), which is a gram-negative bacterium with an outer membrane composed of lipopolysaccharide (LPS). An increased presence of *P. gingivalis* in the oral plaque on the dental surface is associated with chronic inflammation that induces tooth loss due to bone resorption. Previous studies have observed an increased number and activity of mast cells in the oral mucosa during periodontitis. Moreover, mast cell-deficient mice showed reduced bone loss in a model of *P.gingivalis*-induced periodontitis. Therefore, the regulation of mast cell activity could be a therapeutic strategy to control and reduce periodontitis progression. Valproic acid (VPA) is a first-line drug in epilepsy treatment, however, in recent years its ability to regulate different cells of the immune response has been discovered. Remarkably, VPA diminishes mast cell activation through FcεRI crosslinking and during *Listeria monocytogenes* infection. In this study we analyzed the effect of VPA on *P. gingivalis* LPS-mediated mast cell activation. We observed that mast cells treated with VPA and activated with *P. gingivalis* LPS released lower levels of IL-6 and TNFα, compared to non-treated LPS-stimulated cells. This inhibitory effect might be associated with a decreased expression of TLR4, and an increased histone H3 acetylation through a mechanism not yet described. Our study shows that VPA can downmodulate the pro-inflammatory response to LPS by mast cells. To corroborate the role of VPA in regulating periodontitis progression, *in vivo* studies with murine models are required.

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Resumen corto

Gene expression of cytokines in lambs immunized with a native serine protease and two S28 peptides from *Haemonchus* spp.

Duran-Cortes, Z.C. [2], Camas-Pereyra, R. [1], Bautista-García, G.A. [1], Pérez-Anzurez, G. [3], Reyes-Guerrero, D.E. [3], Maza-Lopez, J. [3], López-Arellano, M.E. [1*]

[1] Centro Nacional de Investigación Disciplinaria en Salud Animal e Inocuidad, Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias. Carr. Fed. Cuernavaca-Cuautla Núm. 8524, Jiutepec, Mor., México, C.P. 62550; *E-mail: lopez.mariaeugenia@inifap.gob.mx
[2] Facultad de Biotecnología, Universidad Politécnica del Estado de Morelos, Boulevard Cuauhnáhuac No. 566 Col. Lomas del Texcal, Jiutepec, Morelos. CP 62550. [3]Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Ciudad de México, México, C.P. 04510.

Given the constant research for alternative control methods against *Haemonchus*, one of the most pathogenic gastrointestinal nematodes in ruminants, different proteases as potential vaccine candidates have been studied. Thus, the present study analyzed the local immunogenic effect triggered by a native serine protease (E/S15) and two synthetic peptides (S28) in lambs, after a challenge infection with 10,000 L_3 of *H. contortus*. Four groups of three animals, classified as negative controls (C-), positive controls (C+) and immunized lambs (S28 and E/S15) were established. Abomasal tissue sections were performed for RNA extraction and cDNA synthesis. The relative expression of *IL4, IL5, IL6, CXCL8, IL13* and *FCεR1A* genes was quantified by RT-qPCR in each experimental group. The fold change was analyzed by Student's test ($p \leq 0.05$) with the ΔΔCT method using the GeneGlobe Data Analysis Center® platform. Upregulation of *IL5* and *IL6* was observed in the immunized groups. Additionally, S28 and E/S15 groups showed an up and downregulation of the *FCεR1A* gene, respectively. In contrast, *CXCL8* was upregulated with ES/15 immunized lambs whereas a downregulation in the S28 group was observed. These results indicate that native 15 kDa serine protease and the S28 peptides can stimulate cytokine expression into the abomasal tissue of immunized sheep, suggesting a local immunoprotective effect and a potential as a vaccine candidate that should be evaluated in future studies.

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Resumen corto

Stimulation of TCD4+INF-γ+ and TCD8+INF-γ+ lymphocytes by Rickettsia vaccine candidate pVAX1-OmpB24

Dzul-Rosado, K. [1*], Donis-Maturano, L. [2], Arias-León, J. [3], Machado-Contreras, J. [4], Valencia-Pacheco, G. [1], Panti-Balam, C. [1], Balam-Romero, J. [1], Ku-González, A. [5], Peniche-Lara, G. [3], Mosqueda-Gualito, J. [6], Zazueta, O.E. [7], Lugo-Caballero, C. [1], Puerto-Manzano, F. [1]

[1]Centro de Investigaciones Regionales "Dr. Hideyo Noguchi", Universidad Autónoma de Yucatán, Mérida, Yucatán, México. [2]Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Facultad de Medicina, Universidad Autónoma de Yucatán, Mérida, Yucatán, México. [4]Facultad de Medicina, Universidad Autónoma de Baja California, Mexicali, Baja California, México. [5]Centro de Investigación Científica de Yucatán, Mérida, Yucatán, México. [6]Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Querétaro, México. [7]Secretaría de Salud de Mexicali, Mexicali, Baja California, México.
*E-mail: karla.dzul@correo.uady.mx

In recent years, promising vaccination strategies against rickettsiosis have been described in experimental animal models and human cells. OmpB is considered an immunodominant antigen that is recognized by T and B cells. The aim of this study was to identify TCD4+INF-γ+ and TCD8+INF-γ+ lymphocytes in an autologous system with macrophages transfected with the vaccine candidate pVAX1-OmpB24. Lymphocytes and monocytes from 14 patients with Rickettsia were isolated from whole blood. Monocytes were differentiated into macrophages and trans-fected with the plasmid pVAX1-OmpB24 pVax1. Isolated lymphocytes were cultured with transfected macrophages. IFN-γ-producing TCD4+ and TCD8+ lymphocyte subpopulations were identified by flow cytometry, as well as the percentage of macrophages expressing CD40+, CD80+, HLA-I and HLA-II. Also, we analyzed the exhausted condition of T lymphocyte subpopulation by PD1 expression. Macrophages transfected with pVAX1-OmpB24 stimulated TCD4+INF-γ+ cells in healthy subjects and patients infected with *R. typhi*. Macrophages stimulated TCD8+INF-γ+ in healthy subjects and patients infected with *R. rickettsii* and *R. felis*. Cells from healthy donors stimulated with OmpB-24 showed a higher percentage of TCD4+PD1+. Cells from patients infected with *R. rickettsii* had a higher percentage of TCD8+PD-1+, and for those infected with *R. typhi* the higher number of cells was for TCD4+PD1+. Human macrophages transfected with pVAX1-OmpB24, activated TCD4+IFN-γ+ and CD8+IFN-γ+ in patients infected with different Rickettsia species, however, the PD1 expression played an important role in the inhibition of T lymphocytes with *R. felis*

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Resumen corto

Antimicrobial effect of bimetallic nanoparticles (Np) on *Nocardia brasiliensis*

Elizondo-Solis, C.V. [1], Bretado-Aragon, L.A. [2], Garcia-Gonzalez, G. [2]; Salinas-Delgado, Y., Hernandez-Garcia, M.F. [1], Medina-de la Garza, C.E. [1], Montoya-Rosales, A. [3], Macias-Segura, N. [1], Salinas-Carmona, M.C. [1]

[1]Laboratorio de Inmunología de Sistemas, Departamento y Servicio de Inmunología, Facultad de Medicina y Hospital Universitario, Universidad Autónoma de Nuevo León. [2]Ingeniería en nanotecnología, Universidad de la Ciénega del Estado de Michoacán de Ocampo. [3]Laboratorio de Inmunomoduladores, Centro de Investigación y Desarrollo en Ciencias de la Salud, Universidad Autónoma de Nuevo León. *E-mail: Cesar.elizondosls@uanl.edu.mx

Mycetoma caused by *Nocardia brasiliensis* is a neglected tropical disease, which causes a great burden to sufferers. Recently, cases of antimicrobial resistance have been reported. Among the therapeutic alternatives currently proposed to combat this resistance is the use of metallic nanoparticles. In this study we evaluated the in vitro antimicrobial effect of bimetallic Np against *Nocardia brasiliensis* by determining the minimum inhibitory concentration by microdilution assays; in addition, we determined the cytotoxic effect on splenocytes by cytotoxicity assays with trypan blue staining. The results obtained were promising, with a MIC of 2 ppm and a MIC of 3 ppm, indicating a strong antimicrobial effect against *Nocardia brasiliensis*. Furthermore, in the cytotoxicity assays, the cell viability of splenocytes was determined to be more than 60%, indicating low cytotoxicity of the nanoparticles. These findings suggest that the use of bimetallic nanoparticles could be a potential therapeutic option for the treatment of Mycetoma caused by *Nocardia brasiliensis,* particularly in cases of antimicrobial resistance. However, further validation of these results is required in an *in vivo* animal model.

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Resumen corto

Synthesis of biocompatible and thermosensible hydrogel of alginate-chitosan enriched with iron sulfide nanoparticles

Escamilla-Flores, A.V. [1]*, Núñez-Anita, R.E. [2], Arenas-Arrocena, M.C. [1], Acosta-Torres, L.S. [1]

[1]Escuela Nacional de Estudios Superiores, Unidad León, Universidad Nacional Autónoma de México, Boulevard UNAM no. 2011, Col. Predio El Saucillo y El Potrero, Guanajuato C. P. 37689, México. [2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Michoacana de San Nicolás de Hidalgo, Carretera Morelia–Zinapécuaro Km. 9.5, Tarímbaro C. P. 58893, México

The aim was synthesize and characterize a thermosensitive and biocompatible hydrogel of alginate with chitosan enriched with iron sulfide nanoparticles. The synthesis was carried out from alginate and chitosan 50:50 vol/vol. Three concentrations of FeS_2NPs 0.03905, 0.0781 and 0.2343 mg/ml were used. The elastic force of the gels was determined with rheological studies. Gel swelling was determined using phosphate buffered saline solution at 1, 2, 4, 6, 24, 48, and 72 h. The microstructure was analyzed using optical microscopy. The identification of characteristic functional groups was determined through Fourier Transform Infrared Spectroscopy with a range of 500 to 4000 cm^{-1}. The analysis of morphology was conducted by scanning electron microscopy. Biocompatibility was determined in a murine model, after seven days of subdermal inoculation, histological sections stained with H&E were analyzed, then histopathological features were evaluated. All the compounds obtained showed a loss modulus lower than the storage modulus. The (0.2343 mg/ml) FeS_2NPs hydrogel showed higher swelling compared to the control. Phase contrast micrographs showed that those containing (0.0781 and 0.2343 mg/ml) FeS_2NPs were less porous compared to the control. The characteristic functional groups were identified, such as –OH, NH2, C-H, C=O, N-H, C-N, C-O, C-O-C. The presence of micro hydrogels was confirmed. In the in vivo evaluation, no adverse effects were found. The presence of FeS_2NPs were well tolerated in subcutaneous tissue of mice, according to histopathological analysis. The synthesized hydrogels added with FeS_2NPs present a good swelling ratio, rheological properties and showed good tolerance in subcutaneous tissue.

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Resumen corto

Siglecs as possible negative regulators of innate immune response in T2D

Esparza-Armenta, M. [1]*, Cardona-Alvarado, M.I. [1],
Reyes-Martínez, E. [2], Figueroa-Vega, N. [1]

[1]Departamento de Ciencias Médicas, División de Ciencias de la Salud, Universidad de Guanajuato, León, Guanajuato, México. [2]Departamento de Biología, División de Ciencias Naturales y Exactas, Universidad de Guanajuato, Guanajuato, Guanajuato, México.
*E-mail: miguel.esparza.fb@uas.edu.mx

Immune response impairment in type 2 diabetes (T2D) represents one of the principal subjacent complications of this disease where the high levels of sugars are a major factor that contributes to the immune response impairment, making subjects with T2D more susceptible to recurrent infections. The immune response is regulated by several molecules, among them Siglecs, membrane receptors that inhibits immune responses, plays a crucial role in this homeostatic process. In this way, alterations in the expression of these molecules can lead to immune response impairment. This study aimed to evaluate the expression of CD33 related Siglecs in monocytes and neutrophils of T2D subjects and evaluate the functionality of these cells. To accomplish this objective, a whool blood sample from healthy subjects and T2D subjects was taken to quantify biochemical parameters and to obtain white blood cells by density gradient. After that a flow cytometric approach was conducted to evaluate the expression of Siglecs in monocytes and neutrophils. Although we evaluated neutrophils functionality by measuring NETs formation and ROS production with a flow cytometric approach. In our preliminary results we have encounter diminished expression of Siglec-5/14 in CD14+CD16+ monocytes subpopulation as well as in neutrophils. In addition, the expression of Siglec-3 and Siglec-5/14 negative correlates with HbA1c. The implications of the expression patterns of Siglec-5/14 and the negative correlations of Siglec-3 and Siglec-5/14 with HbA1c will be dilucidated once all the experiments are conducted.

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Resumen corto

Murine extraparenchymal neurocysticercosis. An ideal model for the study of new therapeutic alternatives

Espinosa-Cerón, A. [1], Méndez, A. [1]*, Juárez-González, J.C. [1], Hernández-Aceves, J. [1], Villalobos, N. [2], Hernández, M. [1], Díaz, G., Soto, P., Concha, L. [3], Perez-Osorio, I.N. [1], Bobes, R. [1], Hamamoto-Filho, P. [4], Parkhouse, M. [5], Fragoso, G. [1]*, Sciutto, E. [1]*

[1]Instituto de Investigaciones Biomédicas. Universidad Nacional Autónoma de México, Coyoacán, Ciudad de México 04510, México. [2]Facultad de Medicina Veterinaria y Zootecnia. Universidad Nacional Autónoma de México, Coyoacán, Ciudad de México 04510, México. [3]Department of Behavioral and Cognitive Neurobiology, Instituto de Neurobiología, Universidad Nacional Autónoma de México, Juriquilla, Querétaro, Mexico. [4]Department of Neurology, Psychology and Psychiatry, UNESP-Univ Estadual Paulista, Botucatu Medical School, São Paulo, Brazil. [5]Instituto Gulbekian de Ciência, Portugal. R. Q.ta Grande 6, 2780-156 Oeiras, Portugal.
*Corresponding authors: Gladis Fragoso, Edda Sciutto, Tel.: +52(55)-5622-3152

Neurocysticercosis (NCC) is an helmintic infection that occurs when the larval form of *Taenia solium* is located in the central nervous system. The extra-parenchymal form (EXP-NCC) is the most severe form of the disease and frequently requires several cycles of cysticidal treatment and the concomitant use of glucocorticoids to prevent the increased inflammation that can lead to death by intracranial hypertension. In this study, the experimental murine model of EXP-NCC and the characteristics that establish it as an adequate model to evaluate new therapeutic alternatives are described. EXP-NCC was established by injecting 30 Taenia crassiceps cysticerci less than 0.5mm-diameter into the cisterna magna of Wistar male and female rats. The implantation and evolution of the infection was monitored by detecting the HP10 antigen and antibodies in the serum and cerebral spinal fluid (CSF of the infected rats. Higher levels of HP10 were observed in CSF than in sera, a result that resembles what is observed in EXP-NCC in humans. The presence of parasites in the CNS was confirmed by histological analysis and nuclear magnetic resonance and by detecting live parasites at the moment of the sacrifice. EXP-NCC does not affect the behavior, growth or general status of the rats. After 4 months of infection EXP-NCC is accompanied with a reduced mononuclear cells proliferation resembling what occurs in the human infection. This model will allow the evaluation of new alternatives for the control of neuroinflammation and immunomodulatory treatments to restore and improve the specific anti-cysticercal immunity.

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Resumen corto

Galectin-1 decreases lipoteichoic acid-induced IL-1β and TNF-α response in human placental explants

Estrada-Hidalgo, N. [1,2]*, Rodríguez-Flores, S. [1,2], Flores-Espinosa, P. [1], Olmos-Ortiz, A. [1], Godínez-Victoria, M. [3], Flores-Mejía, R. [4], Mancilla-Herrera, I. [5], Sosa-González, I.E. [6], Velázquez-Sánchez, P. [7], Zamora-Escudero, R. [8], Islas-López, M. [8], Zaga-Clavellina, V. [1]

[1]Departamento de Inmunobioquímica, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes. Montes Urales 800, Lomas Virreyes 11000, Ciudad de México. [2]Sección de Estudios de Posgrado e Investigación. Maestría en Ciencias de la Salud, Escuela Superior de Medicina, IPN. [3]Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Plan de San Luis y Díaz Mirón s/n, Ciudad de México 11340, México. [4]Laboratorio de Inflamación y Obesidad. Inmunología Médica y Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Plan de San Luis y Díaz Mirón, Casco de Santo Tomas, Ciudad de México 11340, México. [5]Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, Ciudad de México 11000, México. [6]Laboratorio de microbiología, Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes. Montes Urales 800, Lomas Virreyes 11000, Ciudad de México. [7] Departamento de Ginecología y Obstetricia, Hospital Ángeles México, Agrarismo 208, Col Escandón, Ciudad México,11800, México. [8]Ginecología y Obstetricia, Hospital Ángeles Lomas-UNAM, Huixquilucan 52763, México.
*E-mail: eh.nayelli.26@gmail.com

Human gestation involves the establishment of the immune privilege in the feto-maternal unit to offer the fetus a tolerogenic environment to avoid rejection. Among the immunomodulatory strategies required during pregnancy, the Galectin 1 (Gal-1), secreted by maternal and fetal tissues, including the placenta, is associated with the resolution of acute inflammation, favoring maternal-fetal tolerance. However, an intraamniotic infection by pathogens such as Group B Streptococcus (GBS) is closely related with multiple adverse outcomes, including premature birth. The present work aimed to evaluate the *in vitro* effect of Gal-1 in physiological (80 ng/ml) and supraphysiological (100 and 500 ng/ml) concentrations on the secretion of inflammatory modulators and prodegradative secreted in response to the stimulation with 5 µg/ml of lipoteichoic acid. Our results demonstrate that the pretreatment of placental explants with Gal-1 prevents the increase in the synthesis and secretion of lipoteichoic acid-induced IL-1beta and TNF-alpha, opposite IL-6, MIP-1α MCP-1, RANTES and proMMP9, which showed no change with the administration of Gal-1.This finding supports the role of Gal-1 as a potent immune-modulator in the fetoplacental interface, trying to reduce the pro-inflammatory and prodegradative environment induced by an infection that is harmful to the continuity of gestation.

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Resumen corto

DRS-DA2N INDUCES THE DEATH OF BOTH, IMMUNE CELLS AND BACTERIA, IN A SIMILAR MANNER BY INTERACTING WITH THE MEMBRANE AND DISRUPTING IT.

Fajardo-Brigido, E. [1], Drujon, T. [2], Flores, A. [1], Sachon, E. [2], Walrant, A. [2], Melchy, E. [1], Rosenstein, Y. [1], Lacombe, C. [2,3], Auvynet, C. [1*]

[1]Instituto de Biotecnologia, Universidad Nacional Autónoma de México, Cuernavaca, Morelos 62270, México.[2]Sorbonne Université, École normale supérieure, PSL University, CNRS, Laboratoire des Biomolécules, LBM, 75005 Paris, France. [3] Faculté des Sciences et Technologie, Univ Paris Est-Créteil Val de Marne, 94000 Créteil, France.
*E-mail: constance.auvynet@ibt.unam.mx

Inflammatory diseases are a major burden for the society today and fighting them is a national and WHO strategic priority.

Nowadays, most of the treatments available to fight inflammatory diseases are anti-inflammatory drugs, such as corticosteroids or immunomodulators that lead to numerous side effects. In addition to suppressing undesired inflammation, these drugs lessen the immune system protective functions.

Thus, specifically controlling the inflammatory process locally without compromising the ability to combat infections is an essential feature of the treating inflammatory diseases.

We recently isolated a new dermaseptin peptide, DRS-DA2N, from the Mexican tree frog *Pachymedusa dacnicolor* that exhibits dual, *i.e* immunosuppressive and antimicrobial activities. It specifically kills bacteria, including multiresistant strains, and human immune cells without compromising other cell types, such as erythrocytes or epithelial cells. *In vivo*, this peptide reduces rapidly and locally inflammation and disease progression in two preclinical murine models of inflammatory diseases, psoriasis, and dermatitis. Thus, this peptide may be a promising drug in the treatment of inflammatory skin diseases.

However, to be considered as a potential candidate in the treatment of inflammatory diseases, it is of great importance to understand how this peptide induces the death of immune cells and bacteria. Using various methods such as apoptotic/necrotic assay, fluorescence microscopy and biotinylated peptide, ONPG release assay, membrane depolarization assay or ANTS/DPX leakage assay, we showed that this peptide induced the death of both immune cells and bacteria in a similar manner by interacting with the lipids of the membrane before inducing it disruption.

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Resumen corto

The plant defensins PaDef and g-thionin inhibit the endothelial cell response to VEGF

Falcón-Ruiz, E.A.[1]*, López-Meza, J.E. [1], Ochoa-Zarzosa, A. [1]

[1]Centro Multidisciplinario de Estudios en Biotecnología, Facultad de Medicina Veterinaria y Zootecnia, Universidad Michoacana de San Nicol´as de Hidalgo, Km 9.5 Carretera Morelia-Zinap´ecuaro, Posta Veterinaria, C.P. 58893 Morelia, Michoac´an, Mexico.
*E-mail: 1919533f@umich.mx

Angiogenesis is involved in wound repair and tissue maintenance but is associated with diverse diseases. Pro-angiogenic factors such as vascular endothelial growth factor (VEGF) regulate this process. Therefore, searching for treatments to regulate angiogenesis is attractive. Reports from our group showed that plant antimicrobial peptides (PAPs) PaDef from avocado and g-thionin from habanero pepper are cytotoxic on cancer cells. However, their functions as angiogenic regulators are unknown. In this work, we evaluate the effect of PaDef and g -thionin on the angiogenic processes of endothelial cell lines: bovine endothelial cells (BUVEC) and human endothelial cell line EA.hy926. The results showed: VEGF (10 ng/mL) stimulated the BUVEC (40 ± 7 %) and EA.hy926 proliferation (30 ± 9 %); however, peptides (5–500 ng/mL) reverted this effect. Besides, VEGF increased the migration of BUVEC (20 ± 8 %) and EA.hy926 (50 ± 6 %), but both PAPs (5 ng/mL) inhibited the VEGF stimulus (100 %). Furthermore, DMOG 50 µM (an inhibitor of HIF-hydroxylase) was used in BUVEC and EA.hy926 to determine the effect of hypoxia on VEGF and peptide activities. The DMOG reverted the inhibitory action of peptides (100 %), indicating that peptides act through a HIF-independent pathway. Also, the PAPs do not affect the tube formation but decrease it in EA.hy926 cells stimulated with VEGF (100 %). Additionally, docking assays showed a possible interaction between PAPs and the VEGF receptor. These results suggest that plant defensins PaDef and g -thionin are potential angiogenic modulators of the VEGF activity on endothelial cells. Fundings: CONACyT (C.B. 2016-287210) and CIC 14.1 from Universidad Michoacana de San Nicolás de Hidalgo to AOZ. EA F-R obtained a PhD Scholarship from CONACyT (743639).

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Resumen corto

Regulation of chemokines expression modulated by E6/E7 oncogenes of HPV frequently detected in cervical cancer in the Mexican population.

Fernández-Avila, L. [1,2]*, Castro-Amaya, A. [2], Jave-Suárez, L.F. [2], Aguilar-Lemarroy, A. [2]

[1]Programa de Doctorado en Ciencias Biomédicas, Centro Universitario de Ciencias de la Salud (CUCS), Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]División de Inmunología, Centro de Investigación Biomédica de Occidente (CIBO), Instituto Mexicano del Seguro Social (IMSS), Guadalajara, Jalisco, México. *E-mail: lfjave@gmail.com (L.F.J.-S.) adry.aguilar.lemarroy@gmail.com (A.A.-L)

In Mexico, Cervical Cancer (CC) is ranked in second and third place in mortality and incidence, among pathologies associated with cancer in women. Being the *Human Papillomavirus* (HPV) considered as main risk factor. The E6 and E7 HPV oncogenes have an immunomodulatory effect that is related to the induction of carcinogenic processes, through the uncontrolled expression of different molecules. Since chemokines play a crucial role in innate and adaptive immune response for HPV elimination. The aim of this study is to evaluate the expression of chemokines modulated by the E6/E7 oncogenes of frequent HPVs in CC in the Mexican population, to analyze their expression and prognostic value in the development of CC. The expression of a chemokines panel was analyzed in overexpression cell models with E6/E7 oncogenes of HPV -16, -18, -38b, -107, and -122; also, in CC-derived cell lines by next generation sequencing (NGS) and validated by qPCR. Additionally, their expression was determined using the OncoDB tool and a database of 324 cervical squamous cell carcinoma (CESC) biopsies. Finally, survival analyzes (Kaplan-Meier) were performed using databases from the repository “The Cancer Genome Atlas” (TGCA). Our results show that CXCL2 and CXCL8 are overexpressed in the presence of E6/E7 of various HPV genotypes and are overexpressed in CC-derived cell lines as well as in CESC biopsies. This behavior has an unfavorably impact in survival index in patients with CC. Thus, measuring the expression levels of CXCL2 and CXCL8 could improve the screening techniques for the diagnosis/prognosis of cervical lesions.

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Resumen corto

Trimethylglycine induces down-regulation of malignancy markers in 5-Fluorouracil chemoresistance colorectal cancer cells.

Fernández-Muñoz, K.V. [1]*, Sánchez-Barrera, C.A. [2], Medina-Reyes, D. [2], Ledesma-Torres, J.L. [2], Meraz-Ríos, M.A. [1], Figueroa-Corona, M.P. [1], Terrazas-Valdés, L.I. [2], Mendoza-Rodríguez, M.G. [2]

[1]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Unidad de Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México. *E-mail: karen.fernandez@cinvestav.mx

The 5-Fluorouracil (5-FU) is the principal chemotherapeutic agent utilized to treat colorectal cancer (CRC). Unfortunately, in advanced stages, most patients develop resistance to this chemotherapeutic. Inflammation is one of the mechanisms used by cancer cells to induce chemo-resistance. The use of alternative treatments such as Trimethylglycine (TMG) has been demonstrated to have anti-inflammatory and antitumoral effects in CRC. However, the role of TMG in the regulation of chemoresistance in colon cancer cells to 5-FU is still not thoroughly explored. In this work, we evaluated the effect of trimethylglycine in the regulation of malignancy and chemoresistance markers in colon cancer cells. Parental HCT-116 cells were stimulated with increasing doses to 5-FU until obtaining stable chemo-resistant cultures to 10 µM of 5-FU (HCT-116-R). Next, the HCT-116-R were exposed to TMG at different concentrations, and levels of malignancy markers were measured. We showed that malignancy markers SNAI1, b-catenin, and PD-L1 increase in cells resistant to 5-FU, and the TMG alternative treatment, significantly reduce their expression and correlates with restored sensitivity to 5-FU. These data point out that anti-inflammatory TMG treatment is a potential inhibitor of chemoresistance in colon cancer cells.

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Resumen corto

Analysis *in situ* of macrophages and ROS in patients with preeclampsia

Flores-Colque, J. [1,2], Calderón-Amador, J. [3], Wong-Baeza, C. [4], Flores-Romo, L. [3], Donis-Maturano, L. [5*].

[1]Instituto Nacional Ingenes, Fertilidad & Genética, CDMX, México. [2]Hospital de Ginecoobstetricia No. 3, Centro Médico Nacional "La Raza", CDMX, México. [3]Departamento de Biología Celular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX,México. [4]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. [5]Carrera Médico Cirujano de la Facultad de Estudios Superiores Iztacala, UNAM, Estado de México, México.
*E-mail: ludoma6@hotmail.com

Preeclampsia (PE) is a hypertensive disorder that involve pregnancy after the twenty weeks of gestation, with a high rate of maternal-fetal morbidity and mortality. Some mechanisms of PE have been described and they are attributed a low trophoblastic cellularity with cytokines and angiogenic factors alterations, also a systemic inflammatory response. However, there are limited studies of the immunological participants *in situ* that help us understand what happens in situ and are mainly related to the inflammatory process. Therefore, we obtained placental biopsies from healthy pregnant women (n=5) and preeclampsia pregnant patients (n=5), from the right and central portions of each placenta, evaluating the presence and distribution of CD14+ cells, CD11b+ cells, as well as the expression of reactive oxygen species (ROS), in the maternal, maternal-fetal and fetal zones of each portion of the placenta. Interestingly, we observed differences in the number of CD14+ cells in both portions of the placenta of PE patients compared to healthy donors, mainly in the fetal zone of the right portion of the placenta. Regarding CD11b+ cells, we observed an increasing tendency in patients with preeclampsia in all portions and areas analyzed. Also, we found a lower intensity of ROS was also found in the placenta of PE patients. Accordingly, we suggest that this difference between the analyzed groups could be determined by the migration of macrophages towards the different areas of the placenta, presenting an environment with low intensity of reactive oxygen species, compensating the inflammatory environment of patients with preeclampsia.

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Resumen corto

Drug-resistant tuberculosis patients have increased the frequency of CD4+ T lymphocytes displaying phenotype and cytotoxic function.

Flores-Gonzalez, J.C. [1]*, Urbán-Solano, A. [1], Ramón-Luing, L.A. [1], Chavez-Galan, L. [1]

[1]Laboratory of Integrative Immunology, Instituto Nacional de Enfermedades Respiratorias Ismael Cosio Villegas, Mexico City, Mexico. E-mail: juliofglez@gmail.com

Tuberculosis (TB) is one of the deadliest infectious diseases worldwide, and its etiological agent is Mycobacterium tuberculosis (Mtb). Although, clinically, TB has a broad spectrum, it is divided mainly into latent TB (LTB) or active TB (ATB). Persistent antigen stimulation leads to an exhausted status in the cell, characterized by the loss of functions such as cytokines production and cytotoxicity. Twenty ATB patients, divided as drug-sensitive (DS-TB) and drug-resistant (DR-TB), and ten LTB were enrolled. Phenotype and cytotoxic proteins delivered at 48 h of stimulation, with Mtb proteins and lipids, were analyzed by flow cytometry, and cytotoxic molecules were evaluated at the transcriptional level. Our data showed that compared to LTB and healthy donors, both ATB groups have a low frequency of CD8+ T cell but with high intensity of CD8 expression; moreover, the distribution of the naïve and memory subsets is altered. CD8+ cells from DR-TB patients have a low activation profile, but these patients have increased the frequency of CD4+ cells with cytotoxic capability, which are positive for FasL, CD107b, and perforin. These CD4+ cells expressed a cytotoxic profile at the transcriptional level, characterized by TBx21, KLRK1, granulysin, and granzyme B expression. Our data suggest that during ATB-induced stress immunologic that decreases the frequency of CD8+ T cells, DR-TB patients increase the frequency of cytotoxic CD4+ T cells, probably to compensate for a deficiency of classical cytotoxic T cells.

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Resumen corto

Lipopolysaccharide responsive and beige-like anchor (Lrba) protein may participate in the differentiation of IgA+ B lymphocytes and IgA-producing plasma cells.

Flores-Hermenegildo, J.M. [1,2*], Hernández-Cázares, F.J. [1], Pérez-Pérez, D. [2,3], Romero-Ramírez, H. [1], Rodríguez-Alba, J.C. [4], Kilimann, M.W. [5], López-Herrera, G. [2], Santos-Argumedo, L. [1]

[1]Departamento de Biomedicina, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV), CDMX, México. [2]Laboratorio de Inmunodeficiencias, Instituto Nacional de Pediatría (INP), CDMX, México. [3]Programa de Doctorado en Ciencias Biológicas, Universidad Nacional Autónoma de México (UNAM) CDMX, México. [4]Unidad de Citometría de Flujo, Instituto de Ciencias de la Salud, Universidad Veracruzana, Veracruz, México. [5]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany.
E-mail: mizael.flores@cinvestav.mx

Lrba was associated with human disease in patients with autoimmunity and immunodeficiency, as it regulates CTLA4 recycling in Treg cells. Lrba role in B cells remain unexplored. Patients with LRBA deficiency show hypogammaglobulinemia, while *Lrba*-deficient (*Lrba*$^{-/-}$) mice have significantly higher levels of IgA both in serum and feces. Both transforming growth factor β1 (TGFβ1) and its receptor (TGFβR) are crucial in differentiating to IgA+ B lymphocytes. The role of Lrba in differentiation to IgA+ B cells is unknown. The higher IgA production in *Lrba*$^{-/-}$ mice suggest a role of Lrba in TGFβR signaling pathway. To test this hypothesis, we evaluated IgA production, B cell differentiation and response to rTGFb in samples from non-immunized *Lrba*$^{-/-}$ mice compared with WT mice. First, we determined IgA levels in the serum and feces and corroborated that *Lrba*$^{-/-}$ mice exhibit significantly higher levels of IgA in both compartments. Then, we analyzed the small intestine and the secondary lymphoid organs (SLOs): spleen, mesenteric lymph node, and Peyer´s patches. All SLOs and the small intestine of *Lrba*$^{-/-}$ mice revealed a significantly higher number of IgA+ B lymphocytes and IgA+ plasma cells compared with WT mice. Following these results, the TGFβR pathway was evaluated. First, we measured the expression of TGFβR1 and 2. Membrane expression of TGFβR1 on B cells was similar in both *Lrba*$^{-/-}$ and WT mice, in contrast, intracellular expression of this receptor was not detected in *Lrba*$^{-/-}$ mice. Finally, we evaluated the phosphorylation of SMAD2 upon stimulation with rTGFβ. We found increased phosphorylation of SMAD2 in *Lrba*$^{-/-}$ B cells. Finally, preliminary data indicates that Lrba interacts with TGFbR. In summary, Lrba may play an essential role in the vesicular trafficking of TGFβR, which may regulate SMAD2 phosphorylation on B cells. Such of mechanism may explain the increase in the differentiation of IgA+ B lymphocytes and IgA-producing plasma cells.

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Resumen corto

Cell-permeable Bax BH3 Peptide restores Apoptosis and induces Chemosensitization in Hematologic Malignant cells

Flores-Martínez, L.F. [1]*, Magaño-Bocanegra, K.J. [1,2], Muñoz-López, P. [1,3], Becerra-Báez, E.I. [1,4], García-Nava, Y.E. [1,5], González-Franco, J. [1,6], Luria-Pérez. R. [1]

[1]Unit of Investigative Research on Oncological Diseases, Children's Hospital of Mexico Federico Gomez, Mexico City, Mexico. [2]Department of Molecular Biomedicine, Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico City, Mexico. [3]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, Mexico. [4]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [5]Faculty of Veterinary Medicine and Zootechnics, National Autonomous University of Mexico, Mexico City, Mexico. [6]Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de Mexico, Mexico.

Hematologic malignancies such as Leukemia and Lymphoma are among the leading causes of pediatric and young adult death worldwide. Although survival rates have improved with conventional treatments, 10-20% of patients develop refractory disease. Likewise, there is no optimally defined treatment for these patients, drastically reducing their chances of cure. In most cases, recurrences are due to the development of drug-resistance cancer cells. The overexpression of anti-apoptotic members of the Bcl-2 protein family, such as Bcl-XL, Bcl-2, and Mcl-1, induces this condition. We have recently shown that a cell-permeable Bak BH3 peptide may antagonize the anti-apoptotic activity of the Bcl-2 family proteins, restore apoptosis, and induce chemosensitization of Hematologic malignant cells. In the present work, we evaluated the ability of the Bak BH3 peptide coupled with the Antennapedia fusogenic peptide (Cell-permeable Bax BH3 peptide, AntBax) to restore the apoptosis and induce chemosensitization of hematologic malignancies cell lines. The bioinformatics analysis showed a corrected folding of the AntBax peptide. After peptide synthesis, we demonstrated that AntBax promotes a significant reduction in the cell viability (measured by MTT assay), increases the apoptosis (measured by caspase-3 active and TUNEL assays), and induces chemosensitization to Cisplatin treatment of the human B non-Hodgkin´s Lymphoma cell line (Ramos) and human B Acute Lymphoblastic Leukemia cell line (RS4-11). Additionally, we found that these effects do not occur in healthy cells, suggesting that this novel therapeutic approach may be a potential alternative for treating relapsed or refractory Hematologic malignancies.

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Resumen corto

The innate sensor NLRP3 is a key component required for cestode establishment

Flores-Sotelo, I.M. [1]*, Juárez-Valencia, N. [1], González, M.I. [1], Terrazas, L.I. [2], Reyes, J.L. [1]

[1]Laboratorio de Inmunología experimental y Regulación de la Inflamación Hepato-Intestinal, UBIMED, FES Iztacala, UNAM, Tlalnepantla de Baz 54090, Estado de México, México. [2]Laboratorio de Inmunoparasitología, UBIMED, FES Iztacala, UNAM, Tlalnepantla de Baz 54090, Estado de México, México. E-mail: warceli_2000@hotmail.com

The NLRP3 receptor is able to assamble inflammasome platforms to trigger inflammatory responses, however, it can also display anti-inflammatory roles. Here, we addressed the role of NLRP3 on experimentally-induced cysticercosis (*Taenia crassiceps)* whose features include immune polarization into a Th2 profile and high dependence on recruiting suppressive macrophages into peritoneal cavity. When *in vivo* infection was conducted, NLRP3 deficient mice (NLRP3-/-), turned out to be more resistant than similarly infected wild-type (WT) mice. A diminished Th-2 response (IL-4) and high levels of IL-15, a growth factor for both innate and adaptive lymphocytes were found. A dramatic decrease in peritoneum-infiltrating suppressive macrophages in NLRP3-/- mice was observed during 8 weeks of follow-up in this helminthic infection. This led us to test the hypothesis of a putative defect on NLRP3-/- macrophages. We carried out a transcriptional analysis on bone marrow-derived macrophages exposed to *Taenia*-secreted antigens and IL-4, where NLRP3-/- macrophages presented significantly reduced expression of Relm-α and PD-1 ligands (PDL1 and PDL2), markers of alternative activation and suppressive ability, respectively. Finally, we tested if the resistance exhibited by NLRP3-/- mice may be transferred through intestinal microbiota exchange. WT mice co-housed for 4 weeks with NLRP3-/- mice were significantly more resistant than WT individuals with their native microbiota. Of note, increased IL-15 was also observed in co-housed animals. Our data demonstrated that NLRP3 is a component of innate immunity required for *Taenia crassiceps* establishment, most likely contributing to macrophage polarization and controlling cytokines such as IL-15.

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Resumen corto

IL-8 Secreted by Gastric Epithelial Cells Infected with *Helicobacter pylori* CagA Positive Strains Is a Chemoattractant for Epstein-Barr Virus Infected B Lymphocytes

Fontes-Lemus, J.I. [1,2*], Domínguez-Martínez, D.A. [1], García-Regalado, A. [1], Juárez-Flores, A. [1,3], Fuentes-Pananá, E.M. [1]

[1]Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México "Federico Gómez", Ciudad de México, CDMX, México. [2]Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México 06720, Mexico. *nachopnc.15@gmail.com

Helicobacter pylori (*Hp*) and Epstein-Barr Virus (EBV) are considered the main risk factors in developing gastric cancer. Both pathogens establish life-lasting infections, and both are considered carcinogenic in humans. Different lines of evidence support that both pathogens cooperate to damage the gastric mucosa. *Hp* CagA positive virulent strains induce the gastric epithelial cells to secrete IL-8, which is a potent chemoattractant for neutrophils and one of the most important chemokines for the bacterium-induced chronic gastric inflammation. EBV is a lymphotropic virus that persists in memory B cells. The mechanism by which EBV reaches, infects and persists in the gastric epithelium is not presently understood. In this study, we assessed employing invasion assays whether *Hp* infection would facilitate the chemoattraction of EBV-infected B lymphocytes. In this work, we identified IL-8 by ELISA as a powerful chemoattractant for EBV-infected B lymphocytes, and CXCR2 as the main IL-8 receptor whose expression is induced by the EBV in infected B lymphocytes. The pharmacologic inhibition of expression and/or function of IL-8 and CXCR2 reduced the ERK1/2 and p38 MAPK signaling which was assessed by western blot and the chemoattraction of EBV-infected B lymphocytes. Here, we found that IL-8 at least partially explains the arrival of EBV-infected B lymphocytes to the gastric mucosa, and that this illustrates a mechanism of interaction between *Hp* and EBV. Funding: CONACyT "FORDECYT-PRONACES", "PRONAII-7-VIRUS Y CÁNCER" and by the Fondo de Apoyo a la investigación, HIMFG (HIM-2017-074, SSA 1403).

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Resumen corto

Antibodies against Epstein-Barr Virus as disease markers of gastric cancer.

Fontes-Lemus, J.I. [1,2]*, Zhao, I. [3], Rabkin, C.S. [3], Fuentes-Pananá, E.M. [1]

[1]Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México "Federico Gómez", Ciudad de México, CDMX, México. [2]Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [3]Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, Maryland, USA.
E-mail: nachopnc.15@gmail.com

Gastric Cancer (GC) is the fourth deadliest cancer worldwide. Due to the lack of specific early symptoms and non-invasive methods for early detection, the prognosis of GC patients is poor. GC has a well-recognized infectious etiology, with *Helicobacter pylori* and Epstein-Barr Virus (EBV) being the main associated infectious agents. Although other EBV-associated malignancies often manifest with abnormal levels of anti-EBV antibodies, it is not clear whether this is also true for GC. Potentially, these antibodies could serve as a non-invasive tool for GC screening or as markers for GC risk and provide a better understanding of the participation of EBV in the development of this neoplasm. We conducted a systematic review of articles analyzing anti-EBV serology in GC and precursor lesions. Patients were classified according to the Correa cascade lesions and whether they were positive or negative by EBER-in situ hybridization (EBVaGC and EBVnGC, respectively). We retrieved 16 articles involving 9735 subjects from 12 different countries. Higher antibody titers were observed in EBVaGC than in EBVnGC, but also in EBVnGC and GC-precursor lesions when compared with patients with mild dyspepsia or healthy controls. In all cases, the associations were predominantly with antibodies directed against lytic cycle antigens. Data support a role for EBV lytic reactivation in the development of advanced gastric lesions. However, more studies are needed to confirm these associations, particularly the association with lesions considered negative by EBER-ISH, and to establish a set of antibodies and thresholds indicative of enhanced risk to develop these lesions.

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Resumen corto

The peptides of Transferon Oral®, a Dialyzable Leukocyte Extract, are absorbed into cervical nodes after oral administration in a murine model.

Fragozo, A. [1,2,3]*, Trejo-Martínez, I. [1,2,3], Valencia-Martínez, L. [1,2], Domínguez-Bernal, K. [1,2], Pavón, L. [4], Vallejo-Castillo, L. [1,2], Pérez-Tapia, S.M. [1, 2,3]

[1]Unidad de Desarrollo e Investigación en Bioterapeuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos (LANSEIDI-FarBiotec-CONACyT), México City, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [4]Laboratorio de Psicoinmunología, Dirección de Investigaciones en Neurociencias, Instituto Nacional de Psiquiatría Ramón de la Fuente Muñiz, México City, México.
E-mail: ana.fragozo@udibi.com.mx

Transferon Oral® is a complex mixture of peptides smaller than 10 kDa. It is used to treat infections, allergies, and autoimmune diseases. Transferon Oral® reduces the production of proinflammatory cytokines such as TNF-α and IL-6 and increases the IFN-γ levels when administered by different routes, including oral. The complexity of oral Transferon Oral® limits the characterization of its Mechanism of Action (MOA) and pharmacokinetics, among other aspects. This project aimed to determine the biodistribution of Transferon oral® peptides to shed light on its Pharmacokinetics and MOA. To achieve this goal, the peptides of Transferon oral® were covalently linked to a fluorophore (Alexa Fluor-488). RP-UPLC was employed to determine the extent of labeling and free fluorophore. In biodistribution assays, the labeled peptides must maintain their biological activity. In this sense, Transferon Oral® labeled and non-labeled peptides increase the survival in an HSV-1-infection murine model. Labeled peptides were orally and subcutaneously administered in nude Foxn1nu mice, and the accumulation kinetic was determined using an in vivo fluorescence/luminescence IVIS equipment imaging system. Imaging analysis revealed that Transferon oral® peptides are absorbed in the gastrointestinal tract, biodistributed, and accumulate in the lymph nodes in both administration routes. In addition, it was observed that labeled peptides are eliminated by renal filtration within 3 hours after administration. In addition, our results suggest that the immune cells related to lymph nodes are relevant for characterizing the MOA of Transferon Oral®.

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Resumen corto

Association of serum levels of interleukins IL-1β, IL-33 and ST2 in intrauterine growth restriction and *Toxoplasma gondii* infection

Franco-De León, K. [1]*, Galván-Ramírez, M.L. [1], Camarena-Pulido, E.E. [2], Pereira-Suárez A.L. [1] Rodríguez-Pérez, L.R. [1], Barrios-Prieto, E. [3], Soto-Venegas, A. [3], Hernández-Nazara, Z.H. [4], Muñoz-Melano, J.R. [2], Luna-Rojas, Y.G. [2]

[1]Departamento de Microbiología y Patología, [4]IECD, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, 44340, México. [2]Departamento de Ginecología y Obstetricia, [3]Unidad de medicina materno fetal, Hospital Civil Juan I. Menchaca, Guadalajara, México. E-mail: karen.franco2307@alumnos.udg.mx

Toxoplasma gondii (T.gondii) is the causal agent of toxoplasmosis. It may produce severe damage in congenital infection and intrauterine growth restriction (IUGR). The prevalence of toxoplasmosis in pregnant women in Mexico is 22.8%. Exist association of interleukin IL-33 and its receptor ST2 in fetal damage, and premature delivery due to infections of various microorganisms. However, IL-33 has not been associated with congenital toxoplasmosis. IL-1β in the acute *Toxoplasma* infection was found. The aim was to analyze the association of the serum levels of IL-1β, IL-33, and ST2 in IUGR and toxoplasmosis during pregnancy. Eighty-four serum samples from pregnant women older than 26 weeks of gestation were grouped: With and without *Toxoplasma* infection and IUGR, and a control group. Anti-*T.gondii* IgG and IgM antibodies, IL-33, IL-1β and ST2 were determined using ELISA. Statistical analyses were performed using Pearson's correlation and Chi-square, Odds Ratio, 95%(CI), and ANOVA. There was a significant association of IUGR with IL-33 ($p<0.01$) and ST2 ($p<0.001$). IL33 and ST2 could be a biomarker to prognostic of IUGR.

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Resumen corto

Effect of Ge/HA scaffold couple with CpGs and MAGE A5 in antigen presents cell from C57BL/6 mice

Fuerte-Pérez, A.E. [1]*, Castell-Rodríguez, A.E. [1], Jarquín-Yáñez, K. [1], Hernández-Téllez, B. [1], Herrera-Enríquez, M.A. [1], Valencia-Escamilla, E.A. [1], García-Ortega, P. [1] ,Piñón-Zárate, G. [1]

[1]Laboratorio de Inmunoterapia e Ingeniería de Tejidos. Departamento de Biología Celular y Tisular, Facultad de Medicina, Universidad Nacional Autónoma de México, México CDMX. E-mail: fuerte_11@ciencias.unam.mx.

Nowadays traditional immunotherapies against cancer have induced side-effects and limited success. By contrast, the immunotherapy based on the use of scaffolds has evidenced better effects in pre-clinical studies. Scaffolds may be constructed with biomaterials such as, Gelatin (Ge) and hyaluronic acid (HA), which are involved in promoting leukocyte adhesion and migration. In addition, immunomodulators as CpG can be couple to scaffolds to support activation of dendritic cells (DC) and macrophages. Also, to mediate a specific immune response, MAGE antigen was used. So, in this research we studied the effect of a GE/HA scaffold couple with MAGE A5 and CpGs in MHCII+ CD11C+ DC and MHCII+ F4/80+ macrophages. For this proposal splenocytes from C57BL/6 mice were treated with Ge/HA scaffolds, then the percentage of DC and macrophages, and the expression of costimulatory molecules CD40, CD80 and CD86 were analyzed by flow cytometry. For *in vivo* experiment, C57BL/6 mice were inoculated with hydrogels made from the GE/HA scaffold couple to MAGE or CpGs, 21 days later mice were challenged with B16-F10 melanoma cells. As a result, significant differences in the percentage of macrophages with GE/HA+CpGs was found. While levels of costimulatory molecules were higher in cell treated with GE/HA+ MAGE A5. In the survival analysis mice with melanoma treated with GE/HA+ MAGE or CpGs showed increased survival and decreased the tumor growth rate. In conclusion, GE/HA scaffold couple with CpGs or MAGE A5 mediated the activation of DC and macrophages and improved the survival of mice with melanoma.

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Resumen corto

Resistance to anti PD-1 immunotherapy explained by the presence of progenitor-exhausted CD8 T cells with impaired function and quiescent cancer cells.

Gajón, J.A. [1,2]*, Juárez-Flores, A. [3], Fuentes-Panana, E. [3]
Bonifaz, L.C. [4]

[1]Unidad de Investigación Médica en Inmunoquímica, Hospital de especialidades "Bernardo Sepúlveda", Centro Médico Nacional Siglo XXI, IMSS, CDMX, México. [2] Posgrado en Ciencias Bioquímicas, UNAM, CDMX, México. [3]Hospital infantil de México Federico Gómez, CDMX, México [4]Coordinacion de Investigación en Salud, Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, México. E-mail: julian.argenis.23@gmail.com

Immunotherapy based on immune checkpoint blockade has revolutionized modern oncology, leading to an improvement in the survival and life quality of patients with advanced cancer, including melanoma. However, a substantial fraction of treated patients does not response to immunotherapy by unknown mechanisms. Recent approaches have suggested that impairment of the functional capacity of CD8 T cells and apoptosis resistance could explain this unresponsiveness. Nevertheless, these approximations have not enclosed Immunotherapy resistance completely, due to the scarcity of integral approach models. Here we describe the isolation and expansion of an PD-1-resistant murine melanoma cell line (R1) which induces an accumulation of progenitor-exhausted CD8 T cells with impaired function and proliferation. This was observed in both tumor-infiltrating lymphocytes and CD8 T cells co-cultured with tumor spheroids. Moreover, differential phenotype (non-replicative subset PD-1- and PD-L1-) was observed by spectral flow cytometry in R1 compared with its parental cell line MO4. In addition, confocal fluorescence microscopy revealed changes in the expression of WNT3a and WNT5a ligands of WNT/ catenin pathway, along with ALDH1 within the tumor, associated with the phenotype of exhausted CD8 T cells. Lastly, an extended analysis of TCGA and anti-PD-1 melanoma-treated databases suggested that tumors enriched with cancer stem cell signature were negatively associated with overall survival and response to PD-1 immunotherapy in melanoma patients. These results suggest that both the phenotype of exhausted CD8 T cells and quiescent cancer cells explain PD-1 immunotherapy resistance.

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Resumen corto

Innate Immune training on dendritic cells enhances CD8 T cell anti-tumor function

Gajón, J.A. [1,2]*, Tepale-Segura, A. [1], Castro-Escamilla, O. [3], Bonifaz, L.C. [3]

[1]Unidad de Investigación Médica en Inmunoquímica, Hospital de especialidades "Bernardo Sepúlveda", Centro Médico Nacional Siglo XXI, IMSS, CDMX, México. [2]Posgrado en Ciencias Bioquímicas, UNAM, CDMX, México. [3]Coordinacion de Investigación en Salud, Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, México.
E-mail: julian.argenis.23@gmail.com

Innate immune training is a metabolic, functional, and epigenetic reprogramming of innate immune cells described in monocytes and macrophages. Different studies have demonstrated that this imprinting reaches hematopoietic precursors in the bone marrow to sustain a memory-like phenotype. However, it is not clear whether this imprinting can be lineage and stimuli restricted. It has been demonstrated that dendritic cells (DCs) acquire training features leaving the question about the functional consequences in the adaptive and protective immune response. In this work we described the induction of innate immune training on murine classic and inflammatory DCs, using the non-toxic beta sub-unit of cholera toxin (CTB). CTB-trained dendritic cells exhibited an increased expression of TNFα and a metabolic reprogramming indicated by the expression of lactate dehydrogenase (LDH). Moreover, we found that innate immune training on DCs increased its infiltration in the inoculation site and activated recruitment of DCs precursors in vivo. Interestingly trained DCs showed a highly costimulatory phenotype. Remarkably, we demonstrated a functional impact of innate immune training on DCs by challenging CTB-trained mice with inoculation of melanoma cells. The protection against melanoma challenge was associated to a highly costimulatory tumor infiltrating DCs (CD86+) and highly functional and proliferative exhausted CD8 T cells (Ki67+, IFNγ+, GZMB+). These results indicate that innate immune training on DCs has an impact in adaptive immune response with potential as an immunotherapeutic approach in tumor growth control.

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Resumen corto

Tγδ cells participation in the development of a mouse model of lupus induced by lipidic particles

Galarce-Sosa, E.I. [1]*, Barrera-Aveleida, G.B. [1],
Sotelo-Rodríguez, A. [1], Isidro-Magallán, J.E. [1], Baeza-Ramírez, I. [1],
Reséndiz-Mora, C.A. [1] Wong-Baeza, C. [1]

[1]Laboratorios de Biomembranas y de Enzimología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México.E-mail: ivan.gal27@hotmail.com

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease with a variable clinical phenotype, where the mechanisms that led to its development are not yet fully understood. In our research group, we have proposed that SLE and other autoimmune diseases are related to cell membrane alterations, where stable lipidic particles induce the formation of autoantibodies. Since Tγδ cells can respond to lipid antigens and participate in the pathogenesis of SLE by secreting certain cytokines. In the present work we studied the participation of Tγδ cells in the development of lupus in mice (BALB/c) induced by lipidic particles. Tγδ cells from spleen and mesenteric lymph nodes were analyzed by flow cytometry to evaluate their activation, cell cycle, mitochondria type and cytokine production after 5, 10 and 15 days of the administration of stable lipidic particles. A statistically significant increase in the absolute number of Tγδ cells from spleen was detected in mice administered with liposomes bearing lipidic particles compared to those that receive saline solution. This increase was also found in the production of IL-4 by Tγδ cells from spleen and mesenteric lymph nodes, and IFNγ by Tγδ cells from spleen. We also found that a higher percentage of Tγδ cells from mice administered with lipidic particles were in the G1 stage of the cell cycle and presented fissioned mitochondria. Our data suggest that Tγδ cells are involved in the processes that allow the establishment of the adaptive response and are possibly involved in the production of lipid antibodies.

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Resumen corto

Effects of glycomacropeptide on biomarkers of atopic dermatitis in human keratinocytes *in vitro*

Gallegos-Alcalá, P. [1], Jiménez, M. [1*], Cervantes-García, D. [1,2], Córdova-Dávalos, L.E. [1] Salinas, E. [1]

[1]Departamento de Microbiología, Universidad Autónoma de Aguascalientes, Aguascalientes, Ags, México. [2]Consejo Nacional de Ciencia y Tecnología, Ciudad de México, CDMX, México. E-mail: mariela.jimwenez@edu.uaa.mx

Atopic dermatitis (AD) is an allergic skin condition present in 15 to 20% of the world´s population. The keratinocytes participate actively in the onset and persistence of the inflammation, pruritus, and the altered wound regeneration, typical signs of AD. The glycomacropeptide (GMP) is a bioactive peptide derived from milk κ-casein that is generated during the cheese-making process or gastric digestion. Experimental models of AD have shown that orally administered GMP decreases the immune response and pruritus related to AD. The aim of this study was to determine the effect of GMP on the expression of genes related to triggering inflammation and pruritus in an *in vitro* AD model of HaCaT keratinocytes induced by TNF-α and IFN-γ. The proliferative and migratory response of HaCaT cells treated with GMP was also evaluated. GMP significantly decreased *TSLP*, *IL33*, *TARC*, *MDC*, and *NGF* gene expression compared to control condition in the AD model of keratinocytes, while that of *cGRP* was enhanced. Under the AD microenvironment, GMP at 25 mg/mL stimulated the proliferation of HaCaT cells, while at concentrations of 0.01 and 0.1 mg/mL promoted keratinocyte migration. In conclusion, GMP regulates gene expression on human keratinocytes under the AD-type microenvironment, in addition to stimulating wound closure. These new findings strengthen the beneficial effects of GMP reported *in vivo* and suggest its potential for topical application. Funding: Autonomous University of Aguascalientes grant PIBB20-1; CONACyT doctoral fellowship 713727.

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Resumen corto

FK13 peptide is a potent microbicide and induces an increased IL6 cytokine in a murine model of trichomoniasis

García- Segoviano, E. [1]*, Olmos- Ortiz, L.M. [1], Alva- Murillo, P.N. [1].
Cuéllar- Mata, P. [1]

[1]Laboratorio de Inmunomicrobiología, Departamento de Biología, Universidad de Guanajuato Guanajuato, Guanajuato, Mexico. E-mail: mata@ugto.mx

T. vaginalis (Tv) is the etiologic agent of trichomoniasis, the most prevalent sexual non-viral disease. Metronidazole (MTZ) and tinidazole are the conventional treatment, nevertheless these drugs are toxic and not well tolerated by patients. Also, it has been detected resistant strains to these drugs. For these reasons it is important to investigate new possible treatments. The use of antimicrobial peptides and derivatives has been proposed as a novel treatment because they can have both microbicidal and immunomodulatory effect against infectious diseases. In this work we evaluated both effects of FK13 (50 µM), an antimicrobial peptide derivative of LL-37, unique known human cationic peptide, in a murine model of trichomoniasis. This derivative showed a trichomonacide effect both in vitro and in vivo model; furthermore, a better trichomonacide effect was observed when the peptide was combined with a low dose of MTZ (4 nM). Additionally, higher doses of the peptide (100 µM) did not present cytotoxic effect on Fibroblasts BJ and differentiated THP-1 monocytes, as observed using LIVE/DEAD kit, suggesting a possible treatment for human. Finally, the parasite survival was decreased, and an IL-6 increased level was detected by ELISA when infected mice were treated with FK13. These results suggest that this peptide has trichomonacide effect and induces a proinflammatory profile which could contribute to infection outcome.

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Resumen corto

Immunological changes in the pattern of exhausted CD8+ T cells in response to treatment in patients with cervical cancer

García-Barrientos, N.T. [1]*, Güitrón-Aviña, M.S. [1], Solórzano-Ibarra. F [1], Rojas-Díaz, J.M. [1], Haramati, J. [2], Cruz-Ramos, J.A. [3], Bustos-Rodríguez, F.J. [4], Vázquez-Limón, J.C. [5], Ayala-Rojas, I.J. [3], Gálvez-Toro, L. [5], Ortiz-Lazareno, P.C. [6], Urciaga-Gutiérrez, [1], Ceja Flores, F.J. [2], Del Toro-Arreola. S [1,7]

[1]Instituto de Investigación en Enfermedades Crónico-Degenerativas, Departamento de Biología Molecular y Genómica, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Laboratorio de Inmunobiología, Departamento de Biología Celular y Molecular, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Guadalajara, Jalisco, Mexico, [3]Instituto Jalisciense de Cancerología, Guadalajara, Jalisco, México, [4]Nuevo Hospital Civil de Guadalajara "Dr. Juan I. Menchaca", Guadalajara, Jalisco, México, [5]Antiguo Hospital Civil de Guadalajara "Fray Antonio Alcalde", Guadalajara, Jalisco, México, [6]División de Inmunología, Centro de Investigación Biomédica de Occidente, Instituto Mexicano del Seguro Social, Guadalajara, Jalisco, México. [7]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México.
*E-mail: dra.nadia.garcia27@gmail.com ; susana.darreola@academicos.udg.mx

Cervical cancer is the second cause of cancer-associated death in mexican women. The risk of recurrence is between 27 to 70% according to the clinical stage with conventional treatment. Therefore, it is important to identify factors that help to predict responses to available therapies.

Tumors can evade the immune system by inhibiting the function of cytotoxic lymphocytes. An increase in the expression of checkpoint inhibitor molecules in CD8+ T lymphocytes has been reported and associated with an exhausted immunophenotype in these cells. This project aims to evaluate the changes in the expression of inhibitory immune checkpoint receptors in CD8+ T lymphocytes in women diagnosed with cervical cancer throughout conventional treatment.

Through flow cytometry, we evaluated the presence of inhibitory checkpoints PD-1, TIGIT, TIM-3, LAG-3, NKG2A, BTLA in CD8+ T lymphocytes from peripheral blood samples and tumor tissue from women with cervical cancer and evaluated their relationship with the response to treatment.

In a cohort of 19 patients with cervical cancer (compared against 10 age-matched controls), the expression of all 6 inhibitory immune checkpoints in CD8+ T lymphocytes in peripheral blood samples was increased, with PD-1, TIM-3 and BTLA significantly increased. PD-1 was the most significantly increased checkpoint marker. When the co-expression phenotype of PD-1+ other checkpoint+ was evaluated, we found significant increases in all double positive populations. The most notable increase was in PD-1+TIM3+ CD8+ T cells, where the increase in cancer was over 300%. This unique cell population may be an important marker to predict patient therapeutic response.

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Resumen corto

Molecular Mechanisms Associated with FOXP3 Overexpression in Non-Tumorigenic Keratinocytes and Cervical Cancer-Derived Cell Lines

García-Becerra, N. [1,2], Águila-Estrada, M.[1,2] , Palafox-Mariscal, L.A. [1,2], Aguilar-Lemarroy, A *[1,2], Jave-Suárez, L.F. *[1,2]

[1]División de Inmunología, Centro de Investigación Biomédica de Occidente, Instituto Mexicano del Seguro Social, Guadalajara, México. [2]Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, México. lfjave@gmail.com

Cervical cancer (CC) is the cancer-related disease with the second highest prevalence and mortality in Mexico. In CC, it has been identified that the expression of the transcriptional factor FOXP3 increases alongside the lesion progression, for this reason, is of our interest to deep into the role in CC. To identify the derived effects of the overexpression of FOXP3 in a cellular model of non-tumorigenic keratinocytes.

The FOXP3 expression of CC-derived cell lines was evaluated by qPCR. The open reading frame of FOXP3 was cloned into the lentiviral vector pLVX and it was sequenced by Sanger method. For the establishment of the overexpression model of FOXP3, the HaCaT cell lines were used. Subsequently, RNAseq analysis was done to identify differentially expressed genes (DEGs) and biological processes modulated by FOXP3. For functional analysis, proliferation was evaluated by impedance detection, cell division rate by flow cytometry and migratory capacity by wound healing assay.

We identified that overexpression of FOXP3 is not induced by HPV infection. Additionally, we assessed that Δ2Δ7 variant is expressed in SiHa, a CC-derived cell line, this variant is identified as protumoral in other cancer types. From the RNAseq data, 50 DEGs were identified with multiple genes related to protumoral and immunological processes; the enrichment analysis allowed us to identify biological pathways of the same processes, protumoral and immunological. Finally, the functional assays demonstrated that overexpression of FOXP3Δ2Δ7 promotes proliferation, cell division and migration.

Keywords: FOXP3, cervical cancer, RNAseq, enrichment analysis.

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Resumen corto

Patients recovered from severe COVID-19 showed impaired cytokine production and premature senescence in monocytes

García-de la Rosa, M.T. *[1,2], Miranda-Cruz, P.E. [1], Torres-Flores, A. [1,2], Juárez-Palacios, J.E. [1,2], Basilio-Gálvez, E. [2], Cérbulo-Vázquez, A. [3], Ferat-Osorio, E.A. [1], López-Macías, C.R. [1], Wong-Baeza, M.I. [2], Arriaga-Pizano, L.A. [1]

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Ciudad de México, CDMX, México. [2]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Hospital General de México, Dr. Eduardo Liceaga, Ciudad de México, CDMX, México. garciarmt13@gmail.com

Severe COVID-19 induce systemic acute inflammation in patients, implying acute respiratory distress syndrome, septic shock or multiple organ system failure similar to sepsis. Recovered patients of sepsis develop immunosenescence, which is defined as the decrease of the immune response. Senescent cells present morphological, phenotypic, and functional changes, that can be caused also by viruses or systemic inflammation due to the release of DAMPs and interferons. We used immunophenotyping and functional assays (evaluated by multiparametric flow cytometry) to determine if monocytes from recovered COVID-19 patients develop a premature senescence phenotype, compared with a control group (persons not previously hospitalized because COVID-19, but with the same co-morbidities that recovered group). We analyzed 28 patients and 14 controls. The proportion of monocytes CXCR2+ are diminished(52±33vs82±8, p=0.0164), p21+ is increased(10±20vs1±1, p=0.0440 p). We also found in recovered COVID-19 patients an increase in the relative expression of CCR2(4012±1251vs788±215, p<0.0001), p16(1248±715vs453±329, p=0.0005), p21(873±494vs519±323, p=0.0117) and a decreased in the TLR-1 expression(1313±1609vs2449±760, p=0.0003). In contrast, cells functionality, phagocytosis and ROS production, were not modified among the groups analyzed. Nevertheless, in basal conditions, monocytes from recovered patients showed increased production of TNF-α compared with controls (58±9vs18±10, p=0.0179). In comparison with the monocytes from recovered patients showed diminished IL-6 production when stimulated with LPS (10±5vs60±22, p<0.0001). In addition, the percentage of monocytes IL-8+ after Pam-3Cys stimulation was higher in the recovered patients (66±31vs33±16, p=0.0163). Our data suggest that the systemic inflammation due to severe COVID-19 requiring hospitalization, induces a premature senescence phenotype in monocytes and compromises their cytokine production capacity.

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Resumen corto

Regulation of moderate aerobic exercise in perialveolar bone loss and its association with colonic bacterial populations

García-Hernández, A.L. [1], Solís-Suárez, D.L. [1], Drago-Serrano, M.E. [2], Guzmán-Mejía, F. [2], Aguilar-González, J.E. [3], Herrera-Uriostegui, M. [3], Godínez-Victoria, M. [3]*

[1]Lab. de Investigacion Odontológica, Facultad de Estudios Superiores (FES)-Iztacala-UNAM.Estado de México, México. [2]Unidad de Sistemas Biológicos, Universidad Autónoma Metropolitana, Campus Xochimilco, CdMx, México. [3]Lab. de Citofluorometría de Flujo y de Investigación en Inmunología Clínica, Escuela Superior de Medicina, Instituto Politécnico Nacional, CdMx, México. *e-mail: mgodinezv@ipn.mx

Alterations in oral health are associated with a lower quality of life in elderly. Results of our working group have shown that moderate aerobic exercise (MAE) improves bone quality by increasing the microarchitecture complexity and decreased bone fragility through the promotion of an antioxidative and anti-inflammatory state. The aim of this study was to evaluate the effect of MAE on perialveolar bone loss (PBL) and to associate PBL with colonic bacterial populations, in aging.

BALB/c male mice (n=10/group) underwent a moderate exercise protocol from 3 to 12 months of age. Age-match sedentary mice were included as a control group. Fecal samples were collected before sacrifice to count colony forming units (CFU) of lactobacilli, bifidobacterial and aerobic bacteria. The upper maxilla was dissected for morphometric and densitometric analysis by computerized microtomography (μCT). Statistical differences were evaluated by *t*-students with P<0.05.

In elderly mice, MAE decreased aging-induced vertical bone loss in several points evaluated. Furthermore, MAE increased the bone volume and area, and decreased the trabecular separation evaluated by μCT. Also, MAE increased CFU of lactobacilli, bifidobacterial and aerobic bacteria in feces. Several parameters evaluated by μCT were associated with measurements of lingual vertical bone ($p<0.05$) and bone area was associated to CFU of lactobacilli ($p<0.0135$).

In conclusion, MAE increased maxillary bone quality in elderly mice. In addition, our results highlight the importance of gut homeostasis and the impact of exercise on the regulation of bone aging.

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Resumen corto

Cell-permeable Bak BH3 Peptide Released from the Surface of Attenuated *Salmonella* Promotes Chemosensitization of the Non-Hodgkin´s Lymphoma cells

García-Nava, Y.E. *[1,2], Flores-Martínez, L.F. [1], Muñoz-López, P. [1,3], Becerra-Báez, E.I. [1,4], Magaño-Bocanegra, K.J. [1,5], González-Franco, J. [1,6], Luria-Pérez, R. [1].

[1]Unit of Investigative Research on Oncological Diseases, Children's Hospital of Mexico Federico Gomez, Mexico City, Mexico.[2] Faculty of Veterinary Medicine and Zootechnics, National Autonomous University of Mexico, Mexico City, Mexico. [3]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [4]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [5]Department of Molecular Biomedicine, Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico City, Mexico. [6]Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, México.
E-mail: yenny.gn97@gmail.com

Drug resistance is a significant impediment to the success of Lymphoma treatments. The overexpression of anti-apoptotic members of the Bcl-2 protein family, such as Bcl-$_{XL}$, Bcl-2, and Mcl-1, can promote this condition. We have recently shown that a cell-permeable Bak BH3 peptide may antagonize the anti-apoptotic activity of the Bcl-2 family proteins, restore apoptosis, and induce chemosensitization of Hematologic malignant cells. In this study, we investigated the feasibility of releasing this peptide into the tumor cells using live attenuated *Salmonella enterica*, which has proven to have an excellent tropism for tumor tissue and successful potential as a delivery system of heterologous molecules. Thus, using DNA recombinant technology, we expressed and released the cell-permeable Bak BH3 peptide from the surface of *Salmonella enterica* serovar Typhimurium SL3261 through the MisL autotransporter system. Our *in vitro* assays, interacting the recombinant bacteria with Ramos cells (a human B Non-Hodgkin´s Lymphoma cell line) in the presence or absence of Vincristine as chemotherapy, demonstrated that the recombinant bacterium that released the cell-permeable Bak peptide decreased significantly the viability (measured by trypan blue assay), increased the apoptosis (measured by caspase-3 active), and induces successful chemosensitization of the Non-Hodgkin Lymphoma cells. Overall, our results documented an attractive approach to improve patient outcomes with relapsed or refractory non-Hodgkin´s Lymphoma cells. Funding: CONACYT CB-2013-01-222446, Fondos Federales (HIM-2015-049 SSA 1217, HIM-2019-061 SSA 1594, HIM-2021-056 SSA 1756).

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Resumen corto

Computational modeling of the non-covalent binding between metabolites secreted by the human microbiota and non-conventional T cell receptors

García-Núñez, A.A. [1*], Castrejón-Flores, J.L. [1],
Hernández-Jaimes, O.A. [1], Gómez-Castro, C.Z.[2].

[1]Laboratorio de Biología Molecular y Cultivo Celular, Unidad Profesional Interdisciplinaria de Biotecnología-Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Química Teórica y Computacional, Universidad Autónoma del Estado de Hidalgo, Hidalgo, México.
agarcian1301@alumno.ipn.mx

MAIT cells are a subset of non-conventional T cells with a unique receptor capable of recognizing low molecular weight molecules presented by the MR1-antigen complex. This quality allows MR1 to directly regulate the activation of MAIT cells. Several bacterial antigens and drugs that are recognized by MAIT cells have been described, including 5-OP-RU, Diclofenac (DCF), and its metabolite 5-OH-DCF, respectively. However, it was recently reported that the DB28 antigen sequesters MR1 in the cell membrane, preventing its expression, and it is still unknown if other metabolites can be presented by MR1 or sequester MR1. To identify potential new metabolites that could activate or inhibit MAIT cells, we are processing a virtual screening of a database of 24,000 microbiome metabolites using the crystals of the TCR-antigen-MR1 complexes DB28 (PDB:6PVC) and Diclofenac (PDB:5U1R). Until now, the screening identified two possible metabolites. The molecular couplings were assessed using binding free energy (values from -7 to -10 Kcal/mol), interaction distance to the center of mass (values > 4 Å) and ligand receptor contact distance (values from 0.7 to 0.99) consensus scores. The leading candidate with reference to DB28 was 3-Hydroxykynurenine, an intermediate of the mevalonate pathway that inhibits T cell activation. On the other hand, the main candidate with reference to DCF was Chanoclavine II, an intermediate in the synthesis of ergolines. Further research into the role of microbiome metabolites in regulating MAIT cells could help us better understand the importance of the microbiome in maintaining homeostasis.

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Resumen corto

Prolactin inhibits and stimulates the inflammatory response of joint tissues in a cytokine-dependent manner

García-Rodrigo, J.F. *, Ortiz, G., Martínez-Díaz, O.F.,
Ruiz-Herrera, X., Ledesma-Colunga, M.G.,
Martínez-de la Escalera. G., Clapp, C.

Instituto de Neurobiología, Universidad Nacional Autónoma de México (UNAM), Campus Juriquilla, Querétaro, México. jose.rodrigo.garcia93@gmail.com

The close association between rheumatoid arthritis (RA), sex, reproductive state, and stress have long linked the hormone prolactin (PRL) to disease progression. However, this role is questioned by the fact that PRL has both pro-inflammatory and anti-inflammatory outcomes in RA. Here, we show that PRL modifies in an opposite manner the inflammatory action of IL-1β and TNF-α in cultures of mouse synovial fibroblasts (SF). SF treated with IL-1β or TNF-α upregulated the metabolic activity and the expression of proinflammatory genes via the activation of NF-κB. However, IL-1β increased and TNF-α decreased the levels of the long PRL receptor (PRLR) and this differential regulation associated with dual effects of PRL. PRL decreased the proinflammatory action and activation of NF-κB in response to IL-1β, but increased the inflammatory response and NF-κB signaling stimulated by TNF-α. The double-faceted regulatory role of PRL against the two cytokines also manifested *in vivo*. IL-1β or TNF-α with or without PRL were injected into the intra-articular space of the knee joint of mice and, joint inflammation was monitored through the expression of pro-inflammatory genes. Both IL-1β and TNF-α upregulated the joint expression of *Il1b* and *Inos*, and PRL inhibited the action of IL-1β but not that of TNF-α. We conclude that the outcome of PRL action on joint inflammation is dependent on its interaction with specific proinflammatory cytokines, the level of the PRLR, and the activation of NF-κB. Opposite effects of PRL may help balance joint inflammation in RA and understanding their mechanisms could provide insights into the pathophysiology of RA. Supported by UNAM-PAPIIT IN202321.

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Resumen corto

Association of the DHCR7/NADSYN1 (rs3794060) polymorphism with serum levels of calcidiol, calcitriol and genetic risk for rheumatoid arthritis

García-Suarez, M. *[1,2]; Rivera-Escoto, M. [1,2];Campos-López, B. [1,2]; Ruiz-Ballesteros, A. [1,2]; Pesqueda-Cendejas, K. [1, 2], Parra-Rojas, I.[1 3]; Montoya-Buelna, M. [1, 4], Cerpa-Cruz, S. [5]; De la Cruz-Mosso, U. [1, 2,]

[1]Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [2]Instituto de Neurociencias Traslacionales, Departamento de Neurociencias, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [3]Laboratorio de Investigación en Obesidad y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, Chilpancingo de los Bravo 39087, Guerrero, Mexico. [4]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [5]Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara 44280, Jalisco, Mexico. Correspondence: Ulises de la Cruz-Mosso, email: ulises_cdm@hotmail.com or ulises.mosso@academicos.udg.mx

Rheumatoid arthritis (RA) is an autoimmune disease that have been associated with alterations in vitamin D metabolites such as calcidiol and calcitriol. In RA patients vitamin D levels correlates negatively with clinical disease activity. 80% of vitamin D is synthetized in the skin by the DHCR7 enzyme. However, DHCR7 also generates cholesterol. Polymorphisms in DHCR7 gene (DHCR7/NADSYN) have been associated with mRNA alterations. Such variants could favor cholesterol synthesis instead of vitamin D and generate hypovitaminosis D. The aim of the study was to determinate the association of the DHCR7/NADSYN1 (rs3794060) polymorphism with calcidiol, calcitriol serum levels and genetic risk for RA.

A cross-sectional study was performed in 104 RA patients and 196 control subjects (CS). Calcidiol and calcitriol levels were measured by ELISA. Allelic discrimination with TaqMan® was used for DHCR7/NADSYN genotyping.

DHCR7/NADSYN1 (rs3794060) polymorphism was not associated with genetic risk for RA.RA patients carriers of the CC genotype of DHCR7/NADSYN had higher clinical disease activity score. CS carriers of CT genotype of DHCR7/NADSYN had lower calcidiol levels and higher frequency of vitamin D deficiency compared to CS carriers of CC and TT genotypes.

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Resumen corto

Bioinformatic analysis of epitopes from SARS-CoV-2 proteins and their potential cross-reactivity with emerging variants and other human coronaviruses

García-Valeriano, M.G. [1], Pacheco-Olvera, D.L. [1], Saint Remy-Hernández, S. *[1], Rivera-Hernández, T. [1,2], López-Macías, C. [1]

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades del Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, CDMX, México. [2]Consejo Nacional de Ciencia y Tecnología, Ciudad de México, CDMX, México. magvaler@ciencias.unam.mx

Today, we are still in the battle to stop the pandemic caused by SARS-CoV-2, responsible for more than 6 million deaths worldwide. The virus is constantly evolving, and the World Health Organization (WHO) currently recognizes five variants of concern (VOC) for SARS-CoV-2 (Alpha, Beta, Gamma, Delta and Omicron) and seven variants of interest (Epsilon, Eta, Iota, Kappa, Lambda, Theta and Zeta), capable of evading infection and vaccine mediated immunity. These numbers are likely to increase in the future as long as the virus continues to actively circulate. Spike (S), membrane (M) and nucleocapsid (N) proteins are some of the most studied protein targets because they are the main immunogens present in SARS-CoV-2. The aim of the study was to identify potential epitopes of SARS-CoV-2 and other medically relevant coronaviruses. Experimental evidence suggests that cross-reactive responses between coronaviruses are present among the population; however, little information is available on the epitopes that might drive these responses. Using different bioinformatics tools to i) Identify new and compile previously reported B and T cell epitopes from SARS-CoV-2 S, M and N proteins; ii) Determine the mutations in S protein from VOC that affect B and T cell epitopes, and iii) Identify cross reactive epitopes with coronaviruses relevant to human health.

The epitopes identified here may contribute to augmenting the protective response to SARS-CoV-2 and its variants induced by infection and/or vaccination and may also be used for the rational design of novel broad-spectrum coronavirus vaccines.

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Resumen corto

TNF-alpha on LT CD8 memory cells in response to *Mycobacterium tuberculosis* antigens

García-Vargas, I.[1] Sandoval-Montes, C. [1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. csandovalm@ipn.mx

TNF-alpha is a potent pro-inflammatory cytokine that can stimulate cell differentiation and proliferation, induces the release of nitric oxide which causes vasodilation and increased vascular permeability, which leads to the recruitment of inflammatory cells, immunoglobulins and complement. The production of pro-inflammatory cytokines is important for the activation of T cells when are infected with *Mycobacterium tuberculosis*, IFN-gamma and TNF-alpha are important for this function. The LT CD8 cells specific for *Mycobacterium tuberculosis* produce TNF-alpha in tuberculosis patients. After BCG vaccination or infection, LT CD8 cells are differentiated on memory T cells. In this study, TNF-alpha production was measured in healthy people vaccinated with BCG by flow cytometry in LT CD8 cells after activation with *Mycobacterium tuberculosis* extracts. TNF-alpha was expressed higher percentage of memory LT CD8 than naïve LT CD8 cells. Therefore, TNF-alpha produced by LT CD8 from memory could mediate the serious immunopathology associated with the infection of this bacterium; and memory-specific antigen T cells will be protecting against a new *Mycobacterium tuberculosis* infection for years.

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Resumen corto

19n01, a broadly neutralizing antibody against Omicron BA.1, BA.2, BA.4/5, and other SARS-CoV-2 variants of concern

García-Vega, M. [1], Melgoza-González, E.A. [1], Hernández-Valenzuela, S. [1], Hinojosa-Trujillo, D. [1], Reséndiz-Sandoval, M. [1], Llamas-Covarrubias, M.A. [2], Loza-Lopez, M. [3], Valenzuela, O. [4], Soto-Gaxiola, A. [5], Hernández-Oñate, M.A. [6], Mata-Haro, V. [7], Cassaniti, I. [8], Camilla-Sammartino, J. [8], Ferrari, A. [8], Simonelli, L. [9], Pedotti, M. [9], Sun, R. [10], Zuo, F. [10], Baldanti, F. [8,11], Varani, L. [9], Marcotte, H. [10], Pan-Hammarström, Q. [10], Hernández, J.[1]*

[1]Laboratorio de Inmunología, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. [2]Research Institute for Microbial Diseases, Osaka University, 3-1 Yamadaoka, Suita, Japan. [3]Laboratory of Functional Analysis in silico, The University of Tokyo, Shirokanedai, Tokyo, Japan. [4]Departamento de Ciencias Químico Biológicas, División de Ciencias de la Salud, Universidad de Sonora, Mexico. [5]Hospital General del Estado de Sonora "Dr. Ernesto Ramos Bours", Secretaria de Salud del Estado de Sonora, Mexico. [6]Laboratorio de Fisiología y Biología Molecular de Plantas, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. [7]Laboratorio de Microbiología e Inmunología, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. [8]Microbiology and Virology Department, Fondazione IRCCS Policlinico San Matteo, Pavia, Italy. [9]Institute for Research in Biomedicine, Università della Svizzera italiana (USI), Bellinzona, Switzerland. [10]Division of Immunology, Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Stockholm, Sweden. [11]Department of Clinical, Surgical, Diagnostics and Pediatric Sciences, University of Pavia, Pavia, Italy. jhdez@ciad.mx

Continued exploration for new, potent, and broad antibodies is needed to develop suitable treatments for the emerging variants of SARS-CoV-2. This study reports the isolation and characterization of a human monoclonal antibody (mAb) called 19n01. This mAb was isolated by using single-cell RNAseq of B cells from donors infected with the ancestral strain. This mAb possesses a potent and broad capacity to bind and neutralize all previously circulating variants of concern (VOCs), including Omicron sublineages BA.1, BA.2, and BA.4/5. The pseudovirus neutralization assay revealed robust neutralization capacity against the G614 strain, BA.1, BA.2, and BA.4/5, with IC50 values ranging from 0.0035 to 0.0164 ug/mL. The microneutralization assay using the G614 strain and VOCs demonstrated IC50 values of 0.013 to 0.267 ug/mL. Biophysical and structural analysis showed that 19n01 cross-competes with ACE2 binding to the RBD and the kinetic parameters confirmed the high affinity against the Omicron sublineages (KD of 61 and 30 nM for BA.2 and BA.4/5, respectively). These results suggest that the 19n01 is a remarkably potent and broadly reactive mAb. Funding: CONACyT grant number 312677.

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Resumen corto

Mycobacterium tuberculosis infects human primary adipocytes and induces extracellular vesicles and of IL-8 and TNF-α production

Garduño-Torres, A.E. *[1,2], Suárez-Cuenca, J.A. [3], Montoya-Ramírez, J. [4], Guzmán-Beltrán, S. [2], Gutiérrez-González, L.H. [5] and González-Hernández, Y. [2]

[1]Departamento de Investigación en Microbiología, Instituto Nacional de Enfermedades Respiratorias, Ciudad de México, México. [2]Universidad Nacional Autónoma de México, Ciudad de México. [3]Laboratorio de Metabolismo Experimental, Centro Médico Nacional 20 de Noviembre, ISSSTE, Ciudad de México, México. [4]Servicio de Cirugía Bariátrica, Centro Médico Nacional 20 de noviembre, ISSSTE, Ciudad de México, México. [5]Laboratorio de Transcriptómica e Inmunología Molecular, Instituto Nacional de Enfermedades Respiratorias, Ciudad de México, México. anagt@ciencias.unam.mx

Adipocytes have been proposed as niches for dormant *M. tuberculosis*; however, the mechanisms of *M. tuberculosis* infection in human adipocytes have not been fully elucidated. In mice and rabbits, *M. tuberculosis* can infect and persist in adipose tissue, which could regulate lung pathology through cytokine production. The cytokines, together with extracellular vesicles (EVs), share several functions as mediators of cellular function. The aim of this work was to evaluate the percentages of *M. tuberculosis H37Ra-Cherry* infected human adipocytes *in vitro*, and the induction of EVs and IL-8 and TNF-α secretion. We obtained adipocytes from six bariatric patients who underwent gastric bypass or sleeve surgery, then the adipocytes were isolated using a tissue dissociator. The adipocytes were stained with fluorescein (CFSE), and $5X10^6$ fluorescent-adipocytes were infected with *M. tuberculosis* H37Ra-Cherry at MOI of 20, and incubated for 4, 48 and 72 h. The colocalization of adipocytes-*M. tuberculosis* was evaluated by fluorescence microscopy. In filtered supernatant, the IL-8 and TNF-α production was quantified by ELISA, and the EVs secretion was identified by western blot. We found that *M. tuberculosis*-cherry is localized within human adipocytes after four hours post-infection, and the percentages increase after 48 and 72 h of incubation up to 45% of adipocytes; *M. tuberculosis* also induced the secretion of TNF-α and IL-8 cytokines and induced the generation of EVs. These data suggest that adipocytes are not just a niche for *M. tuberculosis*, since the infection can also regulate cytokine secretion and the generation of EVs in human adipocytes.

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Resumen corto

Validation of an ELISA assay to determine the toxicokinetic profile of human anti-SARS-CoV-2 antibodies in rodent models

Garzón-Guzmán, C. [1,2], Ramírez-Villedas, F. [1,2], Carballo-Uicab, G. [1,2,3], González-González, E. [1,2], Godínez-Palma, S. [1,2], Vallejo-Castillo, L. [1,2], Almagro, J.C. [1,2,4], Pérez-Tapia, S.M. [1,2,3]

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City 11340, Mexico. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos, LANSEIDI-FarBiotec-CONACyT, Mexico City 11340, Mexico. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), Mexico City 11340, Mexico. [4]GlobalBio, Inc., 320 Concord Ave, Cambridge, MA 02138, USA. cgarzongu@ipn.mx

Validation of an ELISA to quantify human anti-SARS-CoV-2 antibodies using as case study IgG1-A7 in rodent serum is presented. IgG-A7 is a fully human and broadly neutralizing antibody of Wuhan, Delta and Omicron variants described at DOI: 10.3390/antib11030057. The assay was based on binding of IgG1-A7 to the RBD of SARS-CoV2. An anti- human IgG as secondary antibody specific for total that does not cross-react with mouse IgG was used. The assay showed a sigmoidal response curve in the dynamical range of $7x10^{-4}$ – 10^{3} ng/mL, with a detection limit of 2 x 10^{-2} ng/mL and quantitation limit of 23 x 10^{-1} ng/mL. Evinced precision (CV) of <25%, accuracy (spike recovery) of 108 – 140% and high selectivity to RBD in serum, plasma, and hemolyzed samples. It also met dilutional linearity criteria in serum samples (CV) of <25%. The validated assay was then used to determine the TK profile of IgG-A7 at two single doses: 100 and 200 mg/Kg in CD-1 mice. Half-life ($t_{1/2}$) in serum was 402 h for 100 mg/Kg and 237 h for 200 mg/Kg, while the clearance was 0.012 and 0.018 mL/h/Kg, respectively. No adverse effects related to the administration of the IgG-A7 were observed. The TK profile met the standard behavior of a human IgG1 in mouse serum. These results demonstrate the value of this assay as a tool in preclinical testing of human anti- SARS-CoV-2 antibodies in rodents while supporting the first use of IgG1-A7 in humans as part of the clinical development.

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Resumen corto

Immunogenic regions of BIP and α-1 giardin proteins from *Giardia lamblia* as candidates in the design of a multi-peptide vaccine against giardiasis

Garzón-Lizárraga, T.M. [1*], Yescas-Romo, V. [1*], Esparza-Figueroa, K.A. [1], López-Romero, G.C. [1], Rascón-Durán, M.L. [1], Arvizu-Flores, A.A. [1], Velázquez-Contreras, C.A. [1].

[1]Departamento de Ciencias Químico-Biológicas y de la Salud, Universidad de Sonora, Hermosillo, Sonora, México. thania.garzon@unison.mx, velaz2@unison.mx.

Giardia lamblia causes giardiasis, one of the most common gastrointestinal infections worldwide. Children and immunocompromised individuals are the most susceptible to infection, presenting severe clinical manifestations and long-term sequelae. At the present, there is no vaccine against human *giardiasis*. Several *Giardia* proteins have been described as candidates for vaccine development against giardiasis, including the binding immunoglobulin protein (BIP) and α-1 giardin. This work focuses on searching immunogenic regions of these antigens recognized by the humoral immune response. We expressed recombinant BIP and α-1 giardin proteins in *E. coli* BL21 strain cells that were transformed with pJexpress404 and pET-28a vectors, respectively. The recombinant proteins were purified by IMAC. Balb/c mice were immunized orally with BIP and α-1 giardin proteins (each group n=4) during 4 weeks, and the specific antibody response to proteins (IgG and IgA) were evaluated by ELISA. To identify immunogenic regions from *G. lamblia* antigens, we digested BIP and α-1 giardin with trypsin during 30 and 60 minutes, then, we analyzed the protein digestion by SDS-PAGE and Western Blotting. Additionally, we predicted the linear and conformational B-cell epitopes using bioinformatics tools (BCPred and Ellipro). The oral administration of BIP antigen induced a secretory and systemic antibody response. α-1 giardin did not induce antibody production. Both proteins have predicted regions recognized by antibodies. We identified immunogenic B-cell epitopes of BIP and α-1 giardin proteins from *Giardia*. The identification of B-cell epitopes of *G. lamblia* immunogenic proteins could contribute to the rational design of an effective vaccine against the parasite.

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Resumen corto

Activation of G protein coupled estrogen receptor (GPER) regulates migration and invasion in SiHa and HaCaT-16-E6/E7 cells

Gaxiola-Rubio, A. [1,2], Jave-Suárez, L.F. [3], Hernández-Silva, C.D. [4], Villegas-Pineda, J.C. [4], Ramírez-De Arellano, A. [2,4], Pereira-Suárez, A.L.[1,4]

[1]Doctorado en Ciencias Biomédicas, CUCS, Universidad de Guadalajara, Guadalajara, México; [2]Instituto de Investigación en Ciencias Biomédicas, CUCS, Universidad de Guadalajara; [3]División de Inmunología, CIBO, IMSS; [4]Departamento de Microbiología y Patología, CUCS, Universidad de Guadalajara, Guadalajara, Jalisco, México.

The infection of the cervical epithelium by Human Papillomavirus (HPV) is the major risk factor for Cervical Cancer. Co-factors such as the presence of estrogen hormones are necessary. Among the estrogen receptors, G protein-coupled estrogen receptor (GPER) is highly expressed in cervical cancer tissue, GPER in co-expression with claudin-1 predicts poor prognosis in patients with cervical adenocarcinoma. Little is known about the metastatic capabilities of GPER. The aim of this study was to elucidate the impact of GPER activation on the migratory and invasive potential of keratinocytes transduced with HPV16-E6/E7 oncogenes and SiHa cells. Cell lines of SiHa and keratinocytes (HaCaT-16E6, HaCaT-16E7, HaCaT-pLVX) were used. The cells were stimulated with G-1, a selective GPER agonist. Gene expression by RNA-seq. Cell migration and invasion were assessed using transwell assays. Vimentin and αSMA expression by immunofluorescence. The activation of GPER in SiHa cells had no significant difference while in HaCaT-16E6, HaCaT-16E7 and HaCaT-pLVX increases migration and invasion. G-1 enhance these processes only in the presence of oncogenes. The expression of vimentin increases in HaCaT cells meanwhile SiHa doesn't exhibit difference. αSMA expression had no alterations in SiHa and HaCaT cells. In HaCat-16E7, G-1 regulates the overexpression of 25 and underexpression of 10 genes, which modulate pathways such as TGFβ signaling, epithelial-mesenchymal transition, NFκB TNFα pathway, IL-6 signaling and angiogenesis. The activation of GPER induces an oncogenic potential through cellular migration and invasion events in keratinocytes transduced with E6 or E7 oncogenes, which are mediated by vimentin expression and differentially expressed genes.

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Resumen corto

Differentially Expressed Genes of Patients with Lupus Nephritis Through Integrative Bioinformatics

Gelinas-Martin del Campo, M. *[1], Martínez-Canales, R. [1], Rojas-Gutiérrez, S.E. [1], Elizondo-Solis, C.V. [1], Salinas-Carmona, M.C. [1], Montoya-Rosales, A. [2], Macias-Segura, N. [1]

[1] Laboratorio de Inmunología de Sistemas, Departamento y Servicio de Inmunología, Facultad de Medicina y Hospital Universitario, Universidad Autónoma de Nuevo León. [2]Laboratorio de Inmunomoduladores, Centro de Investigación y Desarrollo en Ciencias de la Salud, Universidad Autónoma de Nuevo León
marianagelinas@outlook.com

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease clinically characterized by periods of flares and remissions. Although its pathophysiology is not well understood, it is well documented that SLE is associated with systemic inflammation and multiple organs involvement. Lupus nephritis (LN) is the most common complication and cause of death in SLE patients, often leading to end-stage renal disease. There is no consensus on which genes are expressed in LN. We aimed to identify overlapping DEGs in patients with LN using integrative bioinformatics and functional enrichment analysis. We designed a search strategy in the GEO platform to identify datasets of expression profiling by array of kidney samples from patients with LN. DEGs were filtered if $p < 0.05$ and logfold change > 2 or < -2. We evaluated the DEGs with David database and performed prediction analysis with GeneMania. Protein-protein interaction analysis was performed with STRING by Cytoscape platform. Three datasets met the inclusion criteria and 9 DEGs were identified. Prediction analysis revealed 23 co-expressed genes. Functional analysis recognized the major biological processes involved in these genes. PPI analysis recognized the top 10 genes with the strongest interactions. We aimed to identify DEGs of patients with LN and to recognize those with the strongest interactions. Our results suggest that type I IFN is crucial for the pathophysiology of LN. We propose further *in vivo* studies to validate these findings as they may serve as diagnostic biomarkers and even possible therapeutic targets for LN treatment. FUNDING: CONACYT PCC/2022-320697.

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Resumen corto

Staphylococcus epidermidis planktonic cell supernatants alter osteoblasts function: implications for implant-associated osteomyelitic infections

Gómez-Alonso, I.S.*[1,3], Sánchez-Torres, M.[1,3], García-Pérez, B.E.[2], Cancino-Díaz, J.C.[3], Moreno-Lafont, M.C.[4], Cancino-Díaz, M.E.[5], Rodríguez-Martínez, S.[5], Jan-Roblero, J.[6] Quiñones-Ramírez, E.I.[7]

[1]Posgrado en Ciencias Químicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [2]Laboratorio de Microbiología General, Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [3]Laboratorio de Inmunomicrobiología, Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [4]Laboratorio de Inmunología Celular, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [5]Laboratorio de Inmunología Aplicada, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [6]Laboratorio de Biotecnología Ambiental, Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [7]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México.

*E-mail: itziasidney@gmail.com

Staphylococcus biofilm formation is a significant contributor to the development of implant-associated osteomyelitis (IAO). However, it is important to note that up to 40% of *Staphylococcus epidermidis* isolates from patients with IAO do not produce biofilms. This observation raises questions about the role of biofilms in these cases of infection and underlines the need to investigate *S. epidermidis* isolates that do not form biofilms. This study examined whether *S. epidermidis* planktonic cell supernatants (PCS) can alter osteoblast function, in contrast to biofilm supernatants. Supernatants from biofilm-producing and PCS of *S. epidermidis* clinical isolates were used to stimulate the human osteoblast cell line MG-63 under osteogenic and non-osteogenic conditions. The results showed that PCS showed similar changes in osteoblast function as supernatants from biofilm producing strains. Cell viability (80%), proliferation and mineralization (40%), and apoptosis in osteoblasts (40%) were significantly reduced. In addition, alkaline phosphatase enzyme concentration and calcium deposition were significantly decreased. The expression of genes related to cell differentiation under osteogenic conditions was affected by PCS, and the RANKL/OPG ratio was significantly increased compared to the control. Finally, increased mRNA expression of the IL-36ϒ isoform was observed in cells treated with biofilm supernatant, suggesting cellular behavior such as chronic inflammation. These results suggest that factors generated by PCS of *S. epidermidis* may affect osteoblast function, not just factors generated by the biofilm. These findings have important implications for the study of IAO infections, since so far, the negative effects on osteoblasts have been caused by bacterial biofilms.

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Resumen corto

Discovery and optimization of neutralizing SARS-CoV-2 antibodies using ALTHEA Gold Plus Libraries™

Gómez-Castellano, K.M.*[1,2], Guzmán-Bringas, O.U.[1,2], González-González, E.[1,2], Salinas-Trujano, J.[1,2], Vázquez-Leyva, S.[1,2], Vallejo-Castillo, L.A.[1,2], Pérez-Tapia, S.M.[1,2,3], Almagro, J.C.[1,2,4]

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos, LANSEIDI-FarBiotec-CONACyT CDMX, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), CDMX, México. [4]GlobalBio, Inc., Cambridge, MA, USA.
*E- mail: keyla.gomez@udibi.com.mx

We recently reported (Antibodies. 11 (1): 13, 2022; Antibodies. 11 (3): 57, 2022) the isolation and characterization of anti-SARS-CoV-2 antibodies from a phage display library built with the VH repertoire of a convalescent COVID-19 patient, paired with four naïve synthetic VL libraries. One of the antibodies, called IgG-A7, neutralized Wuhan, Delta (B.1.617.2) and Omicron (B.1.1.529) strains in authentic neutralization tests (PRNT). It also protected 100% transgenic mice expressing the human angiotensin-converting enzyme 2 (hACE-2) from SARS-CoV-2 infection. Here, the four synthetic VL libraries were combined with the semi-synthetic VH repertoire of ALTHEA Gold Libraries™ (mAbs. 11 (3): 516, 2019) to generate a set of fully naïve, general-purpose, libraries called ALTHEA Gold Plus Libraries™. After three rounds of panning in solid phase with SARS-CoV-2 receptor-binding domain wildtype (RBD-WT) as selector, 630 clones were tested for binding to RBD, yielding 125 positive and specific single chain variable fragments (scFvs), with 24 being unique clones. Three out of 24 specific clones with affinity in the low nanomolar range and sub-optimal in vitro neutralization in PRNT, were affinity optimized via a method called “Rapid Affinity Maturation” (RAM). The final molecules reached sub-nanomolar neutralization potency, slightly superior to IgG-A7, while improved the developability profile over the parental molecules. These results demonstrate that general-purpose libraries are a valuable source of potent neutralizing antibodies. Importantly, since general-purpose libraries are “ready-to-use”, it could expedite isolation of antibodies for rapidly evolving viruses such as SARS-CoV-2.

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Resumen corto

The accuracy evaluation of the CYTEK's NL CLC Full Spectrum Cytometer in immunophenotyping hematological malignancies according to CLSI H62 Guidelines

Gonzales-Saravia, S.[1]*, Moya-Naranjo, J.[2], Rodriguez-Torres, R.[2], Sanchez-Jacinto, B.[3], Espiritu-Antezano, J[1].

[1]Clinical flow cytometry laboratory, Cytometric Bioservices SAC, Lima, Peru. [2] Faculty of Medicine, EAP Medical Technology, Universidad Nacional Mayor de San Marcos, Lima, Peru. [3]Universidad Peruana Cayetano Heredia, Lima, Peru.
*E- mail: sany.gonzales@upch.pe

Flow cytometry (FC) is a valuable tool for diagnosing and monitoring of hematological malignancies due to its speed and sensitivity. In view of the limitations of conventional cytometry, spectral cytometry emerged, offering clear advantages in terms of resolution and panel enhancement compared to its counterpart. Originally, the guidelines established for biochemical methods applied to FC had certain limitations. For this reason, CLSI proposed guideline H62, which includes specific validation strategies for cellular assays performed by flow cytometry. Within the quality standards, to introduce a platform in the clinical area, validation is necessary. In this work the accuracy of the full spectrum cytometer Northern Lights 3000 CLC CE-IVD (Cytek™, USA) was evaluated in 22 samples (normal and pathological) of peripheral blood and bone marrow, taking the conventional cytometer Novocyte Advanteon (Agilent, USA) as a reference, under the guidelines of the CLSI H62 guide using 8-color antibody panels proposed by the Euroflow™ group. A 100% concordance was found between both platforms to determine the presence or absence of pathological populations; as for the evaluation of the phenotypic profile of the pathological population, a 100% concordance was found for the 8-fluorescence studied. Furthermore, the correlation of cell percentages between both platforms was evaluated, finding similar results in most of the populations, except for some minority populations. These results demonstrate that the data obtained between both platforms are concordant with each other and applicable to clinical laboratories.

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Resumen corto

Cloning and recombinant expression of PD-1 and PD-L1 IgV-like extracellular domains

González, P.[1], Beltrán-López, E.[1] López-Moreno, H.S.[1]*

[1]Laboratorio de Biomedicina Molecular, CAC-BB-UAS264, Posgrado en Ciencias Biomédicas y Posgrado en Biotecnología, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Sinaloa. Ciudad Universitaria. Culiacán, Sinaloa, México. CP. 80013.
*E- mail: hslmore no@ms.uas.edu.mx

Cancer immunotherapy using monoclonal antibodies (MAb) that block PD-1/PD-L1 interaction have been shown to improve the response to treatment of cancer patients. In the MAb production process, a critical aspect is antigen availability, for which biomedical biotechnology is key. Our objective was Clone and express the immunoglobulin variable (IgV)-like domains of PD-1 and PD-L1. Since the interaction of PD-1/PD-L1 occurs between their IgV-like extracellular domains, specific primers were designed to clone them. Once cloned, they were individuality ligated to the pcDNA6 and inserted into *Escherichia coli*. Transformants were selected and verified by Colony-PCR. A pilot expression was performed with each transformant using 1mM IPTG as inducer and analyzed by 12% SDS-PAGE. The amplicons obtained (375bp for PD-1 and 357bp for PD-L1) were sequenced, aligned, and verified, obtaining 99% identity for PD-1 and 100% for PD-L1, each IgV-like sequence was registered in GenBank OM363223 (PD-1) and OM363224 (PD-L1). In both proteins, 4h post-induction was the optimal expression time, and, in both cases, the electrophoretic analysis shown a 15kDa band according with molecular weight expected. In conclusion, the cloning and recombinant expression of the IgV-like extracellular domains of PD-1 and PD-L1 was achieved, which will allow having a quasi-inexhaustible source of antigen for the eventual production of a humanized MAb or another immunotherapeutic tool, something that has not yet been achieved in Mexico.

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Resumen corto

In vitro and *in vivo* expression of OmpC protein for the development of DNA vaccine candidates

González-Domínguez, G.[1,2], Acevedo-Ochoa, E.[1,3], Valero-Pacheco, N.[1,4], Reyes-Sandoval, A.[5,6], López-Camacho, C.[5], Patiño-López ,G.[7], López-Macías, C.[1]

[1]Unidad en Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Ciudad de México, CDMX, México. [2]Universidad Nacional Autónoma de México, Programa de Maestría y Doctorado en Ciencias Bioquímicas, Facultada de Química, Ciudad de México, CDMX, México. [3]Max-Delbrück-Centrum für Molekulare Medizin, Berlin, Berlin, Deutschland. [4] Center for Immunity and Inflammation, New Jersey Medical School, Rutgers Biomedical Health Sciences, The State University of New Jersey, Newark, New Jersey, USA. [5]The Jenner Institute, Nuffield Department of Medicine, University Of Oxford, Oxford, Oxfordshire, UK. [6]Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [7]Unidad de Investigación en Inmunología, Hospital Infantil de México Federico Gomez, Ciudad de México, CDMX, México.
*E-mail:gonzalo030793@gmail.com

Salmonella Outer Membrane Proteins (Omps), in particular OmpC porin, is a strong immunogen used as experimental against the diseases induced by the pathogenic Salmonellas. Genetic-based vaccines, like DNA vaccines, because of their nature, could activate both, humoral and cellular immune responses, and achieve robust protection. However, the expression of the antigen is a crucial factor that must be carried out to demonstrate that the vaccine candidate could work. The project aimed to prove that *Salmonella* Typhi OmpC protein gene could be expressed in two cell lines and at the site of immunization in mice. Six OmpC gene variants were synthesized and cloned into an expression vector. The purpose of generating different constructions was to polarize different possible immune responses Hek 293 T and HeLa cell lines were transfected with lipofectamine 3000 and identification of the protein was measured by Western Blot and immunofluorescence. Two constructs were chosen to immunize C57BL/6 mice intradermally at the ear. Detection of the antigen was detected by immunofluorescence. We found different expression patterns of the protein were produced and detected in the whole cell lysate, presumably as different post-translational modifications conferred by the nature of the constructions. The immunofluorescence analysis revealed that the antigen remains intracellularly. *In vivo* experiments confirmed the antigen expression at the immunization site. These results indicate that the antigen can be expressed, and therefore, plasmids could be used as DNA vaccines.
Acknowledgment: the student received CONACYT scholarship.

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Resumen corto

Comparative analysis of PD-L1+ cells between tumor-infiltrating leukocytes and peripheral blood in Patients diagnosed with Renal Cell Carcinoma.

González-Garza, R.[1*], Salinas-Carmona, M.C.[1], Gutiérrez-González, A.[2], Flores-Gutiérrez, J.P.[3], Mejia-Torres, M.[1]

[1]Departamento de Inmunología, Hospital Universitario José Eleuterio González, Monterrey, Nuevo León, México. [2]Servicio de Urología, Hospital Universitario José Eleuterio González, Monterrey, Nuevo León, México. [3]Servicio de Anatomía Patológica, Hospital Universitario José Eleuterio González.

E-mail: raquel.gonzalezgrz@uanl.edu.mx

Clear cell renal carcinoma (ccRCC) is the most prevalent subtype of kidney cancer. Despite the availability of treatment options, the overall prognosis for ccRCC remains poor, mainly because of acquired resistance to conventional therapies. Current evidence indicates that the immune system is indirectly involved in tumor progression, where T cells play a critical role in antitumor immunity. The importance of the immune system in therapeutic responses is highlighted by the fact that lymphocyte-infiltrated tumors have a better prognosis than cold or immune-excluded tumors. In addition, the functional state of infiltrating leukocytes predicts the response rate to therapy in most types of cancer. In the latter scenario, several proteins in leukocytes have the potential to be used as biomarkers of lymphocyte dysfunction, thus helping determine the best treatment options for individual patients. In the present study, we describe the nature of myeloid leukocytes infiltrating tumor tissue in patients diagnosed with ccRCC. After phenotypic evaluation, we measured the expression levels of the protein PD-L1 (Programmed-Cell Death Ligand 1) in myeloid cells obtained from blood, peritumoral kidney tissue, and tumor tissue by flow cytometry. PD-L1 activates the inhibitory receptor PD-1 in lymphocytes inducing cell exhaustion and promoting cancer progression. Our results indicate that tumor tissue has a higher number of infiltrating leukocytes compared to peritumoral kidney tissue. More importantly, we found that within the tumor microenvironment, the main sources of inhibitory signals to lymphocytes are monocytes.

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Resumen corto

In Vitro and In Vivo Characterization of a Broadly Neutralizing Anti-SARS-CoV-2 Antibody Isolated from a Semi-Immune Phage Display Library

González-González, E. *[1,2] , Carballo-Uicab, G. [1,2], Salinas-Trujano, J. [1,2], Cortés-Paniagua, M.I.[1,2], Vázquez-Leyva, S.[1,2] , Vallejo-Castillo, L.[1,2] , Mendoza-Salazar, I. [1,3], Keyla Gómez-Castellano, K.[1,2], Pérez-Tapia, S.M.[1,2,3], Almagro, J.C.[1,2,4]

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos, LANSEIDI-FarBiotec-CONACyT CDMX, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), CDMX, México. [4]GlobalBio, Inc., Cambridge, MA, USA.
*E-mail: edith.gonzalez@udibi.com.mx

Neutralizing antibodies targeting the receptor-binding domain (RBD) of SARS-CoV-2 are among the most promising strategies to prevent and/or treat COVID-19. However, as SARS-CoV-2 has evolved into new variants, most of the neutralizing antibodies authorized by the US FDA and/or EMA to treat COVID-19 have shown reduced efficacy or have failed to neutralize the variants of concern (VOCs), particularly B.1.1.529 (Omicron). Previously, we reported the discovery and characterization of antibodies with high affinity for SARS-CoV-2 RBD Wuhan (WT), B.1.617.2 (Delta), and B.1.1.529 (Omicron) strains (Antibodies. 11 (1): 13, 2022). One of the antibodies, called IgG-A7, also blocked the interaction of human angiotensin-converting enzyme 2 (hACE2) with the RBDs of the three strains, suggesting it may be a broadly SARS-CoV-2 neutralizing antibody. Herein, we show that IgG-A7 efficiently neutralizes all the three SARS-CoV-2 strains in plaque reduction neutralization tests (PRNTs). In addition, we demonstrate that IgG-A7 fully protects K18-hACE2 transgenic mice infected with SARS-CoV-2 WT in a similar manner to that reported for other anti-SARS-CoV-2 antibodies. Taken together, our findings indicate that IgG-A7 could be a suitable candidate for development of antibody-based drugs to treat and/or prevent SARS-CoV-2 VOCs infection.

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Resumen corto

Purinergic receptors associated with chemoresistance in breast cancer patients

González-Hernández, O.[1]*, Ruiz-Rodríguez, V.M.[2], Turiján-Espinoza, E.[1], Martínez-Leija, M.E.[1], Layseca-Espinosa, E.[1], Estrada-Sánchez, A.M.[2], Portales-Pérez, D.P[1].

[1] Laboratorio de Medicina Molecular y Traslacional, Centro de Investigación en Ciencias de la Salud y Biomedicina (CICSaB), Universidad Autónoma de San Luis Potosí, San Luis Potosí. [2] Laboratorio de neurobiología, División de Biología Molecular, Instituto Potosino de Investigación Científica y Tecnológica (IPICYT), San Luis Potosí. E-mail: A221014@alumnos.uaslp.mx

Breast cancer continues to be a global health problem, and chemoresistance contributes to the number of deaths. Chemoresistance has been linked to purinergic receptors of the P2X family. The P2X7, P2X1, and P2X4 receptors contribute to the inflammatory process and the immune response by binding to ATP. The P2X7 isoforms (A and B) share a tumor-promoting activity that promotes the growth of cancer cells and are associated with a poor prognosis in different types of cancer. Therefore, the objective was to determine the expression of these receptors and the P2X7 isoforms (A and B) at the RNAm level in peripheral blood mononuclear cells (PBMC) of breast cancer patients with or without chemoresistance. The methodology consisted of isolating PBMC from patients before chemotherapy (cycle 1) and, at the end of it, six months later (cycle six). Compared to control subjects, decreased levels of relative expression of P2X7B, P2X1, and P2X4 were found in patients. When classifying the patients into sensitive and chemoresistant and at chemotherapy 1 (Q1) and 6 (Q6) and comparing them with the control group, a significant decrease in P2X7B was found in resistant patients at Q6. In the case of P2X4, the decrease was observed in the group of sensitive patients in Q6; concerning chemoresistant patients, low levels of P2X4 occurred in both Q1 and Q6. We concluded that the levels of the purinergic receptors on the immune cells could be a biomarker of sensitivity or resistance in the chemotherapy treatment.

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Resumen corto

Extracellular Monomeric Ubiquitin, the major component of Transferon Oral®, binds to CXCL12, revealing a new regulatory role on the CXCR4/CXCL12 axis.

González-Martínez, A.P.[1,2,3], Aguilar-Alonso, F.[1,2], Fragozo, A.[1,2], Domínguez-Sánchez, K.[1,2], Pavón, L.[3], Vallejo-Castillo, L.[1,2], Almagro, J.C.[1,2,4], Pérez-Tapia, S.M.[1,2,3].

[1]Unidad de Desarrollo e Investigación en Bioterapeuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I + D + i) para Farmoquímicos y Biotecnológicos (LANSEIDI-FarBiotec-CONACyT), México City, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [4]GlobalBio, Inc., 320 Concord Ave, Cambridge MA, USA. *E-mail: anethpaola13@gmail.com

Transferon Oral® is a Dialyzable Leukocyte Extract (DLE) with immunomodulatory properties. Its major components are two monomeric Ubiquitin (Ub): Ub^{1-76} and Ub^{1-74}. CXCL12 is a vital signaling chemokine known to bind and activate the G-protein coupled receptors CXCR4 and CXCR7. Dysregulation of the CXCL12/CXCR4 axis can lead to various diseases, including autoimmune disorders, cancer, and chronic inflammation. Therefore, chemokine activity regulation is critical to maintaining immune homeostasis and preventing disease. One such mechanism is the release of Chemokine-Binding Proteins (CBPs) to modulate chemokine activity by altering receptor binding or bioavailability. Although Ub is critical for intracellular signaling, it has been reported to have immunomodulatory activity as an extracellular CXCR4 agonist. In this study, we found by ELISAs that Extracellular Monomeric Ubiquitin (EmUb) does not bind to CXCR4 but to CXCL12, suggesting that Ub may regulate CXCR4 as a CBP. Migration assays on FaDu Cells were also performed, where mUb alone did not affect migration, whereas AMD3100, a CXCR4 blocker, inhibited this process. Interestingly, co-treatment with both compounds decreased the inhibitory effect induced by AMD3100. This suggests a CXCR4-independent role of EmUb in the regulation of migration of FaDu cells. Given the critical roles of the CXCR4/CXCL12 axis in numerous physiological and pathological processes, understanding its regulation is essential for developing novel therapeutic strategies. Further research is needed to elucidate the role of EmUb on CXCL12 activity and determine its potential as a therapeutic agent.

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Resumen corto

Effect of Pentoxifylline and Norcantharidine on endoplasmic reticulum stress in 3D cultures of B16F1 cells.

González-Quiroz, J.L.*[1], Ocampo-Godínez, J.M.[2], Hernández-González, V.N.[1], Lezama-Palacios, R.A.[3], Reyes-Maldonado, E.[3], Vega-López, A.[4], Romero-López, J.P.[1], Domínguez-López, M.L.[1]

[1]Laboratorio de Inmunoquímica I e Inmunología Clínica, departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, IPN, Ciudad de México, CDMX, México. [2]Laboratorio de bioingeniería de Tejidos, Departamento de Estudios de Posgrado e Investigación, UNAM, Ciudad de México, CDMX, México. [3]Laboratorio de Hematopatología, departamento de Morfología, Escuela Nacional de Ciencias Biológicas, IPN, Ciudad de México, CDMX, México. [4]Laboratorio de Toxicología Ambiental, departamento de Ingeniería en Sistemas Ambientales, Escuela Nacional de Ciencias Biológicas, IPN, Ciudad de México, CDMX, México.
*E-mail: manu_joseluis10@hotmail.com

Melanoma is the main skin cancer. In advanced stages, the current treatment has shown low effectiveness causing poor prognosis for patients. Endoplasmic reticulum (ER) stress is a mechanism which support to control proteins synthesis. In chronic ER stress conditions, cell death pathways are activated. Therefore, ER stress has been proposed as a possible therapeutic target in cancer. Autophagy maintains cellular homeostasis and acts as a cellular survival mechanism in starved cells. In cancer cells, autophagy avoids apoptosis by treatments such as chemotherapy. Pentoxifylline (PTX) and Norcantharidine (NCTD) have shown to induce ER stress and activate apoptosis in tumoral cells. In this work, we propose to determinate the effect of both drugs in spheroids of B16F1 melanoma cells. Spheroids were performed by the hanging drop technique using $1x10^3$ cells. Spheroids were treated with PTX, NCTD, combination of both, and the control without stimulus at three times 6, 24 and 48 hours. Furthermore, we used Tunicamycin and Rapamycin as positive controls of ER stress and autophagy respectively. As ER stress markers were evaluated BiP and CHOP, and as autophagy markers were used Beclin-1 and LC3I/II by Western blot. We observed microscopically morphological changes in the proliferative zone cells of the spheroids treated with PTX, NCTD and both drugs. In addition, we observed a higher expression of BiP and CHOP in the spheroid's cells treated with the three drug conditions at 48 hours. LC3II showed less expression with NCTD and the drugs combination at 6 hours.

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Resumen corto

3D co-culture system for the development of a chemoresistance prediction platform in B-ALL.

González-Reyes, N.C.*[1], Delgadillo-Sánchez, E.I.[1], Angeles-Arvizu, A.[1], Casique-Aguirre, D.[2], Pérez-Tapia, S.M[1].

[1]Unidad de desarrollo e investigación en bioterapéuticos, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Centro de Investigación Biomédica de Oriente, Instituto Mexicano del Seguro Social, Delegación Puebla. Atlixco-Metepec. 74360. Pue. México. *E-mail: ncgonzalezr@ipn.mx

The expansion of malignant lymphoid precursors within the bone marrow results in B-cell acute lymphoblastic leukemia (B-ALL), the main population affected are children. In the past decade there have been remarkable advances in the definition of the molecular abnormalities involved in leukaemogenesis and drug resistance, due to ability of hosting and protecting leukemia initiating cells in the leukemic niches.

The objective of the investigation is to evaluate the tumor microenvironmental to establish a 3D co-culture system treated with chemotherapeutics frequently used in the treatment of B-ALL. For this purpose generic organoids were formed from stromal mouse cells OP9 and lymphocyte-like Nalm6 cells, they were treated with concentrations 50,25,12.2,6.25,3.12 ng/ml (Balandran *et al*., 2021). Samples were acquired in the cytometer to detect $CD45^{+}$ and 7AAD to determine the treatment effectiveness on the cells that migrate in the interior of the organoid, and the exterior cells. The results showed there are no significant difference between the different concentrations.

In conclusion the Nalm 6 cell line was shown to have chemoresistance to vincristine, even at concentrations at which cell samples isolated from patients showed sensitivity, which let us establish this cell line as a chemiresistant control to this treatment, and will allow to evaluate new treatments.

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Resumen corto

Identification of Dominant Negative Isoforms of IKZF1 in B-Cell Acute Lymphoblastic Leukemia from RNA-seq

Grandvallet-Contreras, J.[1*], Carrillo-Sánchez, K.[2], Molina-Garay, C.[2], Flores-Espino, M.F.[2], Jiménez-Olivares, M.[2], García-Solorio, J.[2] , Alaez-Verson, C.[2] , Cervera-Taboada, A.[1]

[1]National Insitute for Genomic Medicine CDMX, México. [2]Genomics Diosgnostics Laboratory, National Insitute for Genomic Medicine, CDMX, México. *E-mail: calaez@inmegen.gob.mx, acerverat@inmegen.gob.mx C Correo de contacto*: julian.grandvallet@cua.uam.mx

B-cell acute lymphoblastic leukemia (B-ALL) is the most common pediatric cancer and the leading cause of cancer related deaths in children and young adults. In B-ALL, IKZF1 is recurrently affected by different types of genetic alterations, some of which have been associated with poor survival. Common alterations of IKZF1 involve exon deletions that could result in expression of dominant negative IKZF1 isoforms. The aim of this study is to, first, identify genetic abnormalities in IKZF1 from RNA-seq data using different bioinformatic approaches, and second, to investigate the effects of IKZF1 isoforms on overall gene expression and pathway signaling as well as clinical outcome. We quantified transcript level and exon level expression using Salmon and Rsubread, respectively, and we used Toblerone to identify exon deletions in IKZF1 in a cohort of 189 B-ALL bone marow samples from pediatric patients. Our findings suggest that RNA-seq can be used to identify individual samples harboring IKZF1 alterations. Furthermore, in contrast with copy number alteration methods based on DNA, which are typically used for detection of IKZF1 defects, RNA-seq allows us to quantify and observe the differential isoform usage of IKZF1 in each sample. Further studies are needed to investigate the functional implications of these isoforms and their potential as therapeutic targets in B-ALL.

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Resumen corto

Sensitizing effect of curcumin to sodium arsenite through lytic reactivation of Epstein-Barr virus in a lymphoblastoid model

Guaita-Gavilanes, M.G.*[1], Arenas-Romero, R.M.[1], Suárez-Vargas, R.J.[1], Vargas-Robles, H.[2], Córdova, E.J.[3], Martínez-Castillo, M.[1], Hernández-Zavala, A.[1]

[1]Sección de Estudios de Posgrado e Investigación de la Escuela Superior de Medicina, Instituto Nacional Politécnico, Casco de Santo Tomás, Ciudad de México, México. [2]Departamento de Biomedicina molecular, Centro de Investigación y de Estudios Avanzados, Zacatenco, Ciudad de México, México. [3]Laboratorio Consorcio de Oncogenómica, Instituto Nacional de Medicina Genómica, Clínica de Investigación, Arenal Tepepan, Ciudad de México 14610, México. *E-mail:magabrielaguaita@hotmail.com

Curcumin (CUR) is a phytochemical with an antitumoral activity supported by a sensitizing effect; as a consequence of apoptosis in cells models infected with Epstein-Barr virus (EBV). EBV is a tumoral virus of biphasic cycle life, it's infected in latent phase to 90% of world population causing gastric and nasopharyngeal carcinoma and types of lymphomas in some groups. Recently, it's been described a sensitizing effect of CUR to sodium arsenite (iAs) in EBV-positive cell models; without being explored mechanisms that underlie it. Then, we evaluated if the sensitizing capacity of CUR to iAs has related with a lytic reactivation of EBV in a lymphoblastoid model, we analyzed as lytic markers BZLF1 and BRLF1 gene expression and Zta protein by RT-PCR and immunoblot respectively. In this work we found in the pretreatment group with CUR followed by iAs that decreased BZLF1 and BRLF1 against control group, in consistent with this result found a low protein Zta level; induced with doxorubicin. Thus, in the sensitizing model CUR would suppress the lytic gene expression and viral protein, so we can discard a lytic reactivation as a mechanism of sensitizing of CUR to iAs in a lymphoblastoid model.

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Resumen corto

Detection of Histone H2B in tumor tissue of patients with breast cancer as an indicator of NETs.

Guerrero-López, A.[*1], Martínez-Álvarez, K. O.[1,2], Salinas-Argueta, M. A.[1,2], Pedroza-González, A.[1], García-Romo, G. S.[1]

[1]Laboratorio de Inmunología, Unidad de Morfología y Función, FES Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla de Baz, México. [2] RED MEDICI Carrera de Médico Cirujano, FES Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla de Baz, México.

*E-mail: aurora.gl@comunidad.unam.mx ; garciaromogs@iztacala.unam.mx

Tumor development depends on a complex and orchestrated network of interacting cells that form the tumor microenvironment (TME). It is well known that neutrophils are the most prevalent type of innate immune cell and are the first cells to arrive at sites of developing inflammation, in this context it is to be expected to find neutrophils as part of the TME. Several studies in mouse models have shown that intratumoral neutrophils may induce the progression of the tumor However, the role of neutrophils in cancer has long been a matter of controversy. Neutrophils can die in a peculiar way called Netosis, in this study, we aimed to analyze the frequency of Histone (H2B) as a marker of NETs within tumors from patients with breast cancer. Histones were located in tumor tissue from 10 patients who had not received prior treatment. The detection of histones using a technique such as immunohistochemistry could have prognostic value of tumour-infiltrating neutrophils.

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Resumen corto

Effect of different immunostimulations in glycosylation of hemocytes from *Cherax quadricarinatus*

Guluarte, C.[1], Pereyra, M.[1], Ramírez-Hernández, E.[1], Segura-Pérez, E.[1], Pérez-Echeverria, M.[1], Moreno-Mendieta, S.A.[2], Rodríguez, R.[2], Angulo, C.[3], Zenteno, E.[1], Sánchez-Salgado, J.L.[1]

[1]Departamento de Bioquímica. Facultad de Medicina. Universidad Nacional Autónoma de México, 04510, CDMX. [2]Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, 04510, Ciudad de México, México.[3]Immunology & Vaccinology Group, Centro de Investigaciones Biológicas del Noroeste (CIBNOR), Av. Instituto Politécnico Nacional 195, La Paz, México. *E-mail: crystal@bq.unam.mx

Crayfish (*Cherax quadricarinatus*) is poorly unknow the glycophenotyping which is the glycan structure arrangement in hemocytes. This work is aimed to characterize possible glycophenotyping of subpopulations hemocytes for basal or stimulation with bacteria such as: *V. parahaemolyticus* N16 (Vp) or *Escherichia coli* BL21A1 (Ec); or rice microparticles (MPA) in each population. The experiment was carried out as follows: Vp (1×10^9 cells/mL), Ec (1×10^9 cells/mL) and MPA (200 ng/mL) were used for stimulate to crayfish *in vivo* by injection. Samples were taken at 0-4 h after stimulation. By flow cytometry was characterized subpopulations of hemocytes and measured viability, phagocytosis activity, ROS production, and carbohydrates in the cell surface by lectins (ALL, VVA, ConA, MAA-I, GS-I, GS-II and SBA-I). The results obtained until this moment showed similar viability among groups without cytotoxicity caused by treatments, high increment in the parameters of ROS production with (84.7%) MPA, (79.3%) Vp or (89.3%) Ec after 2-4 h stimulation compared with (50.3%) control. Phagocytosis activity also showed a significant increment in (43.3%) MPA, (45.1%) Vp or (35.5%) Ec compared with (0.53%) control after 2-4h of immunostimulation. Recognition of carbohydrates in membrane by lectins in hemocytes showed changes in treated groups with MPA (85.5% of α-(2,3) NeuAc, 41.2% of α-(2,6) NeuAc, 23.6% of Gal, 46.6% of GlcNAc, 53.6% of GalNAc), Vp(65.3% of α-(2,3)NeuAc, 35.6% of α-(2,6) NeuAc, 23.6% of Gal, 56.3% of GlcNAc) or Ec(25.6% of Gal, 46.7% of GlcNAc, 61.7% of GalNAc) compared with basal and control group. The stimulants used were safe, moreover demonstrates a possible composition of glycans per population of hemocytes by their immunostimulation.

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Resumen corto

Immunotherapy for dogs with oral melanoma: GK-1 increase survival improving peripheral levels of IFNγ

Gutiérrez, A. [1], Guadarrama, M. [2], Belmonte, J. [1], Vargas, H. [1], Alvarado, V. [1], Ramírez, F [1], Hernández-Aceves, J.A. [3]*, Garduño, L.F. [3], Moctezuma, D. [3], Cervantes, A. [4], Romero, L. [2], Sciutto, E. [3], Fragoso, G. [3], Cervantes-Torres, J. [3,5]

[1]Hospital Veterinario Oncocare. Mexico City, Mexico. [2]Departamento de patología. Facultad de Medicina, Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico City, Mexico [3]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Mexico City, Mexico. [4]Hospital de pequeñas especies, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico City, Mexico. [5]Departamento de Microbiología e Inmunología, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico City, Mexico.
*E-mail: angelinaoncocare@gmail.com

Canine oral melanoma (COM) is a common severe pathology of immunocompetent dogs. Surgical treatment is the first-line therapeutic alternative, although by itself, it does not modify the poor prognosis of this disease. The median survival time in dogs with surgically resected melanoma varies from 3 to 18 months depending on the stage at diagnosis. Despite many attempts to use chemotherapy, it does not offer improvement in the clinical course of patients compared to surgical resection. On the other hand, many expectations exist around immunotherapy to improve the prognosis of this disease, particularly considering the success obtained in certain types of cancer. GK-1 has been successfully used to improve the evolution of melanoma and breast experimental murine tumors; besides it exhibited a high anti-metastatic capacity in the 4T1 murine cancer model. This trait is of great importance, because COM is a cancer with high metastatic capacity, which is the most frequent cause of death in these patients. Herein, dogs with confirmed COM in late stages, were treated intravenously or subcutaneously with GK-1 (0.5mg/kg). Treated dogs increased survival time up to 17 weeks (p=0.0082) without changes in hematological and biochemical parameters measured by automatic cytometry and photometric analyses neither any signs of discomfort. GK-1 treatment increased dogs´ weights and plasmatic levels of IFNγ that correlated with the dogs ´surveillance (r=0.88). Overall, these results points to GK-1 as a promising new therapeutic alternative for dogs with CMO. Funding: PAPIIT:IN230320, IN218822, CONACyT: 302961; PROCAVADI

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Resumen corto

Effect of gold nanoparticles on the biological function of human peripheral blood basophils.

Gutiérrez-Cruz, S.G. [1*], Rodríguez-Cortes, O. [2], Díaz-Márquez, A. [2], Muñoz-Diosdado, A [1], Flores-Mejía, R. [2]

[1]Departamento de Ciencias Básicas, UPIBI-IPN, México. [2]Inmunología Médica y SEPI. Laboratorio de inflamación y obesidad, ESM-IPN, México.
*E-mail: gcsina5@gmail.com

Gold nanoparticles (NPOs) have been approved for use in humans because they have chemical and physical characteristics that allow them to have therapeutic and diagnostic applications. Functionalized NPOs have been reported to interact with immune system (IS) cells, but the ability of NPOs alone to interact with IS cells has been scarcely reported. The aim of the present work is to characterize and evaluate the effect of NPOs on the biological function of human peripheral blood basophils. The characterization of NPOs was done with Transmission Electron Microscopy and Nanoparticle Tracking Analysis by checking diameter, shape and dispersion. It was found that the NPOs present shape and size corresponding to the manufacturer's specifications; it is necessary to sonicate the NPOs to avoid agglomeration and to have an adequate dispersion. It was observed that NPOs agglomerate when interacting with PBMC. The degranulation will be done by flow cytometry from PBMC of the leukocyte concentrate of healthy donors and then the cultures of basophils (enriched by magnetic beads) and NPO (at different concentrations, sizes and times) will be performed, to quantify the toxicity 7AAD will be done, the production of cytokines by CBA and their location by fluorescence confocal microscopy.

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Resumen corto

B55β modulates the intensity of germinal center reactions by promoting T follicular helper cells polarization

Gutiérrez-Hernández, J.E. *, Rosetti, F., Crispín, J.C., Madera-Salcedo, I.K.

Departamento de Inmunología y Reumatología, Instituto Nacional De Ciencias Médicas y Nutrición Salvador Zubirán. Av. Vasco de Quiroga 15 Col. Belisario Domínguez Sección XVI, C.P. 14080 Tlalpan, Ciudad de México. *E-mail: jegh1997@gmail.com

T follicular helper cells (T_{FH}) are essential to shape B cell response during germinal center (GC) reaction, that lead to the development of high affinity and long-lasting humoral immunity. Abnormal differentiation and accumulation of T_{FH} can promote an autoimmune response. Patients with autoimmune diseases, like rheumatoid arthritis, have an aberrant expression of B55β in T cells causing apoptosis resistence, contributing to autoimmune pathology. We hypothesized that B55β modulates the differentiation and function of T_{FH} exercising an altered GC response.

To assess this, we elicited a humoral immune response using ovalbumin (OVA) and CFA in CD4.Cre$^{Ppp2r2b-/-}$ (B55β$^{-/-}$) and CD4.Cre$^{Ppp2r2b+/+}$ (B55β$^{+/+}$) mice, and analyzed the proportions of $T_{FH,}$ GC B cells and anti-OVA IgG_1 antibody production at different time points. We found a consistent higher proportion of T_{FH} cells in the draining lymph nodes (dLN) of B55β$^{-/-}$ mice and no difference in the GC B cell population. Furthermore, while no difference in total IgG serum levels was found, significantly higher anti-OVA IgG_1 antibody titers were found in the serum of B55β$^{-/-}$. In addition, equal results were observed transferring OT-II B55β$^{-/-}$ or B55β$^{+/+}$ T cells into CD45.1 mice before an immunization with NP-OVA in CFA.

Altogether, our study illustrates a B55β as a modulator of the GC response by regulating T_{FH} cell polarization. This data favors the understanding of autoimmune pathogenesis and advise the development of therapies for diseases or new approaches to vaccine efficacy.

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Resumen corto

Activating the non-apoptotic pathway of CD95 reverse cell arrest induced by IL-2 in cervical cancer cells

Gutiérrez-Hoya, A. [1,2], Ortiz-Garrido, I. [1], Zerecero-Carreón, O. [1], Weiss-Steider, B. [1], Soto-Cruz, I. [1*]

[1]Laboratorio de Oncología Molecular, Unidad de Investigación en Diferenciación Celular y Cáncer, FES Zaragoza, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Investigador Cátedra CONACYT, Ciudad de México, CDMX, México.
*E-mail: adrianagh85@hotmail.com ; sotocruz@unam.mx

Cervical cancer is the second cause of women's death and is a significant public health problem in Mexico. Therefore, it is necessary to study new molecules that can promote the elimination of tumour cells and serve as therapeutic targets that affect the immune system. We have shown that IL-2 induces cell arrest in cervical cancer cells but does not induce apoptosis. Cancer cells can escape from apoptosis by expressing CD95 at the cell membrane. CD95 signalling cascades are often altered in malignant tumours, leading to non-apoptotic signals that contributes to tumour growth, invasion and pro-inflammatory roles. However, the role of the CD95 pathway is not fully elucidated in cervical cancer. For this purpose, we determined the presence of CD95, its cognate ligand CD95L and its role in cell proliferation of IL-2-arrested cervical cancer cells. CD95 and CD95L staining in HeLa and SiHa cell lines was determined by flow cytometry. Cell lines arrested in the G1 phase by IL-2 were incubated with different concentrations of CD95 agonist to determine its effect on cell proliferation by the cristal violet technique. We found that both cell lines express CD95 and its ligand. Stimulating the CD95 pathway with low concentrations of the agonist induce cell proliferation. The cell arrest induced by 100 IU/mL of IL-2 was reversed when the cells were treated with the CD95 agonist. Our results suggest that cervical cancer cells use the CD95 pathway to promote cell proliferation and survival. Funding: PAPIIT (IN222121) DGAPA, UNAM

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Resumen corto

Enhancing effect on tumor apoptosis with the combined use of pentoxifylline plus chemotherapeutic agents *in vitro* and patients with Hodgkin Lymphoma

Gutiérrez-Ortiz, J.A. [1,4]*, González-Ramella, R.O. [3], Ortiz-Lazareno, P.C. [1], Bravo-Cuellar, A. [1], Aguilar-Lemarroy, A.C. [1], Del Toro-Arreola, S. [2]

[1]División de Inmunología, Centro de Investigación Biomédica de Occidente del Instituto Mexicano del Seguro Social; Guadalajara, Jalisco, México. [2]Instituto de Investigación de Enfermedades Crónico-Degenerativas, Departamento de Biología Molecular y Genómica del Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara; Guadalajara, Jalisco, México. [3]Servicio de Hematología y Oncología Pediátrica, Hospital Civil de Guadalajara Dr. Juan I. Mechaca; Guadalajara, Jalisco, México.[4]Doctorado en Ciencias Biomédicas con Orientación en Inmunología del Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara; Guadalajara, Jalisco, México.
*E-mail: alejandro.gutierrez2329@alumnos.udg.mx

Hodgkin Lymphoma (HL) is a B-cell neoplasm. Its treatment continues to be chemotherapy which causes severe adverse effects, especially with doxorubicin (DOX) and bleomycin (BLM). Therefore, new strategies are required to enhance treatment, reduce its duration and adverse effects, and improve clinical response. Pentoxifylline (PTX) inhibits NF-κB pathway and increases chemotherapeutic-induced apoptosis *in vitro*. It has been used in children with acute leukemia, observing an increase in tumor apoptosis and earlier remissions. PTX is proposed as an adjuvant to increase antitumor effect generated by chemotherapeutics in the Hs-445 cell line and patients with HL. In this work, apoptosis, cell cycle, senescence, and caspases will be evaluated by flow cytometry, and proliferation and mitochondrial membrane potential by spectrophotometry. Patients will be randomly and blindly administered PTX/placebo, serum levels of fortilin and cytochrome c will be quantified by ELISA, also clinical response and adverse effects will be evaluated. The recruited patients continue to be monitored, reporting nausea, vomiting, and menorrhagia as grade II and I. PTX induces greater cell death than DOX and BLM, with a pronounced effect when combined with BLM and triple treatment. PTX and BLM abrogate DOX-induced cell arrest in G2, increasing the percentage in G1. PTX increases the activity of caspases-3, -8, and -9, an effect increased when combined with DOX, BLM, or both, except with caspase-3 whose activity decreases when DOX is added. PTX has been used safely in patients; increasing apoptosis, enhancing when combined with DOX and BLM, by activating caspases and arresting in G1 phase.

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Resumen corto

Inhibitory effect of the human sperm acrosome reaction by the presence of reactive oxygen species in cumulus cells.

Gutierrez-Silva, A.L. [1]*, Berumen-Segura, L.C. [1], Tusie-Sanchez, A.A. [1], Garcia-Alcocer, G. [1], Escobar-Cabrera, J.E. [2], Vergara-Castañeda, H. [1]

[1]Unidad de Investigación Genética, Universidad Autónoma de Querétaro, Querétaro, México. [2]Laboratorio de Fisiología Celular y Molecular, Centro de Investigación Biomédica Avanzada, Universidad Autónoma de Querétaro, Querétaro, México.
*E-mail: agutierrez59@alumnos.uaq.mx

There are an estimated 48 million couples in the world suffering from infertility. In turn, oxidative stress (OS) has become an epicenter of a better understanding of the complexity of this global public health problem. A defense mechanism against OS in the oocyte is the barrier surrounding it, the cumulus cells (CC); beyond this, they reflect the physiological and quality status of the oocyte. One of the most impressive features of these cells is their ability to induce the acrosome reaction (AR), a fundamental step in fertilization. On the other hand, assisted reproduction techniques (ART) are a comprehensive alternative to treat infertility; however, the success rate remains at 30 %. Thus, this work aims to identify the relationship between the OS in the cumulus cells and the AR in human sperm to create strategies that help achieve a pregnancy. In this work, we evaluated the percentage of AR in the presence of CC with OS in human sperm by fluorescence microscopy using a PSA-FITC stain. We found that the oxidative stress induced in CC suppresses AR in a dose-dependent manner, suggesting that reactive oxygen species alter the ability of CC to induce AR and can be used as a predictor for success in ARTs.

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Resumen corto

Fucosyltransferase 4-derived peptides bio-conjugated to carbon nanotubes induce M1-like macrophage polarization

Guzmán-Mendoza, J.J. [1]*, Sánchez-Ramírez, B. [2], Cigarroa-Mayorga, O.E. [3], Orrantia-Borunda, E. [4], Talamás-Rohana, P. [1]

[1]Departamento de Infectómica y Patogénesis Molecular. Centro de Investigación y de Estudios Avanzados, CDMX, México; [2]Facultad de Ciencias Químicas, Universidad Autónoma de Chihuahua, Chihuahua, México; [3]Departamento de Tecnologías Avanzadas. UPIITA-Instituto Politécnico Nacional, CDMX, México. [4]Departamento de Medio Ambiente y Energía. Centro de Investigación en Materiales Avanzados, Chihuahua, México. *E-mail: jose.guzmanm@civestav.mx.

One of the most promising nanomaterials for nanovaccines developing is carbon nanotubes (CNTs), given the ease of bioconjugation and cellular uptake. Recently, we reported that fucosyltransferase-4 (FUT4), an enzyme responsible for aberrant fucosylation, is one important target in ovarian cancer. Here, we synthesize and characterize CNTs bioconjugated with a FUT4-derived peptide and test their biological interaction in J774A.1 macrophages.

For this, antigenic epitopes of FUT4 with affinity to MHC-I and MHC-II were predicted, modeled, and selected according to their best immunogenic characteristics. Peptides were synthesized and bioconjugated to CNTs (f-CNTs), which was confirmed by physicochemical methods. Assays in macrophages showed that f-CNTs induced morphological changes and activation without cytotoxicity. Lysosomal uptake and M1-type cytokine production were induced by f-CNTs in a time-dependent manner. Also, increased nitrite production, downregulation of arginase-1, and upregulation of CD80/86 and MHC-II molecules. These results demonstrate that f-CNTs are not cytotoxic, inducing M1-type activation and polarization in macrophages.

Taken together, CNTs bioconjugated with FUT4-derived peptides can be considered a safe candidate carrier system to be explored in ovarian cancer immunotherapies.

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Resumen corto

Changes in allatotropin levels in ventral nerve ganglia, hemolymph and brain of *Aedes aegypti* after an immune challenge

Guzmán-Rabadán, K.K. [1], Lozano, J. M. [2], Noriega, F.G. [3], Hernández-Martínez, S. [1*]

[1]Research Center for Infectious Diseases. National Institute of Public Health. Cuernavaca, Morelos, México. [2]Pharmacy Department, National University of Colombia, Bogota, Colombia. [3]Florida International University, Miami, FL, USA. * E-mail: shernandez@insp.mx

The neuropeptide allatoropin (AT) elicits immune responses in two important mosquito disease vectors, *Anopheles albimanus* and *Aedes aegypti*, suggesting a new role for AT, the modulation of the immune response in mosquitoes. Here we evaluate changes in AT levels in ventral nerve ganglia (VNG), hemolymph and brain of *Ae. aegypti* adult females after an immune challenge. Samples were obtained from sugar- or blood-fed mosquitoes at different ages or times post-injection of different microorganisms, including Dengue virus (DV) infection. The evaluation of AT was performed by an indirect ELISA and results were expressed as the mean ± SD, $p < 0.05$. The highest AT concentrations was observed in VNG and hemolymph at mosquito emergence (0h, 28.9±7 and 95.8±6 fmols/mosquito respectively). In sugar-fed, the lowest values were at 6-7 days-old (4.3±2 and 50.2±12 fmols/mosquito respectively). In 5-days-old, the highest AT values in VNG and hemolymph were observed at 6h (55.8±5 and 148.8±5 fmol respectively) and the lowest at 72h (3.8±0.5 and 46.9±11 fmols respectively) post-blood fed. In brains, from 0 to 7-days-old, an AT peak was observed at 4 days-old (19.8±3.7 fmol/brain), other days was 4.7±0.7 fmol. The immune challenge was performed at 5 days-old, without AT changes in brains at different times. However, in VNG and hemolymph important changes were observed at 2h post-challenge or during DV infection. In conclusion, AT concentration in VNG and hemolymph were directly proportional in basal conditions, and the immune-challenge or DV infection increase the AT levels in both tissues in similar proportion, suggesting that the AT found in hemolymph comes from VNG.

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Resumen corto

Analysis of antibody response in breast cancer patients

Hernández Aparicio, A.A. [1*], García Romo, G.S. [1],
Alanis López, P. [2], González Bermúdez, E.A. [2],
Pedroza González, A. [1]

[1]Unidad de Morfología y Función. Facultad de Estudios Superiores Iztacala, UNAM. Av. De los Barrios #1, Col. Los Reyes Iztacala, Tlalnepantla, Estado de México, 54090. [2]Unidad Médica de Alta Especialidad Hospital de Ginecología y Obstetricia No. 3, Centro Médico Nacional la Raza. IMSS. Clzd. Vallejo, esq. Antonio Valeriano, Col. La Raza, Ciudad de México. 02990.
*E-mail: aramh2107@gmail.com

Breast cancer is the most common neoplasm in women worldwide and the first cause of death by a malignant tumor. The molecular and cellular complexity of the tumor microenvironment (TME) defines the pathogeny, the therapeutic, and the prognosis of the disease. Although the antibody response is essential in the host's defense against microbes, its relevance and functions in breast cancer are not well understood. Therefore, the purpose of this study is to analyze the capacity of antibodies from breast cancer patients to bind tumor antigens and trigger effector mechanisms. For that, we evaluate the capacity of antibodies obtained from breast cancer patients to recognize antigens derived from tumor tissue lysates by ELISA and western blot. We found that serum antibodies from breast cancer patients were able to bind several tumor antigens, and we also detected the presence of antibodies in the TME. The main antibodies against tumor antigens were IgG, but we also observed other isotypes present in the TME, suggesting the participation of the humoral immune response within the tumor tissue in breast cancer patients.

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Resumen corto

Neutralizing antibody response against the SARS-CoV-2 Omicron BA.1, BA.5.1.6, BQ.1.3 and XBB1.1 subvariants after one dose of Ad5-nCoV and a booster with mRNA-1273 vaccine

Hernández, J. [1]*, Dehesa-Canseco, F. [2], Vázquez-López, A.B. [1], Reséndiz-Sandoval, M. [1], Caire-Juvera, G. [1], Solís-Hernández, M. [2], Valenzuela, O. [3], Gómez-Gil, B. [1], Mata-Haro, V. [1]

[1]Centro de Investigación en Alimentación y Desarrollo, A.C., Hermosillo, Sonora. [2]Comisión México-Estados Unidos para la Prevención de la Fiebre Aftosa y otras Enfermedades Exóticas de los Animales (CPA), SENASICA, SADER, Ciudad de México 05010. [3]Departamento de Ciencias Químico Biológicas, Universidad de Sonora, Hermosillo, Sonora, 83000, Mexico. *E-mail: jhdez@ciad.mx

In this work, we evaluated neutralizing antibodies against the SARS-CoV-2 ancestral strain (B.1.189) and Omicron BA.1, BA.5.1.6, BQ.1.3, and XBB.1 subvariants in serum samples from nonhospitalized adult participants immunized with a single dose of Ad5-nCoV and a booster eight months later with the mRNA-1273 vaccine. We used ELISA to analyze the anti-N and anti-RBD antibodies and a microneutralization assay with live virus to evaluate neutralizing antibodies against the ancestral strain and the Omicron BA.1, BA.5.1.6, BQ.1.3, and XBB.1 subvariants. The results demonstrate that neutralizing antibodies induced by the Ad5-nCoV vaccine can persist after eight months, similar to other COVID-19 vaccines. However, the neutralizing antibodies against Omicron BA.1 and BA.5.1.6 were lower and negative against BQ.1.3 and XBB.1. A heterologous booster with the mRNA-1273 vaccine increases the neutralizing antibodies, especially in previously infected individuals. However, the nAbs against BQ.1.3 and XBB.1 were still low, showing that vaccines, boosters, and infection are insufficient to neutralize these subvariants robustly. In conclusion, the combination of Ad5-nCoV vaccine with mRNA vaccines can be recommended as an immunization protocol against COVID-19.

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Resumen corto

Single-cell transcriptome analysis of B cells from convalescent patients with different clinical manifestations of COVID-19

Hernández, J. [1]*, García-Vega, M. [1], Llamas-Covarrubias, M.A. [2], Loza-López, M.J. [3], Reséndiz-Sandoval, M. [1], Hinojosa-Trujillo, D. [1], Melgoza-González, E.A. [1], Valenzuela, O. [4], Mata-Haro, V. [5], Hernández-Oñate, M.A. [6], Soto-Gaxiola, A. [7], Chávez-Rueda, K. [8]

[1]Laboratorio de Inmunología, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. [2]Research Institute for Microbial Diseases, Osaka University, 3-1 Yamadaoka, Suita, Japan. [3]Laboratory of Functional Analysis in silico, The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo, Japan.[4]Departamento de Ciencias Químico Biológicas, División de Ciencias Biológicas y de la Salud, Universidad de Sonora, Mexico. [5]Laboratorio de Microbiología e Inmunología, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. [6]Laboratorio de Fisiología y Biología Molecular de Plantas, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. [7]Hospital General del Estado de Sonora "Dr. Ernesto Ramos Bours", Secretaria de Salud del Estado de Sonora. Hermosillo, Sonora, Mexico. [8]Unidad de Investigación Médica en Inmunología, UMAE, Hospital de Pediatría, Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, Mexico.
*E-mail: jhdez@ciad.mx

The B cell heterogeneity and antibody-independent functions in response to SARS-CoV-2 infection are still limited. Some studies have suggested alterations in B cell subsets and signatures linked to poor prognosis. Therefore, further characterization is necessary to understand the roles of B cells and their associations to disease severity in COVID-19. Here, we performed single-cell RNA sequencing (scRNA-seq) of circulating B cells from convalescent COVID-19 patients with mild, moderate, severe, and critical manifestations. The transcriptome profiling analysis yielded 10 clusters, then the cell type annotation was performed based on gene expression markers. Within the identified cells, five subsets of memory B cells were observed, including atypical memory B cells (atMBCs), as well as naïve activated B cells, transitional B cells (T1, T2, T3), and antibody-secreting cells. Trajectory analysis showed the differentiation stages and confirmed cell identities. A predominant expansion of transitional B cells was observed in severe and critical donors, as well as atMBC in severe donors. Additionally, the differential gene expression and somatic hypermutation analyses of the different subsets allowed us to identify features associated with clinical conditions. Overall, our results showed a predominant expansion of different B cells subsets that could be associated with the disease severity and may help to better understand the antibody-independent functions of B cells in response to SARS-CoV-2 infection.

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Resumen corto

The immunomodulatory GK-1 peptide reduce the MDSC and the ability to invasiveness of tumor cells in the 4T1 murine model of breast cancer

Hernández-Aceves, J.A. *, Cervantes-Torres, J [2], Patiño, O. [1], Romero-Romero, L.[3], Pérez-Torres, A. [4], Fragoso, G[1], Sciutto, E.

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Mexico City, Mexico. [2]Departamento de Microbiología e Inmunología, Facultad de Medicina, Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico City, Mexico. [3]Departamento de Patología, Facultad de Medicina, Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico City, Mexico. [4]Departamento de Biología Celular y Tisular, Facultad de Medicina, Universidad Nacional Autónoma de México, Mexico City, Mexico.
*E-mail: jhdzaceves@gmail.com

Breast cancer is the most important women's cancer worldwide by its incidence and mortality, in which triple-negative breast cancer (TNBC) is the type with the worst clinical outcome. The experimental model of metastatic 4T1 breast cancer was employed to evaluate new therapies for triple-negative breast cancer. The tumor growth and metastasis are promoted by the tumor microenvironment and the immunosuppression that allow the escape of tumor cells.

GK-1 is an 18 aa peptide with anti-tumor and anti-metastatic effects that revert the intratumoral immunosuppression. Intravenous and subcutaneous administration of GK-1 (5 mg/kg, 4 times weekly) decrease myeloid-derived suppressor cells (MDSC) in the spleen quantified by flow cytometry. Histological analysis reveals that GK-1 reduced the red pulp in the spleen, diminished the granulophilia in peripheral blood, and also the weight and length of the spleens, all markers associated with a poor prognosis. In addition, GK-1 reduces the invasiveness of HS5-spheroids by 4T1 cells, observed by fluorescence microscopy.

Overall, these results point out that GK-1 not only decrease the PD-1 expression and restore the cytotoxicity of CD8 intratumoral cells but also reduces MDSC and limits its escape to other organs, such as the lung or lymph nodes. These results point to GK-1 as a promising molecule to be used in the immunotherapy for triple-negative breast cancer.

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Resumen corto

The Arp2/3 complex inhibitor, Arpin, regulates epithelial barrier functions during Ulcerative Colitis

Hernández-Almaraz, K.B. *, Montoya-García, A., Schnoor, M.

[1]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México.
*E-mail: karina.hernandez@cinvestav.mx

Ulcerative Colitis (UC) is an inflammatory bowel disease characterized by mucosal inflammation that is limited to the colon. Although its incidence has been higher in European and North American countries, other countries such as Mexico which used to have lower incidence rates, have shown a constant increase in recent years, affecting both female and male mostly between 20 to 40 years of age. The etiology of the disease remains elusive; however, the development of UC is influenced by the immune response, genetic factors and microambiental factors that lead to disruption of epithelial integrity leading to increased permeability, dysbiosis and an increase of leukocyte recruitment to the lamina propia. The actin cytoskeleton regulates the integrity of the epithelial barrier by stabilizing tight and adherence junctions; however, functions of actin regulators such as arpin during UC have not been studied in detail. The dextran sulfate sodium (DSS)-induced colitis model was applied in arpin-KO and WT mice and the disease activity index (DAI) was evaluated for 7 days. Arpin-KO mice showed a higher susceptibility for developing colitis with disease symptoms such as lost weight, bleeding in stools, starting much earlier compared to WT mice. Colon lengths were measured, showing around 40% colon length reduction in arpin-KO mice. We evaluated the permeability and TER in C2BBe1-arpinKD cells which have an increase in permeability and a decrease in TER. In future experiments, we will analyze leukocyte recruitment to the lamina propia to unravel whether neutrophil transepithelial migration is also affected in arpin-KO mice during colitis.

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Resumen corto

Antimicrobial effect of Aquiluscidin, a cathelicidin from *Crotalus aquilus,* against *Babesia* spp.

Hernández-Arvizu, E.E. [1,6]*, Rodríguez-Torres, A. [2], León Ávila, G. [3], Vega y Murguía, C. [2], Rivas-Santiago, B.T. [4], Asada, M. [5], Kawazu, S.I. [5], Mosqueda, J. [6]

[1]PhD Program in Natural Sciences, Natural Sciences College, Autonomous University of Queretaro, 76230 Queretaro, Mexico. [2]Natural Sciences College, Autonomous University of Queretaro, 76230 Queretaro, Mexico. [3]Department of Zoology, National School of Biological Sciences, National Polytechnic Institute, Carpio y Plan de Ayala S/N, C.P. 11340, Casco de Santo Tomas, Mexico City, Mexico. [4]Medical Research Unit Zacatecas-IMSS, Zacatecas, 98053 Zacatecas, Mexico. [5]National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Inadacho, Nishi 2-13, Obihiro, Hokkaido 080-8555, Japan. [6]Immunology and Vaccine Research Laboratory, Natural Sciences College, Autonomous University of Queretaro, 76230 Queretaro, Mexico. *E-mail: esau.hernandez@uaq.mx

Babesia spp. are protozoa parasites that infect animals and humans. Drug resistance and unwanted effects by current treatments have motivated research of new anti-babesia components. Antimicrobial peptides are positively charged amphipathic elements, which constitute part of living beings' innate immune mechanisms. Among the animals' produced peptides, cathelicidins stand out, due to their broad spectrum of activity against pathogenic microorganisms and their immunomodulatory functions. These properties have sparked interest in their study as a treatment of protozoan diseases. Aquiluscidin, a cathelicidin from *Crotalus aquilus*, and Vcn-23, its derivative molecule, previously exhibited antibacterial activity with non-detectable hemolytic and cytotoxicity effects on mammalian cells at microbicidal concentrations. This work aimed to characterize the effect of these peptides against three *Babesia* species. A 96-h inhibition assay was performed with *Babesia bigemina* (supplemented with bovine serum), *B. bovis* (two strains, one with serum addition and one without bovine serum), and *B. ovata* (without serum). *In vitro* cell cultures were tested with peptides in serial concentrations. Parasite growth was monitored by counting parasitized erythrocytes in Giemsa-stained smears. Aquiluscidin was effective against all *Babesia* species tested ($p > 0.05$) showing a decrease of 28% in *B. bigemina* growth (20 µM), with an IC_{50} of 14.48 and 20.70 µM against *B. ovata* and *B. bovis*, respectively. The *B. bovis* strain cultured with serum was not inhibited. Vcn-23 did not show babesiacidal activity. Aquiluscidin had anti-babesia activity, but its inhibitory effect is altered by the presence of serum in cell culture. However, this peptide represents a candidate for studying anti-protozoan properties.

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Resumen corto

Melatonin regulates the innate pro-inflammatory response induced by LPS in human fetal membranes

Hernández-Bones, K. [1,2]*, Flores-Espinosa, P. [1], Nájera-García, N. [3], Olmos-Ortiz, A. [1], Velázquez, P. [4], Zamora-Escudero, R. [5], Zaga-Clavellina, V. [1], Torres- Ramos, Y. [1], Mancilla-Herrera, I. [6]

[1]Departamento de Inmunobioquímica, Instituto Nacional de Perinatología, Ciudad de México, CDMX, México. [2]Maestría en Ciencias de la Salud, Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Sección de estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [5]Departamento de Ginecología y Obstetricia, Hospital Ángeles Interlomas, Estado de México, México. [6]Departamento de Infectología, Instituto Nacional de Perinatología, Ciudad de México, CDMX, México.
*E-mail: karlamhbones@gmail.com

Intrauterine infection is one of the main risk factor for premature rupture of fetal membranes (pPROM) a condition associated with 40% of preterm deliveries. The infection triggers an innate inflammatory response in fetal membranes, causing their rupture and compromising their function as a barrier to maintaining sterility and the amniotic cavity's anti-inflammatory milieu. The evidence indicates that antibiotics are ineffective in preventing pPROM because they do not control inflammation. Melatonin is a neurohormone that exerts anti-inflammatory effects in several tissues; this hormone is synthesized in the pineal gland and placenta during pregnancy. In this work, we evaluated the effect of melatonin on inflammatory factors secreted by human fetal membranes after choriodecidual challenge with *E.coli* LPS (*ex vivo* model of independent chambers: amnion and choriodecidua). TNF-α, IL-1β and IL-10 were measured by ELISA in supernatants from independent chambers. We found that melatonin decreases the release of pro-inflammatory factors induced by LPS in both chambers, suggesting that melatonin's immunoregulatory properties can be a possible strategy to repress the harmful effects of infections in fetal membranes.

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Resumen corto

Assessing Hybrid Immunity and Comorbidities in the Education Sector of Mexico: Insights from CANSINO/MODERNA Vaccination against SARS-CoV-2

Hernández-Casiano, J.O. [1], Pérez-Lara, J.C. [2], González-Herrera, S.L. [1], Santiago-Roque, I. [1,3], Lin-Valdivia, J.A. [4], Almanza-Domínguez, M.F. [4], Gallardo-Hernández, C.A. [1,5]*.

[1]Licenciatura de Química Clínica, Facultad de Bioanálisis de la Universidad Veracruzana, Xalapa, Veracruz, México. [2]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Laboratorio de Neurotoxicología, Facultad de Bioanálisis de la Universidad Veracruzana, Xalapa, Veracruz, México. [4]Facultad de Química Farmacéutica Biológica de la Universidad Veracruzana, Xalapa, Veracruz, México [5]Unidad de Servicios Analíticos en Salud Bioanálisis, Facultad de Bioanálisis de la Universidad Veracruzana, Xalapa, Veracruz, México. *E-mail: argallardo@uv.mx

Several vaccines against SARS-CoV-2 have been developed, and a combination of different vaccination schemes has been applied in some sectors of the population. In Mexico, the education sector has been immunized with a combination of CASINO and MODERNA vaccines. Hybrid immunity, which combines natural immunity from previous infection with immunity from vaccination, is an important process that enhances the immune response against infectious diseases. However, there is limited evidence evaluating hybrid immunity in populations vaccinated with the CANSINO/MODERNA scheme. Moreover, it has been demonstrated that comorbidities are a risk factor for developing severe COVID-19, and data on vaccine effectiveness in patients with comorbidities are limited. Therefore, a comparative cross-sectional observational study was conducted in the education sector of the State of Veracruz, involving 43 subjects who had previously been infected with SARS-CoV-2 or not, and who had received CANSINO/MODERNA vaccination. The concentration of anti-Spike IgG antibodies was evaluated using ELISA assay. The results showed that individuals with previous SARS-CoV-2 infection who received the CANSINO/MODERNA vaccination had higher levels of anti-Spike IgG antibodies compared to those who had not previously had COVID-19. Moreover, individuals with comorbidities had impaired anti-Spike IgG production despite having hybrid immunity. These findings indicate that antibodies against SARS-CoV-2 are produced after CANSINO/MODERNA vaccination, emphasizing the significance of hybrid immunity in the context of COVID-19. Additionally, these results underscore the detrimental effect of comorbidities on humoral response, potentially contributing to the increased risk of severe COVID-19 in individuals with underlying health conditions.

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Resumen corto

Histone H3 methylations in the *Aedes aegypti* mosquito during infection with dengue virus serotype-2

Hernández-Díaz, G.G. [1], Cime-Castillo, J. [1], Tello-López, Á. [1], Lanz-Mendoza, H. [1]

[1]Centro de Investigación Sobre Enfermedades Infecciosas (CISEI), Instituto Nacional de Salud Pública. *E-mail: gabriela.hernandez@insp.edu.mx

Dengue is the most prevalent arboviral disease. The *Aedes aegypti* mosquito is the main vector and, therefore, responsible for transmitting the virus to humans. Genes associated with the RNAi pathway, such as DICER-2, have been reported as effector genes that participate in the antiviral immune response (IR). Also described as a QTL related to DENV-2 susceptibility, however, their transcriptional regulation is unknown. Epigenetic mechanisms such as histone modification could be associated in determining a DENV-2 susceptible phenotype. The enrichment of mosquito IR effector genes and transcription factors related to the NOTCH and Jak-STAT pathways was observed in a study mapping epigenetic histone mark such as H3K27ac, H3K9ac, H3K9me3 and H3K4me. Therefore, the objective of the research project is to determine the methylation pattern in histone H3 of mosquitoes infected with dengue virus, as well as to identify the genomic sequences associated with the H3K27me3 and H3K4m3 marks. As a first step, the Rockefeller and Cuernavaca strains of *Aedes aegypti* were determined as strains with a DENV-2 susceptible phenotype, as well as the *in silico* presence of the methyltransferase machinery, and finally a purified extract of mosquito histones was obtained.

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Resumen corto

CRTAM regulates the balance between effector and memory precursors T CD8+ cells.

Hernández-Galicia, G. [1], Medina-Contreras, O. [2], Olvera-Gómez, I. [3], Ortiz-Navarrete, V.F. [1].

[1]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Unidad Zacatenco, Ciudad de México, México. [2]Unidad de Investigación Epidemiológica en Endocrinología y Nutrición, Instituto Nacional de Salud Hospital Infantil de México "Federico Gómez", Ciudad de México, México. [3]Laboratorio de Inmunología, Unidad de Investigación, Hospital Nacional Homeopático, Ciudad de México, México. *E-mail: gabriela.hernandez@cinvestav.mx

CRTAM is an adhesion molecule that belongs to the immunoglobulin superfamily of proteins. Their expression is inducible by the activation of T cells, mainly in CD8+ lymphocytes. It has been shown that CRTAM impacts the polarization of specific proteins like CD3 and CD44 and cytokine production like IFN-γ during the activation process of lymphocytes. Those processes affect the generation of CD8+ memory T cells and their precursors. Thus, we hypothesized a possible role of CRTAM in effector and memory precursor decision fate. To address this, we immunized B6(CRTAM$^{+/+}$) or CRTAM$^{-/-}$ mice with an attenuated *Salmonella enterica* serovar Typhimurium (*aroA*-) and the lymph nodes and spleen were recovered seven days after immunization. CD8+ effector memory precursors (MPECs; CD127+ of CD8+ cells) were identified by flow cytometry. We found an increase in MPECs frequency in lymph nodes from CRTAM-/-. In addition, the lymph nodes recovered from CRTAM$^{-/-}$ mice have increased in size compared to the control group. These results suggest the possible role of CRTAM in the acquisition of effector memory precursor fate.

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Resumen corto

Effect of Isthmin 1 protein on a tumor cell line

Hernández-Guerrero, V. [2,5*], Valle-Rios, R. [1,2],
Ángeles-Floriano, T. [1,3], Jaimes-Ortega, G.A. [2, 4].

[1]University Research Unit, Research Division, School of Medicine, National Autonomous University of Mexico-Federico Gomez Children's Hospital of Mexico (UNAM-HIMFG), Mexico City, Mexico. [2]Immunology and Proteomics Research Laboratory, Hospital Infantil de México Federico Gómez (HIMFG), Mexico City, Mexico. [3]Department of Clinical Diagnostics and Clinical Laboratory Department, Hospital Infantil de México Federico Gómez, Mexico City, Mexico. [4]Postgraduate degree in Experimental Biology, Department of Biological and Health Sciences, Universidad Autónoma Metropolitana (UAM), Mexico City, Mexico. [5]Bachelor's degree in Biology, Department of Biological and Health Sciences, Universidad Autónoma Metropolitana (UAM), Mexico City, Mexico.
*E-mail: valeriahernandezguerrero1@gmail.com

Isthmin 1 (ISM1) is located on human chromosome number 20 and 2 in mouse, it is expressed in skin, tissues, mucous membranes, and lymphocyte populations. It has been demonstrated that ISM1 has a direct link with the immune system in mammals, participating in inhuman and acquired immune responses, expressing directly in NK, CD4+ and TH17 cells. It is also responsible for encoding secreted proteins that present signal peptide domains, adhesion-associated peptide domains (AMOP) and thrombospondin domains (TSR), demonstrating that it has antiangiogenic, antitumor and proapoptotic properties.

Childhood acute lymphoblastic leukemia (ALL) is a type of cancer of the blood and bone marrow, the most common type of cancer and the second leading cause of mortality among Mexican children, with a relapse rate of 20%.

In the present investigation, we set out to analyze the cell viability of SUP-B15; a B lymphoblast cell line isolated from the marrow of an 8-year-old white male patient with acute lymphoblastic leukemia, following treatment with recombinant human ISM1.

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Resumen corto

Altered trafficking receptors in non-conventional T cells in Severe Cutaneous Adverse Reactions

Hernández-Jaimes, O.A. [1]*, Cazares-Olvera, D.V. [1], Rodríguez-Cortés, O. [2], Méndez-Flores, S. [3], Domínguez-Cherit, J. [3], Castrejón-Flores, J.L. [1]

[1]Laboratorio de Biología Molecular y Cultivo Celular, Unidad Profesional Interdisciplinaria de Biotecnología-Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Inflamación y Obesidad, Escuela Superior de Medicina-Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, CDMX, México.
*E-mail: ohernandezj0901@alumno.ipn.mx

Drug hypersensitivity reactions are mediated by T-cells, but non-conventional T-cells like MAIT, NKT, and γδ T-cells are also involved. MAIT cells have been found to be altered in patients with severe cutaneous adverse reactions (SCARs). The objective of this study was to determine the frequency and T-cell trafficking receptors of non-conventional T-cells in SCARs patients using multiparametric flow cytometry analysis. The study analyzed samples from SCARs patients and used markers CD103, CLA, CXCR3, associated with mucosal, skin, and liver tissues, respectively, to identify upregulation of trafficking receptors. The results showed upregulation of trafficking receptors in non-conventional T-cells associated with the severity of the reaction. In conclusion, non-conventional T-cells like MAIT cells are involved in drug hypersensitivity reactions, and their altered trafficking receptor expression may contribute to the severity of these reactions. The findings suggest that targeting these receptors could be a potential therapeutic approach for the treatment of SCARs.

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Resumen corto

Allele specific gene expression during tolerance induction on dendritic cells from Mexican women with systemic lupus erythematosus.

Hernández-Ledesma, A.L. [1*], Nuñez-Reza, K.J. [1], Torres-Valdez, E. [2], Peña-Ayala, A. [3], Tinajero-Nieto, L. [3], Felix-Rodríguez, G. [4], Frontana-Vázquez, G. [2], Rosetti-Sciutto, F. [5], Fernández-Valverde, S.L. [6], Gutierrez-Arcelus, M. [7,8,9,10,11], Alpízar-Rodríguez, D. [12], Medina-Rivera, A. [1].

[1]Laboratorio Internacional de Investigación sobre el Genoma Humano, Universidad Nacional Autónoma de México, Querétaro, México. [2]Hospital General Regional No. 2, Instituto Mexicano del Seguro Social, Querétaro, México. [3]Hospital General Regional No. 1, Instituto Mexicano del Seguro Social, Querétaro, México. [4]Capítulo de Reumatología, Querétaro, México. [5]Departamento de Inmunología y Reumatología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Tlalpan, Ciudad de México, México. [6]Unidad de Genómica Avanzada, Langebio, Centro de Investigación y Estudios Avanzados del Instituto Politécnico Nacional, Irapuato, Guanajuato, México. [7]Center for Data Sciences, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts, USA. [8]Division of Genetics, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts, USA. [9]Division of Rheumatology, Inflammation and Immunity, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts, USA. [10]Program in Medical and Population Genetics, Broad Institute, Cambridge, Massachusetts, USA. [11]Division of Immunology, Department of Pediatrics, Boston Children's Hospital, Harvard Medical School, Boston, Massachusetts, USA. [12]Research Unit, Colegio Mexicano de Reumatología, México City, Mexico.
*E-mail: alhernandezledesma@liigh.unam.mx

Loss of immune tolerance plays a key role in Systemic Lupus Erythematosus (SLE) etiology. Tolerogenic dendritic cells (tolDCs) are a target of interest due its ability to polarize the immune response towards an anti-inflammatory profile, potentially restoring the tolerance. Although the genetic contribution to SLE has been proven there is still scarce information underlying the involved genes and regulatory mechanisms. Allele specific expression (ASE) can establish gene regulatory mechanisms that can be associated with physiopathological processes. This study aims to characterize ASE patterns during tolDC differentiation from monocytes of Mexican women with SLE. Samples were obtained from 30 volunteers with SLE and 10 non-SLE participants. Monocytes were isolated and cultured with GM-CSF and IL-4 for monocyte-derived dendritic cells (moDCs) and GM-CSF, IL-4 and IL-10 for tolDCs. CD14, CD11c, CD80, CD40 and HLA were measured by flow cytometry to evaluate cell isolation and differentiation, RNA sequencing will be performed in all samples and participants will undergo whole genome sequencing. Finally, ASE dynamics will be determined across differentiation and tolerization. The cytometry showed a higher percentage of cells expressing CD14 and CD11c were observed on both dendritic cell cultures when compared to monocytes. Similar pattern was observed for the percentage of cells expressing MHCII, CD40 and CD80 markers in both groups after differentiation. Further integration of RNA and DNA information will allow us to identify ASE patterns associated with the tolerogenic potential of dendritic cells from Mexican women with SLE. Funding: CONACYT-FORDECYT-PRONACES grants no. [11311] and [6390]. Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica–Universidad Nacional Autónoma de México (PAPIIT-UNAM) grants no. IA203021 and IN218023. A.L.H.L. is a doctoral student from Programa de Doctorado en Ciencias Biomédicas, Universidad Nacional Autónoma de México (UNAM) and she received fellowship CVU/Becario (711015/790972) from Consejo Nacional de Ciencia y Tecnología (CONACYT).

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Resumen corto

Standardization of RT-qPCR for the detection of CD4+ T cells biomarkers in PLWH and syphilis co-infection.

Hernández-Pliego, A. [1], Vergara-Ortega, D.N. [1*],
Sánchez-Alemán, M.A. [1].

[1]Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, México.*E-mail: nicte.vergara@gmail.com

Syphilis is a sexually transmitted disease caused by *Treponema pallidum*. According to the CDC, it has been re-emerging powerfully in recent years, especially in men who have sex with men (MSM) and people living with HIV (PLWH). Due to a lack of an accurate animal model and cell culture is complex with the spirochete, the immunological response against the bacteria remains unclear. On previously published work, we established the kinetics of the immune response against syphilis and hypothesized how $CD4^+$ T cells, such as Th17 and T rex cells, worsen the progression of the disease in PLWH through their hallmark cytokines, IL-10 and IL-17, and how these two cytokines may play important roles as biomarkers. To asses this theory, we took MIQE guidelines to standardize RT-qPCR 2-step to associate the immunological profile and syphilis stage (active, latent and treated) in PLWH. We were able to amplify STAT-1, T-bet, Foxp3 and RORc transcription factors to differentiate $CD4^+$ T cell subpopulations (Th1, Trex and Th17) and GAPDH as housekeeping gene with reaction efficiencies greater than 95%. We managed to generate a biobank of cDNA from PLWH and syphilis co-infection (n=400). It is necessary to apply the proposed molecular technology to corroborate the published theoretical data and associate these results to clinical history.

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Resumen corto

Serum expression of TGF-β cytokine as a key to understand latent syphilis in PLWH: a cross-sectional study.

Hernández-Pliego, A. [1*], Vergara-Ortega, D.N. [1], García-Cisneros, S. [1], Olamendi-Portugal, M.L. [1], Román-Acevedo, Y. [2], Sánchez-Alemán, M.A. [1].

[1]Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México.[2]Centro Ambulatorio para la Prevención y Atención de SIDA e Infecciones de Transmisión Sexual, Cuernavaca, Morelos, México.
*E-mail: dcei.ahp@gmail.com

Treponema pallidum subs. *pallidum* is the etiological cause of syphilis. In recent years has been reported to be re-emerging. The CDC estimated a resurgence of 76% especially in men who have sex with men (MSM) and people living with HIV (PLWH). $CD4^+$ T cells are the target cells for HIV, along with CXCR4 and CCR5 receptors. For *T. pallidum*, how people go from active to a latent stage remains unclear. In a systematic review, previously published in our group, we established that, certain cytokines from $CD4^+$ T cells may be playing as hallmark biomarkers in the progression of syphilis in PLWH. Due to a lack of an accurate animal model, it becomes important to study how the immune system works against *T. pallidum* in PLWH. Here we evaluate the serum expression of IFNγ, TNF, IL-10, TGF-β and IL-17 in PLWH and its association in different stages of syphilis (active, latent and treated). Between march to October 2022, we recruited 883 PLWH. Out of all these participants, 78% were MSM and 53% from this, tested positive to syphilis; 24% had active stage, 37% latent and 39% treated or had previously have syphilis infection. From the analyzed cytokines, TGF-β demonstrated to be statistically significative in latent syphilis group versus those who previously had it (treated group). This result suggests that TGF-**β** may be playing as a biomarker in latent stage and could be suppressing the inflammatory response against the spirochete, resulting in elevating the treponemic load and allowing disease progression.

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Resumen corto

Identification of malignant cells through the phenotype associated with the mechanism of activation of the Th2 locus via NLRP3 in patients with CTCL.

Hernández-Rico, B. [1,2]*, Pérez-Koldenkova, V. [3],
Lemini-López, A. [3], Bonifaz-Alfonzo, L.C. [1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, CMN siglo XXI, Ciudad de México, CDMX, México. [3]Laboratorio Nacional de Microscopía Avanzada, CMN siglo XXI, Ciudad de México, CDMX, México. [4]Servicio de Dermatología, CMN siglo XXI, Ciudad de México, CDMX, México.
*E-mail: breen.henzric@gmail.com

Identifying the malignant cells in cutaneous T-cell lymphoma (CTCL) cell has become challenging due to the heterogeneity of the cells present in the skin and the lack of unique markers to identify them. Previous work from our research demonstrated that the malignant cells express IL4 by activating the Th2 locus via NLRP3 in its role as a transcription factor. In this work, we evaluated whether a phenotype associated with the mechanism of IL-4 expression via NLRP3 allows the identification of the malignant cells in skin biopsies of CTCL. Since this disease has a chronic behavior, we evaluated the exhaustion phenotype associated with the NLRP3 mechanism through immunofluorescence. We found that in early stages of the disease NLRP3+ malignant cells express both progenitor (TCF-1+) and terminal phenotype (TIM3+). Remarkably in advanced stages, TIM3 an inhibitor molecule was significantly decreased. When evaluating whether the nuclear localization of NLRP3 could affect TIM3 in a primary CTCL cell line (HTB-176), we observed a significant reduction of TIM3 expression suggesting a new role for NLRP3 down regulating the expression of this inhibitor receptor. Taken together, our results suggest that activation of the Th2 locus via NLRP3, could also be associated with a molecular signature that can help in the identification and prognosis of CTCL patients, as well as in the understanding of the pathogenesis of the disease.

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Resumen corto

Development of Human Antibodies against SARS-CoV-2 Variants of Concern

Hernandez-Rivera, D.V. [1]*, Muñoz-Herrera, J.C. [1], Vázquez-Leiva, S. [1], Pelcastre-Gómez, A.Y. [1], Salinas-Trujillo, J.R. [1], Pérez-Tapia, S.M. [1], Pedraza-Escalona, M. [1].

[1] Unidad de Desarrollo e Investigación en Bioterapeuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México.
*E-mail: dhernandezr1708@alumno.ipn.mx

Although the vaccination schemes against COVID-19 represented a great advance in the reduction of infection severity by increasing the immune response to patients, the high rate of mutation of SARS-CoV-2 maintains the possibility of new outbreaks. In this work, we select and characterize a group of human monoclonal antibodies able to recognize and neutralize SARS-CoV-2 variants of concern (VOC) using the Epstein-Barr virus immortalization human B cells method. From 1.5 to 19 x10E6 B lymphocytes (CD22+), we obtained between 0.073% to 0.29% B cells that produce specific antibodies against RBD. After immortalization, 64 positive clones were obtained from a patient convalescent to Omicron BA.1 variant and 59 from a patient convalescent to Omicron BA.4/BA.5 variant. The lymphoblastic cell line P7F8 produces an antibody (IgG isotype) with a lambda light chain germline genes IGHV3-25*3 and IGHV2*01 and a heavy chain germline genes IGHV6-1*02, IGHJ4*02 and IGHD3-22*01. The last one has a YYDRxG-like motif, which has been reported to be important in the recognition and neutralization to different SARS-CoV-2 RBD variants. The antibody has been purified and the affinity constants towards different variants have been determined: 2.25nM to S1, 1.89 nm to RBD WT, 2.32nM to Beta variant, 3.52nM to Delta, 3.27nM to Delta+ and 1.46nM to Omicron BA.4/BA.5. This antibody targets a highly conserved epitope among the different VOC, which can be used in diagnostic and therapeutic approaches.

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Resumen corto

Intestinal permeability markers and cytokines as early predictors of mortality in COVID-19 patients

Hernández-Solis, A. [1,2], Güemes-González, A.M. [3], Castañeda-Casimiro, J. [3,4], Estrada-Parra, S. [3], Chacón-Salinas, R. [3], Soria-Castro, R. [3], Ruiz-Sánchez, B.P. [5,6], Wong-Baeza, I. [3]

[1]Servicio de Neumología, Hospital General de México "Dr. Eduardo Liceaga", Secretaría de Salud, Ciudad de México, México. [2] Facultad de Medicina, Universidad Nacional Autónoma de México (UNAM), Ciudad de México, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN), Ciudad de México, México. [4]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN), Ciudad de México, México. [5]Facultad de Medicina. Universidad Westhill, Ciudad de México, México. [6]Departamento de Bioquímica, Facultad de Medicina, Universidad Nacional Autónoma de México (UNAM), Ciudad de México, México

Coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), can present mild, moderate or severe symptoms, or critical symptoms that resemble those of sepsis. In the latter case, a deregulated immune response to SARS-CoV-2 infection leads to organ failure and to a high morality risk. It has been suggested that sepsis involves an increase in intestinal permeability, which leads to greater microbial translocation from the intestine to the bloodstream, and hence to a higher inflammatory response in the patient. In this study, we measured the serum concentration of cytokines associated with the innate and the adaptive immune responses, and the serum concentration of molecules associated with the integrity of the intestinal barrier, in patients with moderate, severe and critical COVID-19. Our results indicate that IL-6, IL-10, granulysin, and sFas may be early biomarkers of fatal disease outcomes. In addition, we found that D-lactate, a metabolite produced by bacterial fermentation, and zonulin, a molecule that disassembles the tight junctions of the intestinal epithelial cells, were elevated in the serum of patients with severe COVID-19 and in those patients with secondary infections. These results suggest that, in addition to cytokines, markers of intestinal permeability may be useful for the early identification of fatal outcomes in COVID-19 patients.

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Resumen corto

Comparison of genomic abnormalities between childhood and adult B cell lymphomas

Hernandez-Valenzuela, M.A. [1,2], Fuentes-Pananá, E.M. [2]

[1]Doctorado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Químico Biológicas, Instituto Politécnico Nacional, CDMX, México. [2]Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México "Federico Gómez", CDMX, México.
*E-mail: hv.marcoa@gmail.com

Although lymphomas can affect pediatric and adult patients, they differ in several ways. The incidence of different lymphoma histological subtypes, prognosis and treatments varies with the age. We compared available expression and genetic data from public databases such as NCBI Gene Expression Omnibus and R2genomics to search for the most recurrent genetic abnormalities in pediatric and adult lymphomas, particularly B-cell lymphomas, which account for 90% of all lymphomas. Hodgkin lymphoma (HL) and Burkitt lymphoma (BL) are more common in childhood, contrary to diffuse large B-cell lymphoma (DLBCL) and follicular lymphoma (FL), which are more frequent in adulthood. BL is characterized by rearrangements in the *MYC* gene, usually children have a better prognosis than adults. Most pediatric BL cases, present activating mutations in *TCF3* or inactivating mutations in *ID3*. The genetic hallmark of adult FL is the t(14;18) (q32;q21) translocation in *IGH-BCL2*. However, pediatric FL rarely carry this translocation, instead they tend to have mutations in *MAP2K1* that are uncommon in adults. Pediatric DLBCL rarely exhibit the t(14;18) translocation involving the *IGH-BCL2* genes that is very common in its adult counterpart. In contrast, they often exhibit rearrangements in *MYC* leading to pediatric DLBCL with a signature similar to BL. We found that although pediatric and adult patients could have the same histologic group of lymphoma, the genetic abnormalities in the tumor and its behavior could vary greatly. Identifying genetic differences in tumors from pediatric and adult patients with lymphoma could facilitate diagnosis and better patient stratification, leading to more effective and less toxic treatment in both pediatric and adult patients.

Keywords: Lymphoma, pediatric, adulthood, abnormalities

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Resumen corto

Analysis of the different subsets of effector and memory T cells in individuals with immunity against SARS-CoV-2

Hernández-Valenzuela, S. [1]*, García-Vega, M. [1], Reséndiz-Sandoval, M. [1], Hernández, J. [1]

Laboratorio de Inmunología, Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora, Mexico. *E-mail: sofiahdzval@gmail.com

Since the onset of the COVID-19 pandemic, several research groups have tried to understand the adaptive immune response against SARS-CoV-2 to generate therapies, improve the design and administration of vaccines and define the characteristics of the protective immune response. Moreover, the emergence of new variants brings doubts about the effectiveness of our immunity generated after two years of the pandemic. The response of $CD4^+$ T cells plays an essential role in the control of infection against SARS-CoV-2, and it needs to know the function, conformation, and kinetics of the cellular response to COVID-19. In this work, we evaluated the different subpopulations of $CD4^+$ T lymphocytes by flow cytometry, after the stimulation of mononuclear cells from infected or vaccinated individuals (n=10) against SARS-CoV-2 proteins. In this way, we allowed the activation of $CD4^+$ T different subtypes: Tfh, Th1, Th2, Th17, CM, EM1, EM2, EM3 and EMRA. Early response of $CD4^+$ T cells correlated with a good long-lasting humoral response, highlighting the importance of T cell immunity in defining response to vaccination. Our data revealed that SARS-CoV-2-specific helper and memory lymphocytes expanded upon antigen reencounter. The specific functions and kinetics of these adaptive immune responses are discussed, as well as their interplay with innate immunity and implications for COVID-19 immune memory against reinfection.

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Resumen corto

Detection of *Brucella abortus* in intestinal epithelial cells during an infection kinetic in a murine model intragastrically inoculated

Herrera-Torres, E. [1*], Sánchez-Argáez, A.B. [2],
Moreno-Lafont, M.C. [1], Vega-López, M.A. [3],
López-Santiago, R. [1].

[1]Departamento de Inmunología. Escuela Nacional de Ciencias Biológicas. Instituto Politécnico Nacional. Prol. de Carpio y Plan de Ayala s/n. Del. Miguel Hidalgo. CP 11340. Ciudad de México. México. [2]Departamento de Biomedicina Molecular. Centro de Investigación y de Estudios Avanzados (CINVESTAV). Instituto Politécnico Nacional. Av. IPN No. 2508. Del. Gustavo A. Madero. CP 07360. Ciudad de México. México [3]Departamento de Infectómica y Patogénesis Molecular. Centro de Investigación y de Estudios Avanzados (CINVESTAV). Instituto Politécnico Nacional. Av. IPN No. 2508. Del. Gustavo A. Madero. CP 07360. Ciudad de México. México. *E-mail: estefa_h@hotmail.com.com

Bacteria of the genus *Brucella* are the causal agent of the zoonosis called brucellosis, whose main route of entry is oral. It has been possible to recover the bacteria from Peyer's patches, mesenteric lymph node and feces of intragastrically infected mice even after prolonged periods postinfection. *In vitro* assays have shown that *Brucella* is able to adhere to epithelial cells. Intestinal epithelial cells (IEC) are one of the first points of contact for the bacteria and establish a close communication with antigen-presenting cells and lymphocytes of the lamina propria. In this way, the IEC could play an important role in the infection by *Brucella* and probably in the evasion of the immune response. The determination of *Brucella* associated to IEC in a murine model infected by the intragastric route, will allow to understand the interactions of *Brucella* with the IEC which can influence the immune response and the evolution of the disease. In this model it was detected the presence of the bacteria associated to IEC from mice for 48 hours up to 5 weeks after infection. Histological analysis showed damage in the intestinal tissue as the infection progressed. Detection of the bacteria with immunofluorescence will allow to determine its location within the intestine. These findings reinforce the possibility that IEC play an important role during *Brucella* infection and could act as a reservoir.

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Resumen corto

Evaluation of IL-10 and IL-4 in a cohort of patients with metabolic dysfunction-associated fatty liver disease (MAFLD).

Hipólito-Vicente, A.G. [1,2]*, Hernández-Flores, K.G. [1], Domínguez-Alemán, C.A. [1], Priego-Parra, B.A. [1], Vivanco-Cid, H. [1].

[1]Instituto de Investigaciones Médico-Biológicas, Universidad Veracruzana, Región Veracruz, Veracruz 91700, México. [1,2] Facultad de Bioanálisis, Universidad Veracruzana, Región Veracruz 91700, México. *E-mail: angel_hipolito1@hotmail.com

Metabolic dysfunction associated fatty liver disease (MAFLD) is characterized by an accumulation of lipids in the hepatocytes, causing inflammation and damage of the liver tissue, inducing liver regeneration and scarring by depositing collagen to replace the damaged tissue. If the lesion is persistent, over time the capacity for liver regeneration decreases, which causes fibrosis that can progress to cirrhosis and liver carcinoma. MAFLD affects one third of the world's population with 50.77%, with diabetes mellitus type 2 and obesity being the main factors. In order to understand more about the pathogenesis of this disease and the behavior of these molecules in inflammation and liver fibrosis, we measured the levels of anti-inflammatory cytokines such as IL-10 and IL-4 in MAFLD and fibrosis patients. In this study we evaluated blood serum from healthy subjects, MAFLD subjects without fibrosis and MAFLD subjects with fibrosis by ELISA. In our preliminary results, we found no significant difference in IL-10 levels between the study groups. Other studies have reported that IL-10 levels correlate negatively between healthy subjects and patients with MAFLD, suggesting that there is insufficient anti-inflammatory compensation caused by a defect in its function or in the production of this cytokine related to disease progression.

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Resumen corto

Oral administration of Bacillus thuringiensis Cry1Ac toxin induce changes in the cellular populations in gut mucosal tissue

Ilhuicatzi-Alvarado, D. [1]*, Betanzos-Laguna, X.I. [1],
Bautista-Jacobo, I.S. [1] Moreno-Fierros, L. [1]

[1]Laboratorio de Inmunidad de Mucosas, Unidad de Biomedicina UBIMED, FES-Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Edo. Mex., México.
E-mail:damarisialvarado4@gmail.com

The Bacillus thuringiensis Cry1Ac toxin are widely used as biopesticides and can be expressed by genetically modified plants for human and animal consumption like BT crops. Cry1Ac is not toxic for vertebrates; however, previous studies from our group have shown that recombinant Cry1Ac toxin is able to activate the adherent macrophages, T lymphocytes and B lymphocytes. Here we evaluated the intestinal inflammatory potential of Cry1Ac toxin. We used for these experiments a model of acute intestinal inflammation induced with DSS 3% for 7 days. Mice were administered intragastrically with: i) vehicle phosphate-buffered saline, ii) Cry1Ac toxin 2g/l iii) Cry1Ac toxin 20 g /l iv) Cry1Ac toxin 50 g/l v) DSS 3% for 7 days. After 7 days we evaluated the characteristics like blood in feces, large intestine size, weight loss, inflammatory production of cytokines in explants, and histopathologic changes were evaluated at intestinal and systemic level. The Cry1Ac administered experimental groups; developed moderate inflammation related reactions. While only the positive group DSS 3% presented severe inflammatory features such as blood in feces, weight loss, and reduction of intestinal size. The measure of cytokine levels in the Cry1Ac administered groups in explants showed significant production of IL6 and reduction of IL10 levels with respect to the vehicle group. Interestingly, these Cry1Ac groups also showed colonic lymphoid hyperplasia. The histopathological analysis in these Cry1Ac administered groups revealed edema with apparent recruitment of neutrophils. The outcomes sustain that via intragastric administration Cry1Ac toxin does not provoke severe inflammation but it is not innocuous.

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Resumen corto

Response of NKT cells and Tγδ lymphocytes to mycobacterial antigens in mice

Isidro-Magallán, J.E. [1]*, Galarce-Sosa, E.I. [1], Sotelo-Rodríguez, A. [1], Barrera-Aveleida, G.B. [1], Reséndiz Mora, C.A. [1,2], Baeza-Ramírez, M.I. [1,2], Wong-Baeza, C. [1,2]

[1]Laboratorio de Biomembranas, Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [2]Laboratorio de Enzimología, Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. E-mail: eliazisidro@gmail.com

The Tuberculosis (TB) is a disease caused by Mycobacterium tuberculosis (MTB). According to the WHO, it is estimated that about a quarter of the world's population has been infected with TB, although the development of the disease will depend on the degree of exposure and immune response. The cell wall of MTB is a contributing factor to the establishment of infection, since it provides resistance to different agents. One of the main components of the MTB cell wall are lipids. Natural killer T (NKT) cells and γδ T lymphocytes (Tγδ) respond to lipid antigens, being important to resolve the infection. In this work we will evaluate the mouse response of NKT and Tγδ to lipids isolated from *Mycobacterium tuberculosis* strain H37Rv and *Mycobacterium smegmatis* and compare this response to a murine model of lupus. Lipids will be isolated from each strain and by open column adsorption chromatography, the polar lipid fractions will be separated and administered to C57BL/6 mice via intrasplenic and intraperitoneal; the murine model of lupus will be developed through the administration of liposomes with lipid particles. Flow cytometry will be used to identify and ascertain the activity of NKT and Tγδ.

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Resumen corto

Immunepotent CRP in combination with cyclophosphamide or etoposide induces synergistic cell death in tumoral T-cell lymphoblasts

Izaguirre Rodríguez, M. [1]*, Rivera Lazarín, A.L. [1],
Rodríguez Padilla, C. [1], Martínez Torres, A.C. [1]

[1]Universidad Autónoma de Nuevo León. Facultad de Ciencias Biológicas. Laboratorio de Inmunología y Virología. San Nicolás de los Garza, Nuevo León, México.
E-mail: ana.martinezto@uanl.edu.mx

Chemotherapy such as cyclophosphamide (CTX) or etoposide (ETO) is one of the main treatments for hematologic cancers, however, it lacks selective cytotoxicity. Therefore, its use in combination therapies has been proposed to reduce cell death on healthy cells, and to prevent cell death resistances. Immunepotent CRP (ICRP) is an immunotherapy that induces selective cytotoxicity to cancer cells. However, its effect in combination with chemotherapies against hematologic cancer cells is unknown. To analyze cell death induced by ICRP plus CTX or ETO in tumoral T-cell lymphoblasts and its effect in peripheral blood mononuclear cells (PBMC). Human (CEM) and murine (L5178Y-R) tumoral T-cell lymphoblasts were treated with ICRP, CTX or ETO and ICRP+CTX/ETO at different combination ratios for 24 h. Trypan blue exclusion was used for cancer cell death determination. Combinatorial index (CI) and dose reduction index (DRI) were quantified using Compusyn software. The effect of the combinations on PBMC was evaluated using annexin V and propidium iodide by flow cytometry. ICRP plus CTX/ETO induced synergistic cell death in tumoral T-cell lymphoblasts since sublethal (non-toxic) or low concentrations of ICRP, whereas in PBMC, ICRP did not increased chemotherapy-cell death. Furthermore, DRI showed that ICRP at sublethal or equipotent concentration to chemotherapy promotes a significant dose reduction of CTX/ETO. These results suggest that the combination of ICRP with CTX or ETO is an effective combination therapy, as ICRP doesn't reduce but potentiates chemotherapy-cytotoxicity in hematologic cancer cells.

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Resumen corto

A potential role of Isthmin 1 in the gut

Jaimes-Ortega, G. A. [1,2,3]*, Cruz-Córdova, A. [4], Valle-Rios, R. [2,3]

[1]Posgrado en Biología Experimental, Departamento de Ciencias Biológicas y de la Salud, Universidad Autónoma Metropolitana (UAM), México City, México. [2]Laboratorio de Investigación en Inmunología y Proteómica, Hospital Infantil de México Federico Gómez (HIMFG), México City, México. [3]Unidad Universitaria de Investigación, División de Investigación, Facultad de Medicina, Universidad Nacional Autónoma de México-Hospital Infantil de México Federico Gómez (UNAM-HIMFG), México City, México. [4]Laboratorio de Investigación en Bacteriología Intestinal, Unidad de Investigación en Enfermedades Infecciosas, Hospital Infantil de México Federico Gómez, 06720 Ciudad de México, México.

The gut is constantly exposed to a large antigenic load, this tissue protects the host by competing with pathogens for nutrients and space. Isthmin 1 (ISM1) is a constitutively secreted protein produced by barrier tissues, such as skin and mucous-associated tissues, for example, intestine and lung. Under inflammatory conditions, ISM1 levels are altered, suggesting that ISM1 is a molecule that could be related to the regulation of inflammatory events; for example, during infectious processes. Our group recently described that in a model of intestinal infection, the frequency of ISM1+ cells are increased and levels of luminal/secreted ISM1 are also elevated. However, the different cell subsets of ISM1 producing cells are not known, and more important, the biological role of ISM1 in the gut is missing Therefore,to understand the importance of ISM1 in the physiology of the gut, the objective of this project is to characterize the phenotype of ISM1+ expressing cells in the lamina propria of the small intestine in a model of microbiota depletion and during pathogenic bacterial infection, along with the measurement of inflammatory markers. So far, we found that Isthmin 1 is expressed in CD45+ cells in the intestine, and part of those had a LSK phenotype. Also, ISM1 is expressed in CD3+, CD8+, and Ly6g+ cells. In addition, in experiments to determine the susceptibility of bacteria to ISM1, it was observed that both, mouse and human recombinant ISM1 decreased the growth of *Enterococcus faecalis*. These data suggest that ISM1 is produced by cells related to the immune response and it may react against intestinal pathogenic bacteria. The project was financed with the support of the basic science project 222775 and the project HIM 2019/044 SSA 1598 and federal funds HIM/2022/FF.

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Resumen corto

Phenotypic characterization of innate lymphoid cells and γδ T lymphocytes in the omentum of a mouse model of ovarian cancer

Jimenez-Bernal, A. [1]*, Sánchez-Bello, M.E. [1], Martínez-Vargas, I.U. [1], Guzmán-Mendoza, J.J. [1], Talamás-Rohana, P.[1]

[1]Departamento de Infectómica y Patogénesis Molecular. Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, México.
E-mail: Alondra.jimenez@cinvestav.mx

The omentum is a visceral adipose tissue, considered the first site of metastasis in human ovarian cancer (OvCa). This tissue is composed mainly of adipocytes, and other cells, including immune system cells predominantly of the innate type, such as Innate Lymphoid Cells (ILCs) and γδ T lymphocytes, which are found abundantly. In the tumor context, anti-tumor and/or pro-tumor functions have been described for these cell populations. Therefore, the objective was to phenotypically characterize ILCs and γδ T lymphocytes in the omentum of a mouse model of OvCa (ID8). We analyzed the proportions of both lymphoid populations in the omentum at different times of cancer development using flow cytometry. A non-significant increasing trend in the proportion of γδ T lymphocytes at 16 weeks of disease compared to the control, and a trend, without being significant, in the decrease in the proportion of ILCs were found. In addition, cytokine detection assays performed on omentum samples showed high levels of IL-6, IL-10, TNF-α IFN-γ, IL- 2, IL-4, IL-17. We thus confirmed, in the murine model of OvCa, that after intraperitoneal inoculation with tumor cells, the main site affected was the omentum; moreover, an inflammatory microenvironment composed mainly of γδ T lymphocytes and a decrease in ILCs, as well as an increase in the cytokines was found. In conclusion, an inflammatory environment is present and this could suggest a pro-tumoral function that needs further experiments to confirm.

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Resumen corto

HDAC6 inhibition dampens the invasive capacity of acute lymphoblastic leukemia B cells via cortactin acetylation

Jiménez-Camacho, K.E. [1], Adomako, J. [1]*, Schnoor, M. [1]

[1]Department of Molecular Biomedicine, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Bacional, 07360 Mexico City, CDMX, Mexico.
E-mail: adomjosh@gmail.com

B-cell acute lymphoblastic leukemia (B-ALL) is the most common leukemia in children. B-ALL cells extravasate and infiltrate bone marrow and organs. Actin cytoskeletal remodeling is needed to accomplish transmigration. Cortactin is an actin-binding protein which accumulates at the leading edge of migrating cells. Recently, we showed that cortactin is overexpressed in B-ALL cells, and correlates with bone marrow colonization, organ infiltration, and relapse. Cortactin acetylation diminishes its affinity for F-actin leading to reduced migratory capacity. Cortactin is a substrate of the deacetylase HDAC6, which controls cell migration in solid tumors. However, it is unknown whether HDAC6 also modulates the aggressiveness of B-ALL cells. In this study, we investigated the relevance of HDAC6 for leukemic B cells migration. We found that HDAC6 is overexpressed in the pre-B ALL cell line REH compared to normal B cells, and that it colocalizes with cortactin in the cytoplasm. Inhibition of HDAC6 with Tubastatin-A induces acetylation of cortactin and tubulin leading to reduced transmigration. Additionally, Tubastatin-A-treatment reduced the ability of REH cells to colonize stromal cells organoids. Of note, the functional effects are resembled when inhibiting HDAC6 in leukemic B cells from patients. Xenotransplantation assay in NSG mice revealed that treatment with Tubastatin-A reduced leukemic B cells capacity to infiltrate the brain, spleen, lung and testis. Taken together, these results suggest that HDAC6-mediated deacetylation of cortactin is an important event that triggers leukemic B cell aggressiveness; thus highlighting the potential of HDAC6 inhibition as new therapeutic strategy in B-ALL patients.

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Resumen corto

Parvovirus B19-like particles in bioluminescence-based photodynamic therapy for the induction of immune responses against solid tumors.

Jiménez-Chávez, A.J. [1]*, Bustos-Jaimes, I. [1],
Moreno-Fierros, L. [2]

[1]Departamento de bioquímica, facultad de medicina, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Unidad de biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.
E-mail: jica9204@gmail.com

Photodynamic therapy (PDT) is a very effective therapy for the treatment of superficial cancerous lesions, however, its use in deep solid tumors is limited. The use of bioluminescent proteins and photosensitizers coupled to nanoparticles is a viable alternative to allow the treatment of solid tumors with PDT. In this work we characterized parvovirus B19-like particles as a delivery platform for luciferase and a photosensitizer to mouse solid tumors. For this purpose, Rose Bengal was chemically coupled to VP2 protein, VP2-RB protein was used to assembly VLPs-RB and decorated with firefly luciferase (VLPs-RB-LUC) and RK-10 peptide to form VLPs-RB-LUC-RK by bioorthogonal conjugation systems DogTag/DogCatcher and SpyTag/SpyCatcher respectively. The results showed that VLPs-B19 can be conjugated with RB, luciferase and RK-10 peptide without affecting their stability, and these VLPs-RB-LUC-RK showed the ability to produce light and singlet oxygen in vitro after substrate addition, VLPs-LUC-RK showed binding to MDA-MB-231 cells and VLPs-RB induced apoptosis of CACO-2 cells by illumination with white light. VLPs-RB-LUC-RK applied to mice with tumors induced by the triple negative line 4T1 delaying tumor growth in the days after administration, but not at the end of the scheme, however, there was a significant reduction of lung macro metastases, which may be due to the induction of immune responses to the tumors released after the photodynamic reaction in the main tumor.

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Resumen corto

Chemotactic profile of the human placenta against an *Escherichia coli* infection in a model of severe hyperglycemia

Jiménez-Escutia, R. [1,2*], Villafuerte-Pérez, A. [1,3], Vargas-Alcantar, D. [1,4], Flores-Espinosa, M.P. [1], Zaga-Clavelina, V. [1], Velázquez-Sánchez, M.P. [5], Olmos-Ortiz, A. [1]

[1]Departamento de Inmunobioquímica. Instituto Nacional de Perinatología "Isidro Espinosa de los Reyes" (INPer IER). Ciudad de México, México. C.P. 11000. [2]Posgrado en Ciencias Biológicas. Universidad Nacional Autónoma de México (UNAM). Ciudad de México, México. C.P. 04360. [3]Facultad de Estudios Superiores Zaragoza, UNAM. Ciudad de México, México. C.P. 09230. [4]Maestría en Ciencias de la Salud. Instituto Politécnico Nacional (IPN). Ciudad de México, México. C.P. 11340. [5]Departamento de Ginecología y Obstetricia, Hospital Ángeles México, Ciudad de México, México. C.P 11800.
E-mail: qfb.jimenezescutia.rodrigo@gmail.com

Placenta is a fetal organ that actively participates against infections by secreting cytokines and chemokines. Hyperglycemia observed in Gestational diabetes mellitus (GDM) women, weakens the innate immune defensive properties of the placenta, which resulted in an increased risk for genitourinary infections, premature rupture of membranes and preterm delivery. However, the role of this pathology over the placental secretion of chemokines against an *E. coli* infection has not been studied. In this work, we evaluated the profile of chemokines secreted by the human placenta during an infectious challenge by *E. coli* in culture conditions of hyperglycemia that resemble the environment of GDM. Placental explants were cultured with glucose (10 mM or 50 mM) for 48 hours. Subsequently, they were infected with *E. coli*. The concentration of bacteria was quantified by plating and the secretion of chemokines by commercial ELISA kits. The explants cultured with 50 mM glucose showed a lower ability to defend against infection compared to the 10 mM glucose condition at 4 hours post-infection. Likewise, the explants cultured in 50 mM glucose show a lower secretion of the CCL2 chemokine and do not show changes in the secretion of CCL3, CCL5, CXCL8 and CXCL10 compared to the 10 mM glucose group. The placenta under conditions of hyperglycemia has a lower defense capacity against infection by *E. coli*. In addition, hyperglycemia decreases CCL2 production in this infectious challenge.

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Resumen corto

Influence of COVID-19 infection in the perforin and granzyme expression of ambulatory positive individuals

Juárez Vega, G. [1]*, Rangel Ramírez, V.V. [2], Pérez Urizar, J.T. [3], Lee Rangel, H.A. [2,4]

[1]Red de Apoyo a la Investigación, Universidad Nacional Autónoma de México – instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán Ciudad de México, CDMX, México, [2]Centro de Biociencias de la Universidad Autónoma de San Luis Potosí, [3]Facultad de Ciencias Químicas de la Universidad Autónoma de San Luis Potosí, [4]Facultad de Agronomía y Veterinaria de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, México. E-mail: guillermovega@cic.unam.mx

Coronavirus disease (COVID-19) is the clinical syndrome associated with SARS-CoV-2 infection characterized by a respiratory syndrome with a variable degree of severity. So far, it is largely unknown how SARSCoV-2 manages to evade immune response and drive pathogenesis. Factors associated with alterations in the immune cell function are likely to impact on resistance or susceptibility to COVID-19 infection. The perforin/granzyme system of cytotoxicity is the main mechanism through which cytotoxic cells eliminate virally infected host cells. Upon recognition of foreign cells, these activated lymphocytes release granzyme and perforin onto the surface of infected cells. Perforin forms pores in the plasma membrane, allowing granzyme to enter the infected cell and initiate apoptosis, thereby effectively killing the pathogen and preventing the spread of infection. The objective of this study is to determine the expression of the perforin and granzyme granules in the context of the infection by SARS-CoV-2 by qPCR, between healthy individuals and individuals infected with SARS-CoV-2; clinical characteristics will also be analyzed. We hypothesize that ambulatory individuals infected by SARS-CoV-2 will have a reduced expression of both proteins which can diminish the clearance of the virus. Until now, we have observed a lower expression of perforin in the SARS-CoV-2+ individuals (n=25) when compared with the control group (n=18), however, this does not reach statistical significance, this can be due to the small number of individuals analyzed. We intend to increase our number of individuals so we can assess the perforin/granzyme system as an important mediator of resistance against COVID-19 infection.

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Resumen corto

MIF: a key cytokine in colorectal cancer progression

Juárez-Avelar, I. [1]*, Andrade-Meza, U.A. [1,2],
Mendoza-Sánchez, D.B. [1,3], Rodríguez-Sosa, M. [1]

[1]Biomedicine Unit (UBIMED), Facultad de Estudios Superiores Iztacala (FES-Iztacala), Universidad Nacional Autónoma de México (UNAM), C.P. 54090. Tlalnepantla, MEX, México.[2]Programa de Doctorado en Ciencias Biomédicas, UNAM, México.[3]Programa de Doctorado en Ciencias Biológicas, UNAM, México
E-mail: imelda_juarez@yahoo.com

Colorectal cancer (CRC) is a significant public health problem, as it ranks third in incidence and fourth in mortality among all types of cancer in the world. Macrophages inhibitory factor (MIF) is a pro-inflammatory cytokine with chemokine characteristic, which is expressed significantly in CRC. Here, we explored the role of endogenous MIF in the genesis and progression of CRC. We used MIF gene-deficient (*mif*-/-) and wild-type (*Mif*+/+) C57BL/6 mice to study the impact of MIF on the development of chemically induced CRC with a single intraperitoneal injection of azoxymethane (AOM, 10 mg/Kg), and 1 cycle of 2% dextran sodium sulphate (DSS) diluted in drinking water and 3 cycles of 1.5% DSS. After the induction, the weight of the mice, the clinical signs, and mortality were recorded weekly. At 90 days post-induction, *mif*-/- CRC mice developed fewer tumors, which presented as characteristic polyps that were up to 3 times smaller than those of *mif*+/+ CRC mice, which developed larger tumors that featured serrated adenomas and metaplasia. The tumor tissue of *mif*-/- CRC presented a lower number of infiltrate cells, with low presence of macrophages and NK cells, as well as low expression of arginase and nitric oxide compared to the tumor tissue from *mif*+/+ mice CRC. The results suggest that MIF has an important role as a regulator of tumor maintenance in the CRC, which suggests that MIF could be a possible therapeutic target in CRC.

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Resumen corto

Tissue resident memory T cells and patient survival association in cutaneous melanoma

Juarez Flores, A. [1,2]*, Bonifaz Laura, C. [2],
Fuentes-Pananá, E. M. [1]

[1]Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México Federico Gómez, Ciudad de México, México. [2]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México 06720, México.
E-mail: angel.juarez.bqd@gmail.com

Melanoma is a highly immunogenic cancer but is still one of the deadliest types of cancer, making it a great candidate for immunotherapy. Immunotherapy response relies in the presence of tumor infiltrating effector T cells. Tissue resident memory T cells (Trm) are a subset of T cells associated with inflammation and local protection against infections. Although T cell tumor densities in general correlate with good prognosis, the particular role of Trm has not been extensively studied. In this work, we explored the meaning of Trm density in melanoma prognosis. For this, a Trm transcriptional signature was created, first by evaluating scRNAseq studies, and secondly by contrasting the signature and conducting a gene correlation analysis using the bulk RNAseq data of cutaneous melanoma in the TCGA consortium. Finally, we made a survival analysis comparing patients with or without enrichment of the Trm signature. This analysis led to conclude that Trm enrichment in cutaneous melanoma is associated with favorable prognosis.

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Resumen corto

The phagocytic activity of peripheral phagocytes of patients with common variable immunodeficiency is not related with the CD16 expression.

Juárez-Palacios, J.E. [1,3]*, Miranda-Cruz, P.E. [1], Prieto-Chávez, J.L. [1], Hernández-Rodríguez, D. [1], García-de La Rosa, M.T. [1,2], Basilio-Gálvez, E. [1], Chacón-Salinas, R. [3], O'Farrill Romanillos, P.M. [2], López-Macías, C. [1], Arriaga-Pizano, L.A. [1]

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades Dr. Bernardo Sepúlveda Gutiérrez del Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social (IMSS), Ciudad de México, CDMX. [2]Servicio de Alergia e Inmunología Clínica del Hospital de Especialidades Dr. Bernardo Sepúlveda Gutiérrez del Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, CDMX. [3]Posgrado en Ciencias en Inmunología del Departamento de Inmunología de la Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, CDMX. E-mail: je.juarezpalacioa@gmail.com

Common Variable immunodeficiency (CVID) is the most frequent symptomatic primary immunodeficiency (PI). People whit this PI have low levels or absence of antibodies, mainly IgG. This makes CVID patients more susceptible to recurrent infections and complications such as pneumonia caused by encapsulated microorganisms whose main defense mechanism is antibody-mediated phagocytosis (AMP). In patients with CVID is expected a restriction in the AMP capacity because of the absence of antibodies, which could be restored with immunoglobulin replacement therapy (IVIG). It also may be influenced by the expression of FC receptors, such as CD16, which have been reported to have decreased in some patients. The aim of this work was to establish whether the expression of CD16 in neutrophils and monocytes is related to the phagocytic capacity in patients with CVID receiving or not IVIG. For this, 23 subjects were recruited, patients with CVID(n=11)(five receiving IVIG and 6 without treatment) as well as healthy subjects(n=12). After informed consent signature, peripheral blood sample was drawn from each person, and the phagocytic capacity of neutrophils and monocytes was evaluated with *E. coli*-pHRodoGreen. Even though the phagocytes from some of the patients showed a diminished phagocytic capacity, it was not significant(p=0.7456) and was not related with CD16 expression (r=0.3836, p=0.3082). Likewise, we did not observe differences in the phagocytic capacity related to the administration of IVIG. Even with the limited number of observations, our results suggest that the differential expression of CD16 on monocyte subpopulations is not related to the previously reported decreased phagocytic capacity in CVID patients.

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Resumen corto

Transcriptomic analysis of Neonatal CD4+ T cell responses.

Kempis-Calanis, L.A. [1]*, Ventura-Martínez, C.J. [1], Spicuglia, S. [2], Medina-Rivera, A. [3], Rodríguez-Jorge, O. [1], Santana, M.A. [1]

[1]Centro de Investigación en Dinámica Celular, Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, 62210 Cuernavaca, México. [2]Aix-Marseille University, Inserm, TAGC, UMR1090, 13288 Marseille, France. [3]Laboratorio Internacional de Investigación sobre el Genoma Humano, Universidad Nacional Autónoma de México, Juriquilla, México.
E-mail: linda.kempiscal@uaem.edu.mx

The neonatal period is a highly vulnerable period in our lives. Infections are responsible for 24% of neonatal deaths worldwide. Infections caused by intracellular pathogens are often more severe in newborns than in adults, suggesting that the immune response mediated by T cells is limited in the early stages of life. To characterize the immune response of neonatal T lymphocytes, we performed a transcriptomic (RNA-seq) analysis of naïve CD4⁺ T cells from neonates and adults at basal levels and in response to TCR/CD28 activation. Bioinformatics tools were used to analyze the quality of the data, identify differentially expressed genes (DEGs) under specific conditions, and perform functional annotation of these genes. A total of 1999 DEGs were identified in basal conditions, and functional annotation suggested that neonatal CD4⁺ T cells have a characteristic gene expression profile, in which transcription and regulation of pathways in cancer, central carbon metabolism in cancer, and the HIF-1 pathway are overrepresented. Experimental validation showed that neonatal CD4⁺ T cells have high proliferation, overexpression of homeobox transcription factors and genes related to glycolytic metabolism. On the other hand, in response to TCR/CD28 activation, neonatal T cells fail to express genes of effector response such as Tbx21 and IFNγ, while adult cells do. Our bioinformatics analyses allowed us to shed light on the mechanisms behind the low immune response of neonatal T cells.

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Resumen corto

CFH Y402H increases the inflammatory response and damage induced by oxidative stress in retinal pigment epithelium cells.

Lammoglia, K. A. [1]*, Velazquez-Soto, H. [1], Cruz-Aguilar, M. [1], Groman-Lupa, S. [1], Zenteno-Ruiz, J.C. [2,3] , Jimenez Martinez, M.C. [1,3]

[1]Department of Immunology and Research Unit, Institute of Ophthalmology "Conde de Valenciana Foundation", Chimalpopoca 14, Centro, Cuauhtémoc, Mexico City 06800, Mexico. [2]Department of Genetics, Institute of Ophthalmology "Conde de Valenciana Foundation", Chimalpopoca 14, Centro, Cuauhtémoc, Mexico City 06800, Mexico. [3] Department of Biochemistry, Faculty of Medicine, National Autonomous University of Mexico, Coyoacán, Mexico City 04510, Mexico.
E-mail: aguslmmk@gmail.com

Age-related macular degeneration (AMD) has been associated with oxidative stress (OS) and genetic factors such as Y402H complement factor H (CFH) variant. OS causes retinal pigment epithelium (RPE) damage and chronic inflammatory response resulting in cell death. CFH is a negative regulator of alternative pathway of the complement system which means that in normal conditions, it inhibits the alternative pathway complement system and modulates RPE functions in response to oxidative stress, but the exact mechanism is unknown. To investigate the role of CFH in the inflammatory response of RPE cells and the link to oxidative stress, an in vitro model of OS in human RPE cell line (ARPE-19) with the CFH Y402H variant was analyzed. The oxidative environment induced by H2O2 increased the levels of inflammatory mediators and pro-apoptotic factors in ARPE-19 cells. Cell damage was prevented by the addition of a human wild type recombinant CFH exogenous before or simultaneously to the stress condition into cell culture. The protective effect was related to the negative regulation of proinflammatory cytokines suggesting a role of CFH in the cellular homeostasis and in modulating inflammation response under oxidative stress.

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Resumen corto

SARS-COV-2 linages identification by SANGER sequencing in patients diagnosed with COVID-19 treated at the Civil Hospital of Guadalajara

Lara-López, I.M. [1], Ruelas-Abarca, B.M. [1], Magaña-Torres, M.T. [2], González-Hernández, L.A. [1], Hernández-Flores, T.J. [3, 4]*, Torres-Baez, C. [1], Iñiguez-Gutiérrez, L. [1]

[1]Instituto de Investigación en Inmunodeficiencias y VIH, Antiguo Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara, Jalisco, México. [2]Laboratorio de genética, Centro de Investigación Biomédica de Occidente, IMSS, Guadalajara, Jalisco, México. [3]Departamento de disciplinas filosófico, metodológicas e instrumentales, Centro Universitario de Ciencias de la Salud, Guadalajara, Jalisco, México. [4]Unidad de VIH, Antiguo Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara, Jalisco, México. teresitahflores.nutricion@gmail.com

The SARS-CoV-2 virus that causes COVID-19 shows great evolutionary capacity and adaptability. The new variants have managed to escape immunization or increase the contagion rate. Although the gold standard for diagnosis is PCR real-time, for lineage identification, there are several other molecular techniques; however, sanger sequencing is an alternative technique that allows the molecular characterization of lineages effectively and more cheaply. This study aimed to identify SARS-COV-2 linages in positive SARS-COV-2 samples by SANGER sequencing in patients treated at the Civil Hospital of Guadalajara, Fray Antonio Alcalde. We performed nasopharyngeal sampling in patients with suspected COVID-19 treated at the “Fray Antonio Alcalde” Civil Hospital of Guadalajara from January 2022 to March 2023. RNA extraction was performed using the Invitrogen PureLink™ Viral RNA/DNA Mini Kit and one-step reverse transcription and PCR amplification using the Genes2Life DeCoV19 Triplex kit. Subsequently, the S gene was amplified in three fragments to complete SANGER sequencing. The analysis of electropherograms was with the Sage Sanger trace alignment software. Sixty-seven patient samples were included in the study. Nine needed adequate quality and concentration to carry out the molecular assays, so they were discarded. Of the 58 remaining samples, we found the following lineages: 39 of them carried Omicron BA.1, 11 of them BA.4&5, one of them carried BA 2.12.1, and one more BA.2. Additionally, 2 presented the XBB.1.5 lineage. Finally, we found two lineages with two carriers each; lineages have yet to be reported.

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Resumen corto

Neutrophils roll faster; and adhere and transmigrate less in response to Cxcl1 dimers compared to monomers in venules of the inflamed cremaster muscle

León-Vega, I.I, *[1], Vadillo, E. [3], Vargas-Robles, H. [1], Rajarathnam, K. [2], Schnoor, M.[1]

[1]Department for Molecular Biomedicine, Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico City, Mexico. [2]Department of Biochemistry & Molecular Biology; Sealy Center for Structural Biology. University of Texas Medical Branch, Galveston, Texas, USA. [3]UMEO. Hospital de Oncología de Centro Médico Nacional S.XXI. Laboratorio de Migración y Metástasis, Mexico City, Mexico. ilianaitzel23@gmail.com

In response to an inflammatory insult, neutrophils are rapidly recruited from the peripheral circulation. In mice, the chemokine Cxcl1, or keratinocyte-derived chemokine (KC), is one of the main chemokines that induces the recruitment of peripheral blood neutrophils to sites of injury or infection. KC mediates recruitment by activating the Cxcr2 receptor and binding tissue glycosaminoglycans (GAGs). KC reversibly exists as monomers and dimers; and previous studies have shown that the monomer is a potent receptor agonist and that the dimer binds GAGs with higher affinity. In peritonitis models, neutrophil recruitment is induced by monomers at low concentrations, and by dimers at higher concentrations. Here, we explored the impact of chemokine dimerization on neutrophil recruitment dynamics of the extravasation cascade. We analyzed neutrophil extravasation by intravital microscopy in venules of the cremaster muscle perfused with recombinant WT Cxcl1 or Cxcl1 dimers at low concentrations. KC dimer compared to WT KC induced weak interactions of neutrophils with the vascular endothelium as manifested by much faster rolling and reduced firm adhesion, which, in turn, resulted in a significant decrease of transmigration. In addition, arrest assays after injection of KC dimer via the carotid artery showed that neutrophils do not adhere properly as compared to WT KC. These data suggest that KC dimer is less efficient in inducing neutrophil recruitment, potentially due to incomplete β2-integrins activation. We conclude that the ability of Cxcl1 to exist as monomer and dimer together with their different receptor and GAG affinities coordinate the early events in neutrophil recruitment. We thank Dr. Idaira María Guerrero Fonseca.

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Resumen corto

Leukocyte immunophenotyping for ALL: heterogeneity of the pre- and post-analytical phases between laboratories

Lima-Salinas, V. *[1,2,5], Prieto-Chávez, J.L. [3,5], Zárraga-Vargas, L.C. [4,5], López-Macías, C.R. [1], Pérez-Romano, B. [5], Martinez-Flisser, G. [5], Arriaga-Pizano, L.A. [1,5].

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades Dr. Bernardo Sepúlveda Gutiérrez del Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, CDMX. [2]Programa de Servicio Social en Investigación, modalidad vinculación Escuela Superior de Medicina del Instituto Politécnico Nacional Ciudad de México, CDMX. [3]Laboratorio Centro de Instrumentos, Citometría de flujo, Coordinación de Investigación en Salud, CIS-IMSS. [4] Hospital del Niño Morelense, [5]PRONAII 303064 Conacyt/ PRONACES Salud.mikafarca@gmail.com

Acute lymphoblastic leukemia (ALL) is the most common cancer among young children. Even worldwide the five years survival is above 95%, unfortunately in many Latin American countries, Mexico included, this survival rate is below 60%. Many factors are associated with this poor outcome, such as lack of access to medical service, abandonment of treatment and even late implementation or adjustment of specific therapy. Leucocyte immunophenotyping is one of the most efficient tools that physicians could use for ALL precision diagnosis and treatment monitorization by MRD (measurable residual disease) analysis. However, its usefulness may vary if the information reported by the laboratory cannot be used by the clinician. Even carrying out a good quality control in the reception and processing of the sample, variations in the markers reported and/or the units used could negatively compromise the effectiveness of the immunophenotype report. This could be solved with the national harmonization of at least part of the report, even using different platform. But for this it is necessary to identify how many laboratories and how varied is the way in which different laboratories have implemented the immunophenotyping process. In order to identify the common characteristics and differences between the laboratories that perform immunophenotyping for ALL at a public or private level, we conducted a survey related to human capital, infrastructure and analysis programs. The survey was completed by 26 laboratories (public and private) from 12 Mexican states (representing 37% of states in Mexico). Results indicated that 42% of the laboratories owned their cytometer, 35% were owned by distributors, and 19% had a combination of both. In 54% of laboratories, any team member could perform all sample analysis activities, while 46% specialized in specific activities. Additionally, 88% received training from distributors, 61% shared knowledge within their group, and 60% received training from external institutions. Identifying these characteristics and differences is crucial for improving the harmonization of immunophenotyping reports in Mexico and ensuring effective ALL diagnosis and treatment monitoring.

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Resumen corto

Cytokine profiles associated with clinical characteristics of patients with rheumatoid arthritis

Limón-López, V.M. [1], García-Arellano, S. [1], Sánchez-Zuno, G.A. [1], Cerpa-Cruz, S. [2], Pérez-Guerrero, E.E. [1], Muñoz-Valle, J.F. [1], Román-Fernández, I.V.[1*]

[1]Instituto de Investigación en Ciencias Biomédicas, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Servicio de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara, Jalisco, México. ilce.romanfer@academicos.udg.mx

Rheumatoid arthritis (RA) is a systemic autoimmune disease with heterogeneous clinical presentations, which difficult decision-making regarding treatment. The identification of groups of patients according to the levels of different markers and associated with the presence of different manifestations or clinical parameters could provide useful information for making more personalized clinical decisions. Being an inflammatory entity, cytokines are an attractive option as markers. The levels of 27 different cytokines were determined in 50 rheumatoid arthritis patients and 26 control subjects using a multiplex assay. Using the K-means clustering method, different groups of patients were identified according to clinical characteristics and cytokine levels. Three different groups of patients with RA were identified with the following characteristics: group 1 (n=12) low levels of G-CSF, GM-CSF, IFN-g, IL-12, IL-7, IL-8, IL- 9, MIP-1b, and the highest level of pain evaluated by pain VAS scale; group 2 (n=24): high levels of RANTES, IL-10, IL-15, VEGF without differential clinical characteristics; group 3 (n=14): high levels of bFGF, eotaxin, IL-13, IL-17, IL-1b, IP10, MIP-19, TNF-a, which presented the lowest clinical activity scores assessed by DAS28 and the highest proportion of patients negative for rheumatoid factor. The groups of patients did not show differences according to the HAQ-DI score, painful or inflamed joints, anti-CCP titers, age, evolution time or treatment scheme. These partial results show that clustering methods such as K-means have the potential to identify clinical patterns in patients with RA according to the levels of specific cytokines, however, studies with larger groups of individuals are necessary.
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Resumen corto

Sialic acid expresión in MCF-7 cell stimulated with TNF- α

López-Castellanos, M.S *, Santiago-Olivera, B.I.,
Gallegos-Velasco, I.B., Hernández-Cruz, P.A.,
Caballero-Sánchez, M.D. .

Laboratorio de Genómica, proteómica y Glicobiología del Cáncer del centro de investigación Facultad de Medicina y Cirugía UABJO-UNAM. Oaxaca de Juárez México.
mimilpez256@gmail.com

Glycosylation is a process of post-translational modifications that transfers carbohydrates to proteins and lipids forming glycoconjugates, where sialic acid is located in terminal positions, they participate in biological and pathological processes, alterations whit other molecules, cell signaling, study recognition, cell surface protector. Sialic acid sticks to complete or incomplete structutes, hence the importance of studying incomplete structures by the antigens T, Sialic Tn and sialyl T and other factors that may be associated whit tumor grade, progression, protection and metastasis, masking tumor epitopes protecting cancer cells, and identifying a specific stage that provides information to develop new timely diagnostic techniques and decrease tumor aggressiveness. TNF is a regulator of apoptosis and cell destruction. In order to determine the expression of sialic acid in MCF-7 cells stimulated and not stimulated with TNF- α at a concentration of 5 ng/mL. and different stimulation times 2,4 and 6 hours. Sialic acid expression was evaluated through cytochemistry and flow cytometry. The expression of sialic acid α2,3 and α2,6 recognized by Maackia amurensis (MAA) and Sambucus nigra (SNA) was found in cytochemistry and cytometry, there is expression of sialic acid in basal conditions. The result indicates that α2,3 and α2,6 sialic acid are present in MCF-7 cells in basal and experimental conditions, TNF-α increases the expression of α2,3 and α2,6 sialic acid in MCF-7 cells. Observing greated expression at 6 hours.

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Resumen corto

Inflammatory stimuli enhance CD13 overexpression in monocytes but not in other cells types

López-Cortés, G.I. *[1], Ortega-Soto, E. [2]

[1]Facultad de Química, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Instituto de Investigaciones Biomédicas, Ciudad de México, CDMX, México.
gina.lopez@comunidad.unam.mx

CD13 (Aminopeptidase N, alanyl peptidase) is a glycosylated membrane peptidase expressed on a wide number of cell types, especially on myeloid cells and endothelial cells. Additionally, to its catalytic activity, CD13 can trigger signaling cascades and cellular functions such as phagocytosis, aggregation and cell adhesion. Studies suggest that CD13 increases its activity during inflammatory threats, however it is not known if it is due to overexpression of the protein or to an alteration to its affinity towards its unknown ligand. To address the first hypothesis, we quantified CD13 membrane expression of different cell types under inflammatory stimuli. We found that CD13 actually is overexpressed on human and mouse peripheral blood monocytes stimulated with inflammatory- conditioned media. This was not true for neutrophils, HUVEC endothelial cells and the human monocytic cell line THP-1. Similar results were obtained when we assessed the effect of CD13 expression on human monocytes using specific inflammatory stimuli (IFN and LPS). Thus, CD13 expression in human monocytes, but not in neutrophils and HUVEC endothelial cells, is regulated by different inflammation stimuli.

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Resumen corto

Immunogenicity and vaccine efficacy evaluation of *Rhipicephalus microplus* BmVDAC peptides with conserved B-cell epitopes

López-Díaz, D.G. [*1], Pérez-Soria, M.M. [1], Ocampo-Jiménez, R. [2], Mosqueda, J.[1]

[1]Immunology and Vaccines Laboratory, Natural Sciences College, Autonomous University of Queretaro, Queretaro, Mexico. [2]PhD Program in Natural Sciences, Natural Sciences College, Autonomous University of Queretaro, Queretaro, Mexico. [3] National Institute for Forestry, Agriculture and Livestock Research, Durango, Mexico. dlopez99@alumnos.uaq.mx

The *Rhipicephalus microplus* tick is the most important ectoparasite for the livestock industry in tropical and subtropical regions of the world. These ticks cause direct and indirect damage to livestock. The antitick vaccines are considered sustainable alternatives for tick control, and the identification of protective antigens is a crucial step. The objective of this work was to identify and evaluate peptides with conserved B-cell epitopes of *R. microplus* BmVDAC, a tick vaccine candidate. *R. microplus* ticks from eight different states of Mexico were collected, the BmVDAC alleles were amplified, cloned, and sequenced. By bioinformatics tools, the sequences were aligned and showed a 99% of similarity. Four peptides with predicted B-cell epitopes were designed and synthesized in MAP-8 system. The immunogenicity was evaluated by mixing each with a commercial adjuvant and subcutaneously inoculating into two cattle four times at 21-days intervals. The antibody response was determined with indirect ELISA. Only the VDAC 3 peptide induced antibodies in both immunized cattle and the humoral response stood the same and slightly increased after every boost. This peptide was selected to continue with the vaccine efficacy experiment in which two cattle were immunized and infested with 0.5 g of *R. microplus* larvae. For the vaccine efficacy formula, biological tick parameters were measured. The results showed that this peptide had an efficacy of 40.69%, significantly reducing oviposition of engorged females and larvae viability. The VDAC 3 peptide had a lower vaccine efficacy than recombinant BmVDAC, but it could be integrated in a multi-antigenic antitick vaccine.

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Resumen corto

Evaluation of Myo1g function in primary mouse NK cells

López-Esparza, V.A.Z. [*1], Martínez-Vargas, I.U. [1,2], Miguel-Rodríguez, C.E. [1,2], Hernández-Casares, F.J. [1,3], Santos-Argumedo, L.[1]

[1]Departamento de Biomedicina Molecular, Centro de Investigación y Estudios Avanzados del Instituto Politécnico Nacional, Cuidad de México, CDMX, México.[2]Departamento de Infectómica y Patogénesis Molecular, Centro de Investigación y Estudios Avanzados del Instituto Politécnico Nacional, Cuidad de México, CDMX, México.[3]Departamento de Biología Celular, Centro de Investigación y Estudios Avanzados del Instituto Politécnico Nacional, Cuidad de México, CDMX, México.
vania.lopez@cinvestav.mx

Myo1g is a short-tail class I myosin involved in cellular adhesion, migration, cytokine secretion, and receptor recycling on T and B lymphocytes. However, its role in other immune cell populations has yet to be evaluated. Thus, the objective of this work, using a model of myo1g deficient mice (Myo1g$^{-/-}$), was to analyze the participation of Myo1g in Natural Killers cells (NK). Based on data available in Immgen, we found that NK cells of the spleen and the bone marrow (BM) express Myo1g mRNA. By Western Blot assay in Wild type mice (WT), we confirmed the presence of Myo1g protein in Poly-IC activated splenic NK cells. Subsequently, by flow cytometry, we found a decrease in the proportion of NK (CD3$^-$CD19$^-$NK1.1$^+$) and NKT cells (CD3$^+$NK1.1$^+$) (that have a different differentiation process) of BM, blood, and the spleen in Myo1g$^{-/-}$ mice compared to WT mice. In addition, the expression of NK1.1 on the surface of CD3$^-$CD19$^-$ cells were analyzed, and a reduction of NK1.1 in Myo1g$^{-/-}$ mice was observed. Nevertheless, its intracellular expression was similar between Myo1g$^{-/-}$ mice and WT mice. This suggests that NK1.1 does not reach the membrane. Finally, by degranulation assay, analyzing CD107a$^+$ (degranulation marker), we found a decrease in Myo1g$^{-/-}$ mice than in WT mice. Altogether, these results suggest that Myo1g is involved in the cytotoxicity process of NK cells.

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Resumen corto

Machine Learning-based Prediction of Potentially Neutralizing Antibodies Against SARS-CoV-2 Using Structural Signatures in the Immune Repertoire

López-Hernández, J.L. [1], Aguilar-Vera, E. [1], González-Sánchez, H.M. [1,2], Tellez-Sosa, J.M. [1], Martínez-Barnetche, J.[1], Godoy-Lozano, E.E. *[1]

[1] Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México. [2] Cátedra CONACYT-Centro de Investigación sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, México. elizabeth.godoy@insp.mx

COVID-19 continues to pose a global challenge as new viral variants emerge. In the past years, hundreds of papers have been published characterizing the immune response to SARS-CoV-2, and various platforms have been developed to identify monoclonal antibodies with therapeutic potential against the virus. The structural and functional information, as well as the sequences of different antibodies, have been deposited in public repositories.

In this study, we generate a model that identifies potentially neutralizing monoclonal antibodies against SARS-CoV-2 based on their structural properties at the primary sequence level through machine learning. We utilized the public CoV-AbDab database which contains information on neutralizing antibodies against SARS-CoV-2, and the public cAb-Rep database, which contains information on antibodies from healthy individuals to construct a supplemented database. This database was divided into a training set and a test set using an 80-20% ratio. To prevent overfitting, we employed k-fold cross-validation with 100 and 200 folds during the training process. Variables that generated superior performance were selected for constructing the model using PCA. We evaluated various nonlinear and linear methods, including logistic regression, decision trees (random forest), support vector machines, and gradient boosting trees (XGBoost).

We analyzed the structural characteristics of the heavy chain of 5,937 antibodies using tests from Encoders: Ordinal and OneHot. The results demonstrate that the models achieve a performance greater than 90% in most cases, with the XGBoost model performing the best at 94%. We plan to apply this model to identify monoclonal antibodies with neutralizing potential from COVID-19 antibody repertoires. Funding: CONACyT 320598.

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Resumen corto

In silico analysis of single-cell RNA sequencing data identifies macrophage populations in breast cancer that differ from the M1/M2 paradigm

López-Huerta, E. *[1,2], Fuentes-Pananá, E.M. [2]

[1]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Unidad de Investigación en Virología y Cáncer, Hospital Infantil de México. Federico Gómez, Ciudad de México, CDMX, México.
eric.lopez@cinvestav.mx

Breast cancer (BRCA) is the leading cause of death by cancer in women worldwide. Tumor-associated macrophages (TAMs) are an important component of the tumor since they are associated with poor prognosis, especially in BRCA, and they are reported to facilitate both anti- and pro-tumoral processes. This duality led to the adoption of the M1 (anti-tumoral) and M2 (pro-tumoral) paradigm of macrophage polarization. However, new technologies, such as single-cell RNA sequencing (scRNA-seq), suggest that the M1/M2 paradigm is inadequate to describe the various populations of TAMs observed in different types of cancer. Therefore, we aimed to analyze TAMs heterogeneity in BRCA and its relation with the M1/M2 paradigm, using publicly available scRNA-seq data. In this study, we implemented R programming language, and unsupervised analyses on public scRNA-seq datasets that contained samples of blood, tumoral and non-tumoral mammary tissue (NT-MT) from both BRCA patients and healthy volunteers. We identified 6 different gene signatures, each one identifying different TAM populations displaying either inflammation, interferon response, angiogenesis, phagocytosis, antigen presentation or matrix remodeling functions. The respective gene signatures were found to be enriched in either blood or NT-MT from healthy volunteers, suggesting different ontological origins among these populations. Importantly, none of the 6 TAMs populations completely correlated with M1 or M2 markers, however the expression pattern of these markers did not seem to be random in TAMs. Our findings indicate that M1/M2 paradigm does not reflect TAMs complexity and that, additional markers are needed to better characterize and distinguish each TAMs population.

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Resumen corto

Expression of genes associated with the M1/M2 profile in peritoneal macrophages and development of *N. brasiliensis* mycetoma in BALB/c mice

López-López, N. *[1], Suarez-Vázquez, T.A. [1], Castro-Corona, M.A. [1], Salinas-Carmona, M.C.S. [1].

[1]Servicio y Departamento de Inmunología de la Facultad de Medicina, Universidad Autónoma de Nuevo León, NL, México. nallely.lopezlp@uanl.edu.mx.

Actinomycetoma caused by *N. brasiliensis* is an infectious disease that causes chronic deforming inflammation in the affected tissue. Macrophages are the main cells of innate immunity that are responsible for eliminating this pathogen, and there are two main phenotypes of macrophage activation: classical or M1 and alternative or M2. In actinomycetoma, the local environment of M2 cells predominates; however, the influence of the pathogen on macrophage function at the systemic level is not known. Therefore, it is important to investigate whether the pathogen can modulate beyond the local microenvironment. This study aimed to evaluate the expression levels of INOS, TNFA, ARG1, and CD206 genes associated with the M1/M2 profile in peritoneal macrophages obtained from mice with *N. brasiliensis* actinomycetoma. For this purpose, 15 BALB/C mice were infected with a suspension in the plantar pad of the left forelimb. The clinical evolution at 5, 15, and 45 days post-infection was evaluated by measuring inflammation at the lesion site, the phagocytic capacity of peritoneal macrophages by flow cytometry, and the expression of genes associated with the M1/M2 macrophage profile by RT-qPCR.

Peritoneal macrophages did not express genes associated with the M1/M2 phenotype under the conditions evaluated; therefore, *N. brasiliensis* infection did not regulate the systemic response at the peritoneal macrophage level.

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Resumen corto

The CCR3 receptor antagonist, SB-328437, reduces neutrophil recruitment to the lung during H1N1 influenza infection in a murine model

Lopez-Leal, F. [1], Cabellos-Avelar, T. [1], Mejia-Franco, O.M. [1], Castro-Jimenez, T.K. [1], Cervantes-Diaz, R. [2], Bustos-Arriaga, J. [1], Maravillas-Montero, J.L. [2], Perez-Lopez, A.[1].

[1] UBIMED, Facultad de Estudios Superiores Iztacala, UNAM. [2] Red de Apoyo a la Investigacion, Universidad Nacional Autonoma de Mexico and Instituto Nacional de Ciencias Medicas y Nutricion Salvador Zubiran.

During influenza infection, neutrophils (NPs) constitute the majority of cells infiltrating to the lung and are important virus elimination. However, uncontrolled activation of these cells contributes to acute tissue damage. We have shown tha NPs acquire CCR3 expression at the site of infection, and CCR3 activation boosts their effector functions. Thus, we evaluated whether the blockade of CCR3 by using the specific antagonist SB-328437, is able to reduce neutrophil recruitment to the lung in a murine model of H1N1 influenza infection. To do so, C57/BL6 mice were intranasally infected with H1N1 influenza (10^6 plaque forming units). SB-328437 was intraperitoneally administered at 32 and 72 hours post infection (hpi) (5 g/kg) or vehicle in the control group. At 4 days post-infection (dpi) the bronchoalveolar fluid (BALF) was collected, the total number of cells in BALF was quantified, and the presence of NPs and CCR3 expression were determined by flow cytometry. Our results showed an increase in the presence of total cells in the BALF, corresponding ~70% to NPs, and the vast majority were CCR3+ (75%) in influenza infected mice. When SB-328437 was administered to infected mice, there was a ~5-fold reduction in the presence of total cells in BALF compared to controls. The flow cytometry analysis revealed a ~6-fold reduction of NPs in the SB-328437 treated group compared to the control. Our results show that SB-328437 administration reduces NP recruitment to the lung during H1N1 influenza infection. Therefore, CCR3 blockade could be used as a strategy to modulate NP recruitment to the lung during acute inflammatory processes.

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Resumen corto

Analysis and immunoproteomic characterization of *Klebsiella pneumoniae* originating from clinical isolates

López-Moreno, H.S. [1], Velarde-Félix, J.S. [2], Vega-Castillo, U. [1]*

[1]Universidad Autónoma de Sinaloa. Doctorado en Ciencias Biomédicas. Laboratorio de Biomedicina Molecular. Boulevard Josefa Ortiz de Domínguez s/n. Cd Universitaria. Z.P. 80013. Culiacán Sinaloa, México.
E-mail: ulisesvega.fcqb@uas.edu.mx

Klebsiella pneumoniae strains resistant to various antibiotics have emerged as a result of life-threatening infections in immunocompromised individuals, the consequent resistance of K. pneumoniae to the vast majority of antibiotics used in clinical practice (eg, carbapenem), and indiscriminate use of these throughout the world, highlights the importance of its study to reveal molecules potentially involved in giving it these characteristics. In this work, the identification of soluble proteins in culture medium was evaluated using a proteomic approach, analyzed by means of a combination of two-dimensional electrophoresis and the western blot technique used for the analysis of the recognition of immunodominant antigens by sera of patients who had a K. pneumoniae infection. The results obtained show a total of 147 identified proteins belonging to K. pneumoniae cultivated in Brain Heart Infusion (BHI) medium. Of which, 42 were recognized by antibodies from diagnosed patients. The results suggest that these immunodominant proteins derived from K. pneumoniae interact with patients and evoke a specific response, being possible therapeutic targets for the development of new drugs and therapies such as vaccines.

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Resumen corto

Study of the immunomodulatory activity of Artemisia mexicana

López-Padilla, M.S. *[1], Legorreta-Herrera, M. [1]

[1]Facultad de Estudios Superiores Zaragoza, Campus II, UNAM, Batalla del 5 de mayo esq. Fuerte de Loreto, Col. Ejército de Oriente, Deleg. Iztapalapa, C.P. 09230, Ciudad de México· alcume_100@hotmail.com

Malaria is the parasitic disease with the highest number of deaths in the world, the high mortality is explain for exaggerated inflammatory response that is not regulated by the immune system. In addition, with the development of strains resistant to antimalarials, it makes its control and eradication difficult. Therefore, new therapeutic strategies are searched to regulate the immune response and delay the development of resistant parasites. The use of plants with antimalarial activity represents an alternative to these problems, since components of a plant interact synergistically and enhance antimalarial activity, delaying resistance to treatment. The Mexican Artemisia known as estafiate or ajenjo, is used in traditional medicine for different conditions. In my research group it was shown that the plant has antimalarial activity, so in this work its immunomodulatory effect on the concentration of cytokines was evaluated by flow cytometry. The results show that the administration of the plant in infected mice significantly increases the concentration of IFN-γ, IL-10 and IL-17. This suggests that the plant promotes a greater activation of the immune response to control the parasite through IFN-γ, but this is regulated by the anti-inflammatory components of the plant that probably promote the synthesis of IL-10. On the other hand, the function of IL-17 is not entirely clear, but studies suggest that it protects against serious complications. Therefore, continuing to evaluate the potentially beneficial effects of the plant will be an effective tool to control and eliminate the parasite.

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Resumen corto

Pulmonary Arterial Hypertension promotes metabolic changes in circulating cells modifying the inflammatory response

López-Velázquez, R. [1,2*], López-Morán, S. [1,2], Jerjes-Sánchez, C. [1], Ramírez-Rivera, A. [1], Castillo, E.C. [1], García-Rivas, G. [1,2], García-Ramírez, N. [1,2l]

[1]Tecnológico de Monterrey, The Institute for Obesity Research, Nuevo León, México. [2] Escuela de Medicina y Ciencias de la Salud, TecSalud, Tecnológico de Monterrey, Nuevo León, México.
Rodrigo.jess@hotmail.com

Pulmonary Arterial Hypertension (PAH) is a progressive disease of the pulmonary vascular system that alters clinical parameters and the site of involvement. Important changes in the tissue have been reported, such as the activation of the Hypoxia Inducible Factor 1 alpha (HIF1α), which is responsible for modifying the activity of other metabolic enzymes such as glucose transporters, but little is known about the changes that occur in the periphery under this condition.

This work searches for metabolic changes in peripheral blood mononuclear cells (PBMC), especially monocytes and T lymphocytes from a blood sample of PAH patients, at the mRNA (gene expression) level by RT-qPCR, as well as at the protein through Western Blot to correlate them with immunological parameters (cytokines and immune cell populations) that have been previously reported in the cohort. Gene amplifications by PCR show important change trends in expression of genes such as HIF1α, Glut1, PDH and Complex IV (MTCO1 and MTCO4) from electron transport chain with an increase in patients with PAH, highlighting GLUT1 and PDH as the points of change in gene expression. These results indicated that changes in PBMC populations could be related to metabolic changes induced by HIF1α.

Important metabolic changes are occurring in the PBMC of patients undergoing PAH, especially in mononuclear cells at the level of gene expression, where such changes could promote immune changes that have been found in these patients. However, we need to finish analyzing the protein levels, as well as their activity.

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Resumen corto

Immunogenic study of porins from three different *Salmonella enterica* serovar Typhi strains

Lozano-Cisneros, D.[1]*, Morales-González, C.[1], Gordillo-López, S.[1], Torres-Flores, A.[1], García-Valeriano, M.[1], Calva-Mercado, E.[2], Rivera-Hernández, T.[1], López-Macías, C[1].

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, México. [2]Departamento de Microbiología Molecular, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México. *E-mail:dlc99236z@gmail.com

The diseases produced by *Salmonella enterica* are still a major health problem around the world. Our laboratory has developed a multivalent vaccine against these diseases based on outer membrane proteins (OMP) named porins, which have been shown to be highly immunogenic antigens. To produced vaccine at industrial level for the subsequent commercialization, a *Salmonella* strain that highly express porins is needed. The objective of these study is to determine the antibody response and protection capacity of porins purified from 3 different *S.* Typhi strains. For this, total IgG antibody titer was determined by ELISA. The protection level was determined through an *in vivo* infection model with *S.* Typhi and subsequent quantification of CFU/g of organ in liver and spleen. The antibody titer of the 3 strains was obtained without a significant difference between the study strains. At once, it was determined that the strain number 3 induced a higher level of protection with respect to the rest of the strains. Therefore it is concluded that strain number 3 is the best candidate to be used a for porins vaccine production.

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Resumen corto

The immunomodulator Transferon® induces changes in cortisol and catecholamines to improve survival in puppies with sepsis.

Lucas-Gonzalez, A.[1,2], Muñoz, A.I.[3,4], Maldonado-García, J.L.[3,5], Fragozo, A.[1,2,3], Vallejo-Castillo, L.[1,2], Trejo-Martínez, I.[1,2,3], Pavón, L.[5], Pérez-Sánchez, G.[5], Cobos-Marin, L.[4] , Pérez-Tapia, S.M.[1,2,3].

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I + D + i) para Farmoquímicos y Biotecnológicos (LANSEIDI-FarBiotec-CONACyT), Mexico City, Mexico. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico. [4]Laboratorio de Virología,Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de Mexico, Mexico City, Mexico. [5]Laboratorio de Psicoinmunología, Dirección de Investigaciones en Neurociencias, Instituto Nacional de Psiquiatría Ramón de la Fuente Muñiz, Mexico City, Mexico. *E-mail: amellalli.lucas@udibi.com.mx

The Neutrophil-to-lymphocyte ratio (NLR) is a cheap and easy-to-obtain biomarker that mirrors the balance between innate and adaptive immunity. Cortisol and catecholamines have been identified as major drivers of NLR. High cortisol levels increase neutrophils while simultaneously decreasing lymphocyte counts. Likewise, endogenous catecholamines may cause leukocytosis and lymphopenia. Thus, NLR allows us to monitor patient severity in conditions such as sepsis. Twenty-six puppies with sepsis secondary to canine parvoviral enteritis were S.C. treated with (I group) and without the immunomodulator Transferon® (CT group). We determined the NLR and the plasmatic cortisol levels by chemiluminescence, and norepinephrine (NE) and epinephrine (E) by HPLC during the first 72 h of clinical follow-up. Our results showed that, at admission, puppies presented an NLR value of 1.8, cortisol of 314.9 nmol/L, NE 3.7 pmol/mL, and E 3.3 pmol/mL. Both treatments decreased the NLR values after 24 h of treatment. However, only the puppies treated with the immunomodulator (I) remained without significant changes in NLR (0.7–1.4) compared to the CT group, which showed a significant difference ($P \leq 0.01$) in their NLR value (0.4–4.6). In addition, we found significant differences in the slope values between the admission and final values of NLR ($P < 0.005$), cortisol ($P < 0.02$), and E ($P < 0.05$) between treatments. Our data suggest that the immunomodulator positively affects the NLR and major drivers like cortisol and epinephrine, reflected in clinical parameters and survival in puppies with sepsis.

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Resumen corto

Generation of germinal center organoids for the identification of human monoclonal antibodies against SARS-CoV-2

Lucio-García, C.*[1,2,3], Martinez-Barnetche, J.[1] Gonzalez-Sanchez, H.M.[1]

[1]Centro de Investigación Sobre Enfermedades Infecciosas del Instituto Nacional de Salud Pública. [2]Coordinación de Investigación de la Facultad de Medicina del Campus Universitario Siglo XXI. [3]Facultad de Medicina de la Universidad Autónoma del Estado de México. *E-mail: cesar.lucio@insp.edu.mx

Introduction. The pandemic caused by SARS-CoV-2 represents a global health problem with multiple challenges to address, including the lack of specific, effective, and safe treatments. The use of monoclonal antibodies (mAbs) against SARS-CoV-2 has been proposed, which are highly specific and exert their therapeutic action in a highly selective manner. Naturally, the highest affinity antibodies are formed at microanatomical sites known as germinal centers (GCs). In GCs, antigen-activated B cells undergo a series of fundamental processes that favor the development of high-affinity mAbs such as somatic hypermutation (SHM) and affinity maturation. Class switching (CSR) and proliferation of B lymphocytes also occur at these sites, as well as their differentiation into antibody-producing plasma cells and memory B cells. Therefore, GCs represent an essential element during the humoral adaptive immune response.

This work developed a stimulation protocol for human B cells based on the combination of cytokines, non-B cells, and the SARS-CoV-2 RBD antigen. The use of this stimulation protocol allowed cell survival, production of antigen-specific mAbs, and the differentiation of cells into the germinal center phenotype (CD27+CD38+) and into plasma cells (CD38+CD138+).

In addition, a 3D culture platform based on a sodium alginate hydrogel was developed, which, compared to conventional culture (2D), proved to have better cell survival, greater production of anti-RBD mAbs, and a higher proportion of cells with the phenotype of anti-RBD. CG, like a human germinal center organoid.

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Resumen corto

Molecular pathways associated with NK cell function in Septic Arthritis (SA) in pediatric patients.

Macias-Segura, N.[1], Elizondo-Solis, C.V.[1], Rojas-Gutiérrez, S.E.*[1], Gelinas-Martin del Campo, M.[1], Salinas-Carmona, M,C,[1], Montoya-Rosales ,A.[2]

[1]Laboratorio de Inmunología de Sistemas, Departamento y Servicio de Inmunología, Facultad de Medicina y Hospital Universitario, Universidad Autónoma de Nuevo León. [2]Laboratorio de Inmunomoduladores, Centro de Investigación y Desarrollo en Ciencias de la Salud, Universidad Autónoma de Nuevo León *E-mail: Cesar.elizondosls@uanl.edu.mx

Pediatric SA is an infectious disease that can become a surgical emergency, with a low incidence in developing countries. The involvement of various cellular groups is known, but there is little evidence on the molecular mechanisms. Integrative bioinformatics analysis can provide new insights into the cellular and molecular mechanisms involved in the disease.

The aim of this work was to identify molecular pathways associated with AS using mRNA expression databases in pediatric patients. A meta-analysis was performed using gene expression databases obtained from GEO in pediatric patients with S. aureus infection who developed AS. Differentially expressed genes were those with an Adj. P <0.05 and a log2 fold-change > -1. To obtain the co-expressed genes, GENEmania and then STRING was used to obtain the protein interaction network (PPI). Main modules were determined by MCODE, and functional enrichment was obtained. A total of 12 down-regulated genes present in both bases were obtained. Co-expression analysis revealed 19 related genes. From the PPI network, 2 modules were identified, one of which is involved in biological processes of NK cell-mediated immunity, NK cell-mediated cytotoxicity, graft-versus-host disease, cell death, defense response to other organisms, and MHC class I binding molecular functions. In the present work, we identified a reduction in the innate immune response mediated by NK cell gene expression. Furthermore, the identified genes have great potential as diagnostic biomarkers and further studies are needed to validate them in a clinical context.

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Resumen corto

Phenolic glycolipid from *Mycobacterium bovis* BCG Mexico strain modulates dendritic cells maturation via TLR-2

Magallanes-Puebla, A.[1]*, López-Vidal, Y.[2],
Pérez-Serrano, R. M.[3], López-Marín, L. M.[1]

[1]Centro de Física Aplicada y Tecnología Avanzada. Universidad Nacional Autónoma de México, Querétaro, México.[2] Programa de Inmunología Molecular. Microbiana, Facultad de Medicina. Universidad Nacional Autónoma de México, Ciudad de México, México. [3]Laboratorio de Genética y Biología Molecular. Facultad de Medicina. Universidad Autónoma de Querétaro. Querétaro, México. *E-mail: magallanes@fata.unam.mx

Tuberculosis remains one of the major public health problems worldwide. Currently, the only licensed vaccine to control the disease is Mycobacterium bovis bacillus Calmette-Guérin (BCG), a live attenuated strain with a protective effect on infant tuberculosis, but less efficient against the more infectious form of the disease in adults. From the parental BCG, multiple substrains have emerged around the world; however, determinants of their protective efficacies are largely unknown. In this work, the major glycolipid component of M. bovis BCG strain Mexico 1931 was isolated and characterized in terms of chemical and immunological features. The molecule was identified as a phenolic glycolipid (PGL), a lipid family typifying some other BCG substrains. The effects of PGL on murine bone marrow-derived dendritic cells were explored by analyzing the expression of cell surface markers (MHC-I, MHC-II, CD40, CD80, and CD86) by flow cytometry; and the secretion of cytokines (TNF-α, IL-12, and IL-10) by ELISA method following different incubation periods (6 and 24 h). Our results show that the purified PGL induced a modulatory effect on dendritic cells, namely by increasing the expression of antigen-presenting molecules, but down-regulating co-stimulatory molecules induced by lipoteichoic acid, a TLR-2 agonist; additionally, PGL upregulated the production of IL-10, an anti-inflammatory cytokine. Altogether, these data revealed PGL as a modulator of dendritic cell function, shining the light on possible differences in the protective efficacy of distinct vaccine substrains.

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Resumen corto

Rickettsial pathogens drive microbiota assembly in *Hyalomma marginatum* and *Rhipicephalus bursa* ticks

Maitre, A.[1,2,3*], Wu-Chuang, A.[1], Mateos-Hernández, L.[1], Piloto-Sardiñas, E.[4], Foucault-Simonin, A.[1], Cicculli, V.[3], Moutailler, S.[1], Paoli, J. C.[2], Falchi, A.[3], Obregón, D.[5], Cabezas-Cruz, A[1].

[1]ANSES, INRAE, Ecole Nationale Vétérinaire d'Alfort, UMR BIPAR, Laboratoire de Santé Animale, Maisons-Alfort, F-94700, France; [2]INRAE, UR 0045 Laboratoire de Recherches Sur Le Développement de L'Elevage (SELMET-LRDE), 20250 Corte, France; [3]EA 7310, Laboratoire de Virologie, Université de Corse, Corte, France; [4]Direction of Animal Health, National Center for Animal and Plant Health, Carretera de Tapaste y Autopista Nacional, Apartado Postal 10, San José de las Lajas, Mayabeque 32700, Cuba; [5]School of Environmental Sciences, University of Guelph, Guelph, ON, Canada. **Autor contact:** Alejandro Cabezas-Cruz (alejandro.cabezas@vet-alfort.fr) and Apolline Maitre (apolline.maitre@anses.fr).

Most tick-borne pathogens are secondarily acquired by ticks during feeding on infected hosts, which imposes 'priority effect' constraints, as arrival order influences the establishment of new species in a microbial community. Here we tested whether once acquired, tick-borne pathogens contribute to bacterial microbiota functioning by increasing community stability.

For this, we used *Hyalomma marginatum* and *Rhipicephalus bursa* ticks collected from cattle in different locations of Corsica and combined 16S rRNA amplicon sequencing for bacterial microbiota and co-occurrence network analysis, with high-throughput pathogen detection, and *in silico* removal of nodes to test for impact of rickettsial pathogens on network properties.

Despite low centrality, *Rickettsia* showed preferential connections in the networks, notably with a keystone taxon in *H. marginatum*, indicating a possible facilitation of the keystone taxa for *Rickettsia* colonisation. In addition, conserved patterns of community assembly in both tick species were affected by *Rickettsia* removal, suggesting that privileged connections of *Rickettsia* in the networks make this taxon a driver of community assembly, but with minor impact on the conserved 'core bacterial microbiota' of *H. marginatum* and *R. bursa*. Interestingly, networks of the two tick species with *Rickettsia* have similar node centrality distribution, a property that is lost after *Rickettsia* removal, suggesting that this taxon drives specific hierarchical interactions between bacterial microbes in the microbiota.

Results suggest that tick-borne pathogens occupy a low centrality but influential position in tick bacterial microbiota to potentially conserve 'core bacterial microbiota' and community stability.

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Resumen corto

Effects of inhibition of TGF-β signaling on the antitumor response in a murine melanoma model

Marcial-Medina, M.C.*[1], Ramos-Balderas, J.L.[1], Licona-Limón, P.[1]

[1]Departamento de Biología Celular y del Desarrollo, Instituto de Fisiología Celular, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.
*E-mail: cleofas@ifc.unam.mx

Transforming Growth Factor beta (TGF-β) promotes the progression of many different types of cancer, including melanoma. In advanced cancer, TGF-β can inhibit dendritic cells, macrophages, natural killer cells, CD4 and CD8 cells, creating a cancer-permissive microenvironment. Thus, we are interested in investigating the therapeutic effect of blocking the TGF- β signal transduction pathway in the tumor and CD8 T lymphocytes. To achieve this objective, we evaluated the efficiency of the adoptive transfer of transcriptional intermediary factor 1 γ (TIF1γ)-deficient CD8 cells into mice with melanoma and the outcome of inhibiting TGF-β signaling in the tumor. In addition, using the CRISPR-Cas9 system, transforming growth factor beta receptor 2 (TGFbR2) was deleted in CD8 T cells. Our results showed that the adoptive transfer of TIF1γ-deficient CD8 cells into melanoma tumor-bearing mice improved tumor control growth compared to the control group. The inhibition of TGF-β signaling in the tumor increased the infiltration of CD3-positive cells, the percentage of NK and CD8 cells positive for granzyme B (GzmB) and IFNγ. Moreover, this treatment significantly decreased the tumor volume compared to the control group. These findings suggest that TIF1γ could be a critical regulator in the antitumor CD8 T-cell immune response in our tumor model. The blocking of the TGF-β signaling in the tumor turned out to be a promising strategy for the treatment of melanoma.
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Resumen corto

Implementation of pharmacy therapy follow-up

Mancilla-Villeda, M.P.[1], Rivera-Bañuelos, J.H.[1], Martínez-Torres, R.E.[2], González-López, K.[3], Abundes-Recilla ,P.*[4], Álvarez-Cortes, V.E.[4]

[1]Facultad de Medicina/Universidad Nacional Autónoma de México. Ciudad de México, [2]Instituto de Ciencias de la Salud/Universidad Autónoma del Estado de Hidalgo. San Agustín Taxiaca, Hidalgo, [3]Facultad de Ciencias Químicas/ Benemérita Universidad Autónoma de Puebla, Cuidad de Puebla/Puebla, [4]Facultad de Farmacia/Universidad Autónoma del Estado de Morelos. Cuernavaca, Morelos.
*E-mail: alrep.ar@hotmail.com

The study of drug-related problems (DRP) monitored during pharmacotherapeutic follow-up in hospitalized patients is currently a vitally important topic, since they are associated with high morbidity and mortality that cause significant costs to health systems. The identification and reporting of medication errors as well as the results of the interventions have a direct impact on the patient's pharmacotherapy and the quality of care in health institutions. Implement pharmacotherapeutic monitoring in a public hospital, as indicated in the supplement for establishments dedicated to the sale and supply of medicines and other health supplies and the corresponding analysis according to the classification of the National Coordination Council for Prevention and Report of Medication Errors (NCCMERP) to analyze and resolve negative results associated with medications. A prospective and descriptive study was carried out with a sample of 351 patients in a public hospital that has 60 census beds of 2nd level of care, pharmacotherapeutic follow-up was carried out in the period March to December 2021 to patients with more than 24 hours of hospitalization. In all the services of the hospital unit, of the 351 registered cases, 62% correspond to male patients and 38% to female patients, 377 problems related to medications were registered, of which 93% correspond to safety errors. 3% necessity and 4% effectiveness in pharmacological therapy. The detection and attention to the results obtained during the pharmacotherapeutic follow-up has contributed to the reduction of errors within the medication process in hospitalized patients, working hand in hand with the multidisciplinary health team to achieve a safe and rational use of medications.

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Resumen corto

Effect of Human Papillomavirus Positive and Negative Oral Cancer Cell Supernatants on Neutrophil Functional Phenotype

Martínez-Barajas, M.G.*[1], Zepeda-Nuño, J.S.[2], Ramírez-de-Arellano, A.[1], García-Chagollán, M.[1], Jave-Suárez, L.F.[3], Villegas-Pineda, J.C.[2], Bueno-Urquiza, L.J.[1], Godínez-Rubí, J.M.[2], Pereira-Suárez, A.L[2].

[1]Instituto de Investigación en Ciencias Biomédicas, CUCS, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Departamento de Microbiología y Patología, CUCS, Universidad de Guadalajara, Guadalajara, Jalisco, México. [3]División de Inmunología, Centro de Investigación Biomédica de Occidente, IMSS, Guadalajara, Jalisco, México.
*E-mail: marcela.martinez8631@alumnos.udg.mx

Head and neck squamous cell carcinoma (HNSCC) has a high incidence worldwide. More than half of oropharyngeal carcinoma is associated with human papillomavirus 16 (HPV16) infection. Tumor-associated neutrophils (TANs) are classified into two functional phenotypes, N1-antitumor and N2-protumor. HPV16+ HNSCC has a better prognosis and lower infiltrate of TANs, but to date, the phenotype of these neutrophils is not known. This work aimed to evaluate the effect of HPV- and HPV+ oral cancer cells on the functional phenotype of neutrophils. The neutrophils were stimulated with supernatants of SCC-9 (HPV-) and UPCI:SCC154 (HPV16+) oral cancer cell lines, HaCaT keratinocytes transduced with the HPV16 E6/E7 viral oncogenes, and LPS as control, to study the functional phenotype by assessment of metabolism with the MTT assay and quantification of reactive oxygen species, CD66b and elastase (NE) expression by immunofluorescence, apoptosis by flow cytometry, and cytokine secretion by multiplex immunoassay. We identified that compared to UPCI:SCC154, SCC-9 induced in neutrophils a higher metabolism, CD66b expression, cell viability, and cytokine production, add to a dispersed intracellular pattern of NE, characteristics associated with a neutrophil activated state; similar results were obtained with HaCaT 16-E7. In the context of cancer, proinflammatory functions of neutrophils can exert protumor activity, so modulation of the TANs activation state by tumor cells could contribute to the improved prognosis of HPV16+ HNSCC. Is relevant to know the functional phenotype of TANs in HNSCC to correctly direct therapeutic strategies focused on modulating neutrophil infiltrate and polarization.

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Resumen corto

Methadone induces Mast Cell Extracellular Traps (MCETs) through the activation of m-opioid and Toll-like (TLR)-4

Martínez-Cuevas, F.L.[1], Cruz, S.L.[1], González-Espinosa ,C.[1]

[1]Departamento de Farmacobiología, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, México City, México. cgonzal@cinvestav.mx ; slcruzm@cinvestav.mx

Mast cells (MCs) express different types of receptors, such as opioid receptors and TLRs. Methadone (Mth) is an m-opioid receptor agonist, that also binds to the TLR4 receptor. This project aims to describe the effects of methadone on MCs. To address that, we stimulated murine bone marrow-derived MCs (BMMCs) with increasing methadone concentrations (0.1, 0.5, or 1 mM) for 10 min and tested cell viability by flow cytometry. We found that methadone induces BMMCs cell death (54.1 and 76.75% when treated with 0.5- and 1-mM Meth respectively). Meth-cell death was found to be associated with the formation of extracellular traps (ETs). To study the mechanism that produces cell death and ETs, the 0.5 mM methadone concentration was chosen and the production of reactive oxygen species (ROS) and Ca2+ mobilization were determined. Methadone produces ROS in a time-dependent fashion and increases Ca2+. Then, BMMCs we pre-incubated with an antioxidant, Trolox, and the calcium chelator, BAPTA, and decreased of percentage Meth-cell death to 28.6, and 25.5% respectively. Next, BMMCs we pre-incubated with naloxone and β-FNA, two m-opioid receptor antagonists. Naloxone pre-incubation plus Meth has 34.7 % of cell death and β-FNA plus Meth shows 40.4% cell death. Additionally, we evaluated the participation of the TLR4 in methadone-induced cell death. The absence of TLR4 reduced cell death to 26.4% after Meth-treatment. In conclusion, our results show that methadone activates the m-opioid receptor and TLR4, and Meth induced cell death by the formation of extracellular traps (ETosis).

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Resumen corto

Persistent infection with *Brucella abortus* 2308 induces senescence in B lymphocytes

Martínez-González, K.[1]*, Sánchez-Argáez, A. B.[2], Garrido-Guerrero, J. E.[3], Moreno-Lafont, M. C[1.], López-Santiago, R.[1]

[1] Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas. Instituto Politécnico Nacional. Prol. De Carpio y Plan de Ayala s/n. Del. Miguel Hidalgo. CP 11340. Ciudad de México. México. [2] Departamento de Biomedicina Molecular. Centro de Investigación y Estudios Avanzados (CINVESTAV). Instituto Politécnico Nacional. Av. IPN N°. 2508. Del. Gustavo A. Madero. CP 07370. Ciudad de México. México. [3] Departamento de Biologia Molecular. Centro de Investigación y Estudios Avanzados (CINVESTAV). Instituto Politécnico Nacional. Av. IPN N°. 2508. Del. Gustavo A. Madero. CP 07370. Ciudad de México. México.
*E-mail: Karinamtzinmuno@gmail.com

Brucellosis is a zoonotic disease caused by bacteria of the genus Brucella that affects half a million people each year. Infection caused by *Brucella* is characterized by persistent and affects various types of cells, including macrophages, dendritic cells, epithelial cells, and B lymphocytes. In infections caused by HIV and hepatitis B virus, or by bacteria such as *Ehrlichia muris*, an increase of B cells with exhausted phenotype has been observed, characterized by low expression of CD23, CD21/CD35 and increased expression of CD11c. These infections alter B cell activation and proliferation through the BCR which are associated with immunosenescence. In this study, the effect of *B. abortus* 2308 infection on B cells from BALB/c mice was determined by flow cytometry. It was found that *B. abortus* 2308 infection induced an increase of CD19+B220+CD11c+CD23-CD21/CD35- B cells after 14 months of infection. These results suggest that B. abortus infection may give rise to an enabling microenvironment for the appearance of B cells with immunosenescent characteristics, which could affect B cell activation and proliferation in response to other infections or stimuli.

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Resumen corto

In vitro expanded purified allospecific CD27^{+}CD70^{-} regulatory T cells are functionally stable in the presence of inflammatory cytokines.

Martínez-Iturbe, I.I.[1,2]*, Cortés-Hernández, A.[1,2], Rosas-Cortina, K.[1,2], Arteaga-Cruz, S.[1,2], Alvarez-Salazar, E.K.[1,2], Reyes-Barrientos, J.E.[1,2], Morales-Buenrostro, L.E.[3], Alberú-Gómez, J.M.[4], Soldevila, G.[1,2]

[1]Department of Immunology and [2]National Laboratory of Flow Cytometry, Biomedical Research Institute, National Autonomous University of Mexico, Ciudad de México, Mexico. [3]Department of Transplantation, National Institute of Medical Sciences and Nutrition Salvador Zubirán, Mexico City, Mexico. [4] Monterrey Technological Institute, School of Medicine and Health Sciences. Mexico City campus.
*E-mail: Iyari689@ciencias.unam.mx

The therapeutic use of allospecific FOXP3+ regulatory T cells (AE-Tregs) in human transplantation patients has been limited due to low numbers of these cells in peripheral blood and the scarce development of efficient protocols to ensure their purity, expansion and stability. In this context, a report has demonstrated that a CD70-CD27+ cell population isolated from *in vitro*-stimulated polyclonal Tregs, gave rise to Tregs with high hypomethylated TSDR. Here, we describe a new protocol that allows to isolate and expand functionally stable CD27+CD70- AE-Tregs. First, we cultured Tregs with allogeneic dendritic cells in the presence of IL-15, IL-2 and retinoic acid. Then, proliferating CD25+CD27+CD70- Tregs (AE-Tregs) were FACS-sorted and polyclonally stimulated with anti-CD3/CD28 in the presence of IL-15, IL-2, and TGF-β. After three weeks, AE-Tregs were expanded up to 570 times the initial numbers with a purity of >95% (CD25+FOXP3+) and maintained a high percentage (>60%) demethylation of *Foxp3*-TSDR. In addition, expanded Treg-AE showed functionally Treg-markers including CTLA-4, Helios and CD39, indicative of a suppressive phenotype and high expression of chemokine receptors important for grafting such as CCR2, CCR4, CXCR3 and CCR7. Accordingly, the AE-Tregs efficiently suppressed T-cell proliferation in an antigen-specific manner, even in the presence of inflammatory cytokines (IFN-γ, IL-1, IL-6, or TNF-α). Finally, our results showed that AE-Treg cells maintain a stable phenotype and function after being stimulated one more week in an inflammatory microenvironment, demonstrating the potential use of this cellular product for customized Treg-therapy in transplanted patients.

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Resumen corto

Evaluation of mast cells in the lung of COVID-19 patients.

Martínez-Martínez, R.E. [1]*, Soria-Castro, R. [1], Meixueiro-Calderón, C. [2], Renata-Fores, E.A. [2], León-Contreras, J.C. [3], Gamboa-Domínguez, A. [3], Hernández-Pando, R. [3], Ponce Regalado, M.D. [4], Becerril-Villanueva, E. [5], Chacón-Salinas, R. [1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Departamento de Patología, Centro Médico Naval, Ciudad de México, CDMX, México. [3]Departamento de Patología, Instituto Nacional de Ciencias Médicas y Nutrición S.Z CDMX, México. [4]Departamento Ciencias de la Salud, Centro Universitario de los Altos Universidad de Guadalajara. [5]Laboratorio de Psicoinmunologia, Instituto Nacional de Psiquiatría R.F.M CDMX, México.
*E-mail: rmartinezm1401@alumno.ipn.mx

Since 2020, COVID-19 has become a worldwide health issue. The emergence of the virus and the high number of deceases associated with the infection, makes important to understand its pathogeny. The main entrance of SARS-CoV 2, and therefore the first contact with the host cells is through the respiratory system, causing on the whole, an exacerbated inflammatory response. Mast cells reside in the lung tissue and are involved in the recognition of different pathogens. Recent reports indicate that patients infected with SARS-CoV 2 show increased levels of mast cell proteases in serum, which is associated with disease severity. In this work, we analyzed the frequency and distribution of mast cells in postmortem lungs tissue of COVID-19 patients. The presence of mast cell and its mediators in lung tissue were analyzed through immunohistochemistry, studying the preparations through optical microscopy to detect the presence of CD117⁺ cells. We found high amounts of CD117⁺ especially surrounding thrombotic vessels, pneumonic and fibrotic zones, suggesting an important role of these cells in the severe manifestations of the disease.

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Resumen corto

Evaluation of the active immunity induced by outer membrane proteins of *Klebsiella pneumoniae* in a murine model

Martínez-Mora, A.Y.*[1], González-Sánchez, H.M.[2], Téllez-Sosa, J.M.[3], Martínez-Barnetche, J.[3]

[1]Facultad de Ciencias Biológicas, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México. [2]CONACYT-Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México. [3]Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México. *E-mail:alondra.martinezm@uaem.edu.mx

The indiscriminate use of antibiotics has provoked the appearance and spread of multidrug-resistant bacteria. Among these, *Klebsiella pneumoniae* is clinically relevant because of the emergence of strains that are resistant to carbapenems and that can spread their resistance genes to other bacterial species. Faced with the constant threat of the declining effectiveness of antibiotics, the development of vaccines can help to prevent bacterial infections, minimizing the selection pressure that may lead to the emergence of resistant strains. In this work, we aimed to evaluate the protective capacity of 3 outer membrane proteins (OMP) of *K. pneumoniae* identified as OMP40, OMP61, and OMP70 in Balb/c mice against a lethal challenge. Cultures of E. coli BL21-A1 previously transformed with a plasmid coding for the OMPs were used. Protein expression was induced in the presence of arabinose and their production was verified in polyacrylamide gels by SDS-PAGE. Subsequently, the proteins were purified by affinity chromatography and their purity was evaluated by SDS-PAGE. The OMPs were dialyzed in PBS and quantified with a bicinchoninic acid assay. The OMPs were used in combination to immunize subcutaneously groups of 6 Balb/c mice, and via intraperitoneal 10 and 20 days later. The seropositivity of the immunized mice was verified by ELISA. We found that the mice immunized with the combination of the OMPs and the mice immunized with a lysate of *Klebsiella* generated antibodies against each of the OMPs analyzed. As expected, mice receiving PBS did not generate a detectable level of antibodies against *Klebsiella* OMPs.

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Resumen corto

Intracellular NAD⁺ dictates proliferation in Jurkat CD4 T cells independently of metabolism.

Martínez-Moreno, M.F. [1,2*], Díaz-Basilio, C.F. [1], Vergara-Mendoza, M. [3], Marín-Hernández A. [4], Romero-Rodríguez, D.P. [5], Reyes-Terán, G. [6], Vázquez-Pérez, J.A. [7], Gutiérrez-Ruiz, M.C. [8], Viveros-Rogel, M. [3], Espinosa, E. [1]

[1]Laboratory of Integrative Immunology, National Institute of Respiratory Diseases "Ismael Cosío Villegas", [2]National School of Biological Sciences, National Polytechnic Institute (ENCB, IPN), [3]Department of Infectious Diseases, National Institute of Medical Sciences and Nutrition "Salvador Zubirán". [4]Department of Biochemistry, National Institute of Cardiology "Ignacio Chávez", [5]Flow Cytometry Core Facility, National Institute of Respiratory Diseases "Ismael Cosío Villegas", [6]Centre for Research in Infectious Diseases (CIENI), National Institute of Respiratory Diseases "Ismael Cosío Villegas", [7]Laboratory for Emergent Diseases and COPD, National Institute of Respiratory Diseases "Ismael Cosío Villegas", [8]Experimental Medicine Laboratory, Unit of Translational Medicine, Institute of Biomedical Research, UNAM, National Institute of Cardiology "Ignacio Chávez", Mexico City, Mexico.

Previously, we observed that selective ablation of CD38 nucleotidase activity in activated Jurkat CD4 T cells decreases OCR/ECAR ratio and increases proliferation, survival, and CD40L induction. Nevertheless, whether these effects are mediated by intracellular NAD⁺ (iNAD⁺) is uncertain. To answer this, we compared TCR response in ectoCD38-inhibited or supplemented (with NMN and NR, NAD⁺ precursors) cells. Proliferation, survival, and mitochondrial morphofunction were assessed by flow cytometry; iNAD⁺ levels by competitive enzyme immunoassay, and oxidative (OCR) and glycolytic (ECAR) metabolism by Seahorse XF Analyzer. CD40L expression, proliferation, and iNAD⁺ increased in supplemented cells. Proliferation increased proportionally to iNAD⁺, but CD40L only tended to correlate under TCR stimulation. iNAD⁺ did not correlate with OCR/ECAR ratio. Our results suggest that ectoCD38 controls T-cell proliferative response via iNAD⁺ via a mechanism independent of metabolic reprogramming.

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Resumen corto

Antitumor-specific immunity induced by an oncolytic adenovirus encoding E7 HPV-16 antigen and SA-4-1BBL in a cancer mouse model

Martinez-Perez, A.G. [1*], Perez-Trujillo, J.J. [1], Garza-Morales, R. [2], Loera-Arias, M. [1], Villa-Cedillo, S.A. [1], Garcia-Garcia, A. [1], Rodriguez-Rocha, H. [1], Flores-Maldonado, O.E. [3], Valdes, J. [4], Saucedo-Cardenas, O. [1], Montes-de-Oca-Luna, R. [1]

[1]Departamento de Histología, Facultad de medicina, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México. [2]Departamento de Medicina Interna, Universidad de Texas Rio Grande Valley, Edinburg, Texas, USA. [3]Departamento de Microbiología, Facultad de medicina, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México. [4]Departamento de Bioquímica, Centro de Investigación y de Estudios Avanzados-Mexico, San Pedro Zacatenco, CDMX, Mexico.
*E-mail: alejandra.martinezpr@uanl.edu.mx

Conventional cancer therapies have significant side effects due to low specificity, a high recurrence, and the need for further treatment. Gene therapies encoding tumor antigens and vector-released immunostimulatory molecules, such as oncolytic viruses, are well-supported as potentiators of therapeutic effects against tumor progression. An oncolytic adenovirus (OAd) encoding SP-SA-E7-4-1BBL exhibits a potent therapeutic antitumor effect. Herein, the prophylactic effect of such a vector and the induction of the antitumor immune response are examined. C57BL/6 mice (n=5) were immunized twice intraperitoneally with OAds encoding SP-SA-E7-4-1BBL, SA-E7-4-1BBL, or SP-SA-4-1BBL [2.5 × 10^8 infectious units (IU)] and then were challenged with TC-1 cancer cells to assess tumor development over time. The DNA construct SP-SA-E7-4-BBL (1 µg) by biobalistcs or PBS injection was used as the control. To assess long-lasting protection, a rechallenge assay was performed in the groups without tumor development 47 days after the first tumor challenge, and the follow-up lasted day 90. In addition, OAd doses were compared to determine the lowest dose required for the antitumor effect. Flow cytometry and the ELISPOT assays evaluated splenocyte-specific antigen cytokines from mice immunized with OAds. The biodistribution and safety of OAd administration were assessed by histological, immunohistochemical, and qPCR organ analysis. *In vivo* immunization with OAd SP-SA-E7-4-1BBL confers a prophylactic, long-lasting, antigen-dependent antitumor effect shown by specific IFN-γ-producing cells. The biodistribution of OAd is found in highly vascularized organs and fades over time without causing detectable tissue injury, in contrast to tumor tissues, where the OAd signal persists over time, causing tumor shrinkage.

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Resumen corto

Sex bias in mycobacterial pulmonary infections

Martínez-Sanabria, C.A. [1], Sartillo-Mendoza, L.G. [1,2], Becerril-Vargas, E. [3], González-Hernández, Y. [4]*, Juárez-Carvajal, E. [4]

[1]Facultad de Medicina, BUAP Puebla, México [2]Becario de la Dirección General de Calidad y Educación en Salud, Secretaría de Salud, CDMX, México. [3]Laboratorio de Microbiología Clínica, INER, CDMX, México. [4]Departamento de investigación en microbiología, INER, CDMX, México.
*E-mail: ygonzalezh@iner.gob.mx

Tuberculosis has an incidence rate, lung damage, coinfections, and other severity parameters that are higher in men than women, likely related to excess inflammation that causes more significant damage to the lung parenchyma. Whether this phenomenon happens in lung disease caused by other mycobacteria is unknown. This project investigated if lung disease caused by other mycobacteria occurs more frequently in men resembling *Mycobacterium tuberculosis* proportions.

We carried out an observational, retrospective, and cross-sectional study that consisted of the active search for cases with suspected pulmonary tuberculosis that had a positive culture for any mycobacteria from individuals of 18 years and older that received medical assistance during the years 2016 to 2018 in the Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas (INER). We selected from the Service of Clinical Microbiology records only the patients with complete medical files in the INER.

The study group consisted of 553 patients. The evaluated samples included bronchoalveolar lavage fluid, sputum, bronchial aspirate, and lung biopsy. *Mycobacterium tuberculosis* was found in 67% of the cases, followed by *M. avium*, *M. bovis*, and *M. intracellulare*, comprising 22.61%, and the other mycobacteria comprised 9.95% of the cases. Most patients were men (60.58%), and a higher proportion of men was observed regardless of the species causative of the infection. The sex bias of lung disease caused by mycobacteria calls for further research focused on the clinical management of the disease and the search for the intrinsic determinants of the susceptibility of men to suffer from it.

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Resumen corto

Myo1f has an essential role in gdT intraepithelial lymphocyte adhesion and migration

Martínez-Vargas, I.U. [1,2]*, Sánchez-Bello, M.E. [1], Miguel-Rodríguez, C.E. [1,2], Hernández-Cázares, F. [2,3], Santos-Argumedo, L. [2], Talamás-Rohana, P. [1]

[1]Departamento de Infectómica y Patogénesis Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Mexico City, Mexico. [2]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Mexico City, Mexico. [3]Departamento de Biología Celular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Mexico City, Mexico. *E-mail: irving.martinez@cinvestav.mx

Intraepithelial gdT lymphocytes represent up to 60% of cells present in the small intestine intraepithelial compartment. They are highly migratory cells that constantly interact with the epithelial cell layer and the lamina propria cells. This migratory phenotype is related to small intestine homeostasis, bacterial and parasitic infection control, and intestinal epithelium repair. Several proteins are involved in the migration of gdT lymphocytes, including CCR9, $\alpha 4\beta 7$, occludin, GPR18 and GPR55 but the function of class I myosins has not been addressed in these cells. This work shows that long-tailed class I myosins are expressed by intestinal intraepithelial lymphocytes. Using long-tailed class I myosin deficient mouse models, we identified the requirement of Myo1f for the lymphocyte migration to the small intestine intraepithelial compartment. The absence of Myo1f affects the intraepithelial gdT lymphocyte homing due to a reduction in the CCR9 and a4b7 membrane expression. In vitro, we confirm that adhesion to MadCAM-1, fibronectin, and collagen is reduced in the absence of Myo1f. Moreover, CCL25-dependent intraepithelial gdT lymphocyte migrations are Myo1f-dependent. Mechanistically, Myo1f deficiency prevents filopodia and lamellipodia formation due to decreased polymerization of the actin cytoskeleton. Thus, Myo1f plays an essential role in the adhesion and migration of intraepithelial gdT lymphocytes in the small intestine.
Funding: Fondo SEP-CINVESTAV (Project 194 to PTR) and CONACYT fellowships to IUMV (780744), MESB (780755), CEMR (780860), and FHC (780260).

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Resumen corto

Long-Non-Coding RNA's expression profile in Minimal Residual Disease in B cell Acute Lymphoblastic Leukemia patients

Mata-Moreno, G. [1,2*], Correa-González, L.C. [3], Niño-Moreno, P. [2], González-Amaro, R. [1], Turrubiartes-Martínez, E. [2], Layseca-Espinosa, E. [1]

[1]Sección de Medicina Molecular y Traslacional, Centro de Investigación en Ciencias de la Salud y Biomedicina, Universidad Autónoma de San Luis Potosí, San Luis Potosí, SLP, México. [2]Sección de Medicina Genómica Médica, Centro de Investigación en Ciencias de la Salud y Biomedicina, Universidad Autónoma de San Luis Potosí, San Luis Potosí, SLP, México. [3]Departamento de Hematología, División de Medicina Interna, Hospital Central "Dr. Ignacio Morones Prieto", San Luis Potosí SLP, México.

B cell Acute Lymphoblastic Leukemia (B-ALL) is the most commonly diagnosed childhood cancer worldwide. Proper monitoring of the response to treatment requires the quantification of minimal residual disease (MRD) at the end of the induction therapy, which is currently evaluated by multiparametric flow cytometry. However, due to the high cost and complexity of this methodology, it is of interest to explore novel options useful for a reliable and simple detection of MDR in these patients. Long-Non-Coding RNAs (lncRNAs) that have been shown to participate in neoplastic processes, particularly those involved in leukemia, such as BALR-6, linc-PINT, ZEB1-AS1 and MEG3, are candidates to be evaluated as potential markers of MDR. In the present study, we analyzed the expression of these lncRNAs in patients with B-ALL, by RT-qPCR, at the time of diagnosis and at the end of induction treatment. A seven-color flow cytometry technique was employed for the detection of MDR at the end of induction treatment. Preliminary results showed discrete differences in the expression profile of these lncRNAs between MDR+ and MDR- patients. A significant decrease in the expression of MEG3 was observed in MDR- patients at the end of the induction treatment compared with their expression at the time of diagnosis. As expected, the expression of BALR6 tended to be higher whereas the expression of linc-PINT tended to be lower at the end of the induction treatment in MDR+ patients.

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Resumen corto

Transitional dendritic cells: the role of a novel innate immune cell population during murine coronavirus infection

Maqueda-Alfaro, R.A.*[1], Sulczewski, F.[1], Arroyo-Hornero, R.[1], Idoyaga, J.[1]

[1]Dept. of Microbiology & Immunology, Stanford University School of Medicine, Stanford, CA, USA.
*Em-mail: ibq.maqueda@gmail.com

High-dimensional approaches have revealed emerging heterogeneity within dendritic cells (DCs), including a conserved population of transitional dendritic cells (tDC). These cells harbor phenotypic features of both plasmacytoid DCs (pDCs) and conventional type 2 DC (DC2s). However, tDC function *in vivo* has yet to be determined. Given their developmental relationship with pDCs and their expression of TLR7/9, we hypothesized tDC could play a role during murine coronavirus (M-CoV) infection. Using models for specific depletion of pDC and tDC vs pDC only ($pDC^{\Delta}tDC^{\Delta}$ vs pDC^{Δ}), we evaluated tDC function during infection. By 5-days post-infection (p.i.) pDC^{Δ} mice were moribund experiencing severe pathology with exacerbated liver damage. Surprisingly, $pDC^{\Delta}tDC^{\Delta}$ mice displayed milder pathology characterized by a decrease in liver damage, and extended survival. Severe pathology in pDC^{Δ} mice, but not $pDC^{\Delta}tDC^{\Delta}$ mice, correlated with a significant increase in IL-1β suggesting that tDC producing this cytokine promote liver damage. Indeed, in vitro experiments demonstrated that mouse and human tDC secreted IL-1β in response to viruses or virus products. Finally, blockade of IL-1β produced by tDC significantly reduced pathology to murine coronavirus in pDC^{Δ} mice. Our findings indicate that tDC have a unique proinflammatory function during viral infections.

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Resumen corto

Evidence for the localization of the oxytocin receptor in human dental pulp

Mayemi Santiago, M. [1*], Condés-Lara, M. [2], Martínez-Lorenzana, G. [2], González-Hernández, A. [2], Espinosa de los Monteros-Zúñiga, A. [2]

[1]Universidad Autónoma de Querétaro, Facultad de Medicina, Querétaro, México, [2]Instituto de Neurobiología, Universidad Nacional Autónoma de México, Campus UNAM-Juriquilla, Querétaro, México.
*E-mail: condes@unam.mx

The interactions between the different cellular elements within the dentin-pulp complex allow us to postulate homeostatic mechanisms that determine the functional state of teeth. In this sense, the presence of calcitonin gene-related peptide (CGRP), a molecule that activates nerve fibers, could indicate possible severe damage to dental structure. On the other hand, oxytocin, a widely distributed peptide, has recently been shown to produce potent analgesic effects through activation of its receptor (OTR). That is why, the present work is an approximation to the study of the CGRP and the OTR on the nerve fibers of the dental pulp, which transmit pain. Samples of third molars were used, from which the dental pulp was extracted, later they were frozen with isopentane at -20°C and 20 µm cuts were made in a cryostat. The tissues were processed with immunofluorescence techniques to localize the CGRP and the OTR in the dental pulp. The analysis of the tissues was carried out in a confocal microscope that allows to see the preparations in three dimensions. The co-localization of CGRP and OTR in the pulp-dentin complex was observed, mainly in the coronal portion, although it was also found in other portions of this complex. These results could help generate therapeutic opportunities in the dental area for the treatment of pain.

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Resumen corto

CD66b⁺ neutrophils are recruited to peri-implant crevicular fluid in peri-implantitis

Medina-Merchán, A. [1*], Saldívar-Salas, S. [1*], Zermeño-Loredo, M.T. [1], Santamaría-Herrera, M.A. [2], Santiago-Martínez, M.P. [1,3], Secundino, I. [3,4]

[1]Universidad La Salle Bajío, Facultad de Odontología. Posgrado en Prostodoncia e Implantología. León, Guanajuato, México. [2]Universidad La Salle Bajío. León, Guanajuato, México. [3]Universidad La Salle Bajío, Facultad de Odontología. León, Guanajuato, México. [4]Universidad La Salle Bajío. Escuela de Veterinaria. León, Guanajuato, México. *E-mail: isecundino@lasallebajio.edu.mx

Peri-implant disease is an inflammatory pathology that damages the tissues surrounding a dental implant. At the initial phase of the disease called peri-implant mucositis, a reversible inflammation occurs around the implant. This stage is followed by chronic inflammation known as peri-implantitis, and clinical signs are loss of bone that supports dental implant, presence of bleeding upon probing, and probing depth >6 mm. Previously, it´s been reported a predominant infiltrate of CD20+ cells (B lymphocytes), followed by CD3⁺ cells (T lymphocytes), CD68⁺ cells (macrophages) and myeloperoxidase⁺ cells (neutrophils) in biopsies from implants affected by peri-implantitis. The aim of this study is to define the phenotype of leucocytes present in peri-implant disease focusing on neutrophils based on the presence of CD45, CD15 and CD66b markers by flow cytometry. Samples of peri-implant crevicular fluid surrounding implants of patients with peri-implantitis, peri-implant mucositis and healthy donors were analyzed. A predominant infiltrate of neutrophils defined by the expression of CD45⁺CD15⁺CD66b⁺ was found around dental implants with diagnosis of peri-implantitis, such CD66b⁺ neutrophils expressed higher level of CD11b and CD64 activation markers compared with samples from patients with peri-implant mucositis. The presence of CD45⁺ leucocytes was not observed in samples from healthy peri-implant tissue. We are currently elucidating the mechanism involved in activation of CD66b⁺ neutrophils. These results will provide an insight into the role of neutrophils in the rapid progression of peri-implantitis in dental implant failures.

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Resumen corto

Analysis of the recruitment of CCR3⁺ and CCR10⁺ cells to the tumor microenvironment in colorectal cancer

Mejia-Franco, O.M. [1], Cabellos-Avelar, T. [1], Juarez-Macias, B. [1], Correa-Becerril, D.A. [1], Juarez-Avelar, I. [1], Cervantes-Diaz, R. [2], Rodriguez-Sosa, M. [1], Maravillas-Montero, J.L. [2], Perez-Lopez, A. [1]

[1]UBIMED, Facultad de Estudios Superiores Iztacala, UNAM. [2]Red de Apoyo a la Investigacion, Universidad Nacional Autonoma de Mexico and Instituto Nacional de Ciencias Medicas y Nutricion Salvador Zubiran.

The tumor microenvironment includes the production of soluble mediators such as chemokines and recruitment of cells of the immune system. Among the chemokines present in various types of cancer is CCL28, which binds to CCR3 and CCR10. Although an increase in the expression of CCL28 has been observed in colorectal cancer (CRC) tumors, the role of CCL28 in the recruitment of cells of the immune system to the tumor microenvironment is unknown. Therefore, we evaluated the presence of CCR3 and CCR10 in the immune cells recruited to the tumoral microenvironment in CRC. We used the AOM/DSS CRC model, and after DSS cycles 3 and 4 a cell suspension was prepared and the expression of CCR3 and CCR10 on the surface of the cells of the immune system infiltrated into the tumor was analyzed using flow cytometry. Analysis showed that at week 11 of AOM/DSS treatment, ~12% of macrophages and ~65% of neutrophils express CCR3, while at week 13, only neutrophils maintain expression of this receptor. Regarding CCR10, we observed that ~25% of B cells and CD4 T cells, and up to ~75% of CD8 T cells express this receptor after DSS cycle 3. However, the proportion of B cells and T cells CD4+ expressing CCR10 is halved, whereas the percentage of CD8, CCR10 T cells was maintained at 13 weeks. In addition, neutrophils acquired CCR10 expression after DSS cycle 3. Immune system cells located in the tumor microenvironment express CCR3 or CCR10, however, expression of these receptors occurs temporarily. These data suggest that the temporary expression of the receptors in the cells of the immune system could play a role in tumor development.

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Resumen corto

Sucralose consumption during pregnancy increases colitis-associated colorectal cancer through the deregulation of the intestinal immune system

Mejía-Muñoz, A.D. [1,2*], Moreno-Tovar, V. [1], León-Cabrera, S. [1,2]

[1]Unidad de Biomedicina. Facultad de Estudios Superiores-Iztacala. Universidad Nacional Autónoma de México, Tlalnepantla, Edo. De México. México. [2]Carrera de Médico Cirujano. Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Edo. De México. México.

Colorectal cancer (CRC) is one of the most common malignant neoplasms and a leading cause of death. Recently, young adults from developed countries presented increased CRC incidence, possibly associated with increased intake of food additives such as artificial sweeteners. Sucralose is among the most ingested non-nutritive sweeteners, especially by women of reproductive age. Sucralose intake during gestation can predispose the offspring to metabolic disturbances and low-grade systemic inflammation. However, if maternal sucralose intake alters the intestinal homeostasis of offspring and exacerbates colitis-associated colon cancer (CAC) in adulthood remains to be elucidated. Therefore, we aim to determine intestinal immune deregulation in offspring that receive sucralose and aggravate CAC illness. In this study, sucralose was included in the drinking water of C57BL/6 pregnant and lactation mice to analyze the role of sucralose in tumorigenesis. After weaning, offspring were fed a control diet until ten weeks of age and treated with an AOM/DSS regimen to induce CAC. Body weight changes, disease activity index, colon length, and tumor burden were assessed for ten weeks. Also, the severities of colon inflammation and carcinogenesis markers were evaluated. Mice whose mothers received sucralose increased inflammatory cell infiltration and faster tumor development, consistent with more signs of the disease, damage, and reduced survival compared with WT animals. This increased tumorigenicity was associated with pSTAT3 and beta-catenin expression in the intestine and augmented expression and production of inflammatory cytokines. These data show that sucralose intake during pregnancy and lactation alters the offspring's intestinal homeostasis and increases tumorigenesis.
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Resumen corto

Chronic stimulation with LPS induces the expression of senescence markers in mast cells

Mendoza-Montiel, P. *, Ibarra-Sánchez, A., González-Espinosa, C.

Departamento de Farmacobiología, Centro de Investigación y de Estudios Avanzados (Cinvestav) del IPN, Sede Sur, Ciudad de México, CDMX, México.
*E-mail: paola.mendoza@cinvestav.mx

Cellular senescence (CS) is a hallmark of aging. It comprehends an irreversible arrest on G1 phase of cell cycle and is accompanied by the overexpression of negative regulators of cell proliferation, such as $p21^{(CIP1/WAF1)}$ and $p16^{(Ink4a)}$ proteins, changes on cell morphology, an increase in lysosomal activity reflected by a rise in the β-galactosidase enzymatic activity, and the acquisition of the senescence associated secretory phenotype (SASP). CS is triggered by distinct inductors. Recent hypothesis proposes that continuous activation of innate immune response could activate stress induced premature senescence (SIPS) of myeloid cell lineages, contributing to inflammaging. Utilizing mature young cultures of bone marrow-derived mast cells (BMMCs) from C57BL6/J mice, we analyzed if chronic exposure to bacterial lipopolysaccharide (LPS; 0 to 7 days) from *E. coli* at 50 or 100 ng/mL could induce the expression of CS markers in a premature fashion. Expression of CS markers was determined by western blot and enzymatic assays and data were corroborated by light and confocal microscopy. Collected results were compared with those obtained from cells treated with vehicle or the well-described senescence inductor, phorbol myristate acetate (PMA). Our results show that young cultures can express senescence markers after three to five days of LPS treatment, whereas old cultures expressed them around 11-15 weeks old. Obtained results strongly suggests that chronic exposure of PAMPs or continuous stimulation of TLR-4 signaling system can induce SIPS in innate immune cells.

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Resumen corto

Evaluation of immune response induced by a plasmid that codify a SARS CoV-2 chimeric protein in a mouse model.

Mendoza-Ramírez, N.J. [1*], García-Cordero, J. [1],
Moreno-Licona, N.J. [2], Morales-Ríos, E. [2], Cedillo-Barrón, [1]

[1]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX. [2]Departamento de Bioquímica, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX.
*E-mail: noe.mendoza@cinvestav.mx

Second generation of COVID-19 vaccines have focused on the use of more than one SARS CoV-2 antigen to induce a long-lasting immune response. In the present work we design a plasmid that code for a chimeric protein that include the most immunogenic regions of S and N protein of SARS CoV-2. Most immunogenic regions were determined by Insilco approaches. Once the sequences were selected, we generate the structure of this chimeric protein and determined physicochemical and immunogenic properties in many platforms. Docking molecular was performed to predict the capacity of chimeric protein to be recognized by innate receptors. The sequence was cloned in pcDNA3.1 and named pcDNA3.1/SRN. The expression of the plasmid was evaluated by immunofluorescence. BALB /c mice were immunized with 20µg or 40µg of pcDNA/SRN. Three doses of DNA were performed at interval of 20 days. After immunization, bleedings were performed, and serum samples were obtained. Mice immunized with parental vector pcDNA3.1 were used as control. Bioinformatics analysis of chimeric protein showed a molecular weight of 50.8kDa, isoelectric point of 9.3, four sites of glycosylation and 90% of immunogenicity. Furthermore, capacity of binding to TLR3 and TLR4 was determined. Specific antibody response of IgM and IgG against N and S1 proteins from SARS CoV-2 were observed in immunized mice. Our results indicate that DNA vaccination with pcDNA3.1/SRN generated by our working group is capable to inducing a specific humoral immune response.

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Resumen corto

Molecules derived from *Taenia crassiceps* improve 5-FU activity in colon cancer treatment, through NK cell recruitment to the tumor site.

Mendoza-Rodríguez, M.G. [1*], Fernández-Muñoz, K.V. [1,2], Sánchez-Barrera, C.A. [1], Medina-Reyes, D. [1], Ledesma-Torres, J.L. [1], Meraz-Ríos, M.A. [2], Terrazas-Valdés, L. I. [1,3]

[1]Unidad de Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México. [2]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Laboratorio Nacional en Salud: Diagnóstico Molecular y Efecto Ambiental en Enfermedades Crónico-Degenerativas, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México (UNAM). *E-mail: monica.mendoza@iztacala.unam.mx

Colorectal cancer (CRC) is one of the most prevalent and deadly neoplasia in worldwide. The 5-fluorouracil (5-FU) is the main drug utilized for CRC treatment despite their low effectiveness and chemoresistance that lead to death in around 50% of the patients. The search for new compounds that improve and restore the activity and signaling pathways that favor tumor cell death is necessary. Recently we evaluated molecules, excreted/secreted by Taenia Crassiceps (TcES), which suppress colorectal cancer development as a prophylactic treatment. To assess the effect of these molecules in established and advanced stages of colorectal cancer, we analyzed the potential role of adjuvant TcES effect on 5-FU in mice induced to colitis-associated colon cancer (CAC) utilizing AOM/DSS. The mice with established tumors in 54 days received 200ug of TcES and 30mg/kg of 5-FU, three times per week, as individual therapies and a group of CAC received combinatory therapy of TcES+5-FU. All the groups were treated until 90 days. We found that the use of TcES have a potential combinatory effect with 5-FU, sensitizing tumoral cells through low expression of cytokines Il-10, Tgfb and Il-17a, inhibiting colon tumorigenesis by increasing recruitment of NK cells at the tumor site and consequent Granzyme B Release and P53 expression restored. Our data identify TcES as a valuable adjuvant therapy in colon cancer.
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Resumen corto

Anti-SARS-CoV-2 Omicron Antibodies Isolated from a SARS-CoV-2 Delta Semi-Immune Phage Display Library

Mendoza-Salazar, I. [1,2,3*], Gómez-Castellano, K.M. [1,3], González-González, E. [1,3], Gamboa-Suasnavart, R. [1,3], Rodríguez-Luna, S.D. [1,3], Santiago-Casas, G. [1,3], Cortés-Paniagua, M.I. [1,3], Pérez-Tapia, S.M. [1,2,3], Almagro, J.C. [1,3,4]

[1]Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico, [2]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (ENCB-IPN), Mexico City, Mexico, [3]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I+D+i) para Farmoquímicos y Biotecnológicos, LANSEIDI-FarBiotec-CONACyT, Mexico City, Mexico, [4]GlobalBio, Inc., Cambridge, MA, USA.
*E-mail: ivette.mendoza@udibi.com.mx

We describe the discovery and characterization of antibodies with potential broad SARS-CoV-2 neutralization profiles. The antibodies were obtained from a phage display library built with the VH repertoire of a convalescent COVID-19 patient who was infected with SARS-CoV-2 B.1.617.2 (Delta). The patient received a single dose of Ad5-nCoV vaccine (Convidecia™, CanSino Biologics Inc.) one month before developing COVID-19 symptoms. Four synthetic VL libraries were used as counterparts of the immune VH repertoire. After three rounds of panning with SARS-CoV-2 receptor-binding domain wildtype (RBD-WT) 34 unique single chain variable fragments (scFvs), were identified, with 27 cross-reactive for the RBD-WT and RBD Delta (RBD-DT), and seven specifics for the RBD-WT. The cross-reactive scFvs were more diverse than the RBD-WT specific ones, being encoded by several IGHV genes from the IGHV1 and IGHV3 families combined with short HCDR3s. Three cross-reactive scFvs and one RBD-WT specific scFv were converted to human IgG1 (hIgG1). The four antibodies blocked the RBD-WT binding to angiotensin converting enzyme 2 (ACE2). Importantly, one of the antibodies also recognized the RBD from the B.1.1.529 (Omicron) isolate, implying that the VH repertoire of the convalescent patient would protect against SARS-CoV-2 Wildtype, Delta, and Omicron. From a practical viewpoint, the triple cross-reactive antibody provides the substrate for developing therapeutic antibodies with a broad SARS-CoV-2 neutralization profile.

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Resumen corto

Inhibition of MIF by CPSI-1306 in Colitis-Associated Colorectal Cancer

Mendoza-Sánchez, D.B. *, Andrade-Meza, U.A., Juárez-Avelar, I., Sánchez-Arteaga, D.A., Rodríguez-Sosa, M.

Laboratorio de Inmunidad Innata, Unidad de Investigación en Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México (UNAM), Tlalnepantla de Baz, Estado de México, México.
*E-mail: mendoza.sa.danae@gmail.com

Macrophage Migration Inhibitory Factor (MIF) is present in chronic inflammatory processes, such as colitis, as in colitis associated colorectal cancer (CAC). Previous studies suggest that MIF favors the development and malignancy of CAC, however, there are no clear results of the benefits of chemically inhibiting MIF on the development and malignancy of CAC in vivo. The main goal is to determine the effect of CPSI-1306 on colon cancer cell lines, as well as its in vivo effect on the development and progression of CAC in a murine model. The in vitro assay of CPSI-1306 were performed on CRC cell lines treated with various doses for 48h, to establish the CI 50. In vivo assays were performed on 6-8 week old female BALB/c mice that were induced with CAC for 68 days by a single dose of i.p. azoxymethane, followed by 3 cycles of DSS (2%) in drinking water for 7 days with DSS-free water intervals for 14 days as rest. On day 40 after CAC induction, CPSI-1306 (1mg/kg) in corn syrup was administered orally. Mice were euthanized on day 68 post-induction. The clinical course, tumor burden, immune cell populations, as well as histopathological characterization in the colon of the mice were determined. CPSI-1306-treated CAC mice had fewer clinical symptoms, small tumors, lower grade of malignancy and increased T CD8+ cells, compared to untreated CAC mice. These preliminary results suggest that MIF inhibition improves the prognosis of this pathology.

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Resumen corto

Immunoregulatory effect of prolactin on plasma cytokine concentration in a mouse model of cerebral malaria

Menera-Jimenez, J.M. [1]*, Legorreta-Herrera, M. [1]

[1]Laboratorio de Inmunología Molecular, Unidad de Investigación Multidisiplinaria FES Zaragoza, UNAM. Batalla 5 de Mayo Esq. Fuerte de Loreto, Iztapalapa, Ciudad de Mexico, México CP. 09230.
*E-mail: drmenera@gmail.com

Malaria is the deadliest parasitic disease in the world. The most severe complication is cerebral malaria (CM). Symptoms and mortality are more serious in men than in women; that is, there is sexual dimorphism. Prolactin (PRL) is an immunomodulatory hormone, and its binding to the prolactin receptor (PRL-R) activates signaling pathways that promote the synthesis of the cytokines INF-γ, IL-6 and IL-10, the latter decreasing synthesis of the first 2 In this work we used female C57Bl/6 mice with the non-functional receptor for PRL (KO PRL-R) and infection with P. berghei ANKA, which is a recognized experimental model for cerebral malaria, and we evaluated the effect of PRL on plasmatic concentration of INF-γ IL-6 and IL-10 in a MC model. We infected 1 WT group and a KO PRL-R group. Parasitaemia was measured from day 3 and sacrifice and blood collection were performed on day 9 to obtain plasma.

The concentration of IL-6 and IL-10 increased in uninfected PRL-R KO mice to almost the same level as infected PRL-R KO mice, although the differences were not statistically significant compared to WT mice. Regarding the concentration of INF-γ, the significant differences were due to infection. Interestingly, parasitemia in PRL-R KO mice was lower on day 9 compared to WT. We are currently studying the possible causes of these differences.

These results indicate that prolactin is an immunoregulator of the inflammatory and anti-inflammatory cytokines analyzed, although the results are not conclusive, so it is important to analyze the mechanisms.
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Resumen corto

Evaluation of mast cell tryptase as a biomarker for SARS-CoV-2 infection

Meneses-Preza, Y.G. [1]*, Soria-Castro, R. [1], Alfaro-Doblado, A.R. [1], Gómez-Martín, D. [2], Torres-Ruiz, J. [2], Hernández-Solis, A. [4,5], Wong-Baeza, I. [1], Pérez-Tapia, M. [1,3], Estrada-Parra, S. [1], Maravillas-Montero, J.L. [6], Chacón-Salinas, R. [1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, ENCB-IPN, Mexico City, Mexico. [2] Departamento de Inmunología y Reumatología del Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Mexico City, Mexico [3]Unidad de Desarrollo e Investigación en Bioprocesos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, ENCB-IPN, Mexico City, Mexico. [4]Servicio de Neumología, Hospital General de México "Dr. Eduardo Liceaga", Secretaría de Salud, Mexico City, Mexico. [5]Facultad de Medicina, Universidad Nacional Autónoma de México (UNAM), Mexico City, Mexico. [6] Red de Apoyo a la Investigación, Universidad Nacional Autónoma de México e Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Mexico City, Mexico.
*E-mail: yatsiri.meneses@gmail.com

COVID-19 is an infectious disease, caused by SARS-CoV-2, that can exhibit an asymptomatic course or present mild to severe symptoms. Immune cells play a crucial role in the pathogenesis of the disease, as they can either control the infection with minimum lung damage or promote tissue damage. Mast cells reside in human lungs and are increased in the lungs of patients who died of COVID-19. MCs are cells from the innate immune response which release different inflammatory mediators either from storage granules or through *de novo* production. MCs are known to participate during the pathogenesis of viral infections; however, the role the MCs' mediators play during SARS-CoV-2 infections remain understudied. To address this gap, this research focused on the study of the main proteases stored by MCs in the serum of COVID-19 positive patients. Our results demonstrate that COVID-19 positive patients have significantly higher serum tryptase concentration compared to the control group, with a greater increase in the most severe cases. Notably, tryptase levels were found to be a reliable indicator of SARS-CoV-2 infection and disease severity. Furthermore, we observed a positive correlation between serum tryptase levels and inflammatory markers such as C-reactive protein and qSOFA score, suggesting a potential involvement of MCs in the development of severe forms of COVID-19. These findings propose tryptase as a promising biomarker for SARS-CoV-2 infection and may contribute to the development of targeted therapeutic strategies to improve patient outcomes.

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Resumen corto

Co-stimulation factors of the immune response expression in diazinon-pre-exposed tilapia leukocytes, challenged with Aeromonas hydrophila

Mercado-Salgado, U. [1,4]*, Bernal-González, K.G. [3], Toledo-Ibarra, G.A. [2], Covantes-Rosales, C.E. [2], Barcelos-García, R.G. [2], Bueno-Durán, A.Y. [2], Ventura-Ramón, G.H. [2], Martínez-Pérez, V.E. [3], Girón-Pérez, D.A. [2], Girón-Pérez, M.I. [2]

[1]Doctorado en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [2]Laboratorio Nacional para la Investigación en Inocuidad Alimentaria (LANIIA) Unidad Nayarit. Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [3]Maestria en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Tepic, Nayarit, México.[4] Licenciatura en Químico Fármaco Biólogo, Universidad Autónoma de Nayarit, Tepic, Nayarit, México
*E-mail: ulises.mercado@uan.edu.mx

Pesticides are substances used to prevent, destroy or control pests, especially, unwanted insects for plants. Its application also causes harmful effects on non-target organisms. Organophosphates family (OPs) are the most widely used pesticides worldwide. Diazinon is a widely used OP pesticide in Mexico. The toxic action of diazinon is the inhibition of acetylcholinesterase (AChE, EC 3.1.1.7) activity through phosphorylation of the serine hydroxyl group in the substrate-binding domain of the enzyme, resulting in the accumulation of acetylcholine and its associated neurotoxicity. It is known that OPs can also cause structural or functional alterations in the innate or adaptive immune response in fish, leading to an increase in susceptibility to infections that affect the aquatic ecosystem and fish production. The aim of the present study is to evaluate the *in vivo* effect of exposure to diazinon on the immune response of tilapia (*O. niloticus*), by determining its ability to facing an antigenic challenge.

The gene expression of specialized immune cells is characteristic, where CD40, CD40L, CD28, and CTLA-4 are molecules that play an important role in establishing cell interactions such as the antigen-presenting process.

The proposed study consists in evaluating the expression of CD40, CD40L, CD28, and CTLA4 in mononuclear spleen cells of tilapia (*O. niloticus*), which were pre-exposed 24 hours to 0.97 mg/L (1/8 CLD_{50}) of diazinon and then challenged with an *A. hydrophila* antigenic preparation.

This study is intended for a better understanding of the affections on the immune response of living organisms that are exposed to pesticides.

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Resumen corto

Association of high calcitriol serum levels and its hydroxylation efficiency ratio with disease risk in SLE patients with vitamin D deficiency

Meza-Meza, M.R. [1] *, Ruiz-Ballesteros, A.I. [1], Pesqueda-Cendejas, K. [1], Campos-López, B. [1], Mora-García, P.E. [1], Montoya-Buelna, M. [1,2], Rivera-Escoto, M. [1], Parra-Rojas, I. [1,3], Vizmanos, B. [1], Cerpa-Cruz, S. [4], de la Cruz-Mosso, U. [1]

[1]Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes; Centro Universitario de Ciencias de la Salud; Universidad de Guadalajara; Guadalajara Jalisco, México.[2]Laboratorio de Inmunología, Centro Universitario de Ciencias de la Salud; Universidad de Guadalajara; Guadalajara Jalisco, México.[3]Laboratorio de Investigación en Obesidad y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, Chilpancingo de los Bravo, Guerrero, México. [4]Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara, Jalisco, México.
*E-mail: monica.meza7057@alumnos.udg.mx

Calcidiol deficiency in systemic lupus erythematosus (SLE) is more frequent than in healthy subjects (HS); it is associated with clinical activity in SLE. Although calcidiol is considered the best indicator of vitamin D serum status, its deficiency could not reflect its hydroxylation efficiency and calcitriol levels. The aimed was to assess the association of calcidiol and calcitriol serum levels and its hydroxylation efficiency with clinical and renal activity risk in SLE patients. Cross-sectional study in 308 SLE and HS women; calcidiol and calcitriol serum levels were evaluated by immunoassays. SLE patients showed lower serum calcidiol *vs.* HS (21.2 *vs.* 24.2 ng/mL; $p<0.001$). Active SLE patients presented higher calcidiol/calcitriol ratio *vs.* inactive patients (2.78 *vs.* 1.92 pg/ng; $p=0.02$), and SLE patients with renal activity showed calcidiol deficiency (19.5 *vs.* 25.3 ng/mL; $p<0.04$), higher calcitriol levels (47 pg/mL *vs.* 41.5 pg/mL; $p=0.02$), and calcidiol/calcitriol ratio (2.13 *vs.* 1.54 pg/ng; $p<0.02$) than patients without renal activity. Calcidiol was negatively correlated with calcitriol ($r=-0.26$; $p=0.001$), and urine proteins ($r=-0.39$; $p<0.01$); calcitriol was positively correlated with blood lymphocytes count ($r=0.30$; $p<0.001$), and negatively with the glomerular filtration rate ($r=-0.28$; $p=0.001$); and the calcitriol/calcidiol ratio was positively correlated with urine proteins ($r= 0.38$; $p<0.01$). The calcidiol deficiency (OR=2.27; 95% CI= 1.15-4.49; $p<0.01$), high calcitriol levels (T3rd, OR=4.19, 95% CI=2.23-7.90; $p<0.001$), and a high calcitriol/calcidiol ratio score (T3rd, OR=5.93, 95% CI: 3.08-11.5; $p<0.001$) were associated with SLE. A pattern of calcidiol deficiency, high calcitriol serum levels and high vitamin D hydroxylation efficiency were associated with SLE risk. Funding UDG-PTC 1401 UDCM, PRO-SNI 2017-2020, UDCM.

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Resumen corto

CD44 is a receptor of murine norovirus 1 in B cells.

Miguel-Rodriguez, C.E. [1,2], Antonio-Buendia, J.I. [1,3*], Cancio-Lonches, C. [2], Gutierrez-Escolano, L. [2], Santos-Argumedo, L. [1].

[1]Departamento de Biomedicina Molecular, [2]Departamento de Infectómica y Patogenesis Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Departamento de Ciencias de la Salud, Universidad Autónoma Metropolitana, Unidad Ixtapalapa, Ciudad de México, CDMX, México.
*E-mail: antonioivan332@gmail.com

Murine Norovirus (MNV) can infect B cells, but little is known about the interaction of noroviruses with these cells and the receptors used. CD300ld and CD300lf were described as the primary MNV-1 receptors on macrophages, but other molecules, such as CD44, have been suggested as MNV receptors in dendritic cells. We found that CD44 and CD300lf are expressed in B cells through bioinformatic analysis. The expression of both molecules on the B-cells membrane was confirmed by western blot and flow cytometry. Since we have previously demonstrated that stimulation of B cells favors the infection with MNV-1, we evaluated the expression of CD44 and CD300lf in these cells by flow cytometry. CD44 but not CD300lf increased in stimulated B cells; thus, the importance of CD44 in MNV infection was evaluated in B cells from $CD44^{+/+}$ or $CD44^{-/-}$ mice by confocal microscopy. We found a significant decrease in the binding of MNV-1 to $CD44^{-/-}$ but not to $CD44^{+/+}$ B cells suggesting the role of this molecule in MNV-1 binding to B cells. To confirm the role of CD44 in MNV-1 binding to mouse B cells, we blocked this receptor using two different monoclonal antibodies: IM7 and NIM-R8. We found that the treatment with the NIM-R8 antibody but not IM7 caused a decreased in MNV-1 infection, suggesting that MNV-1 interacts with CD44 in a site recognized by the NIM-R8 antibody. Together, these data demonstrate the importance of CD44 as a receptor for MNV-1 in B cells.

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Resumen corto

IL-36γ expression in adipocytes

Miguel-Suárez, S.I. [1*], Jiménez-Pineda, A. [1],
Gutiérrez-Román, C.I. [1], Sandoval-Montes, C. [2],
Medina-Contreras, O. [1]

[1]Unidad de Investigación Epidemiológica en Endocrinología y Nutrición, Hospital Infantil de México Federico Gómez, Ciudad de México, CDMX, México, [2]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México.
*E-mail: saitmisu@gmail.com

Adipose tissue is an endocrine organ fundamental for homeostasis regulation. Its main cellular components are adipocytes, macrophages, T cells, neutrophils and mast cells. The excessive accumulation of adipose tissue results in overweight and obesity.

In obesity, chronic inflammation develops in the adipose tissue, triggering cells immune infiltration and an increased pro-inflammatory cytokine secretion. The IL-1 family of cytokines is central during acute and chronic inflammation. Among this family, IL-36γ is an early pro-inflammatory cytokine that modulates inflammation in psoriasis, IBD and other inflammatory diseases, through cytokine production and cell differentiation.

Serum levels of IL-36γ are increased in obese individuals; however, the source of this cytokine is unknown. Here we evaluated IL-36γ production in adipose tissue *in vitro*. We established an efficient model of adipocytes differentiation using 3T3-L1 cells. We confirmed adipocytes differentiation quantifying the amount of intracellular lipid droplets by flow cytometry. Finally, we characterized the profile of pro- and anti-inflammatory cytokines and adipokines by RT-PCR. We observed a high expression of IL-36γ and IL-36R in differentiated adipocytes, suggesting that adipocytes are the main source of IL-36γ in obesity. Interestingly, stimulation with recombinant IL-36γ induces a decrease in the lipid content, which requires further characterization.

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Resumen corto

Cervical cancer cells stimulated with adenosine increase PD-L1 expression via A2AR and induce an exhaust phenotype on T CD8+ cells

Monroy-García, A. [1*], García-Rocha, R. [2], Weiss-Steider, B. [2], Hernández-Montes. [2], Don-López, C.A. [2], Mora-García, M.L. [2].

[1]Laboratorio de Inmunología y Cáncer, UIMEO H de Oncología, CMN SXXI IMSS, Ciudad de México, México. [2]Laboratorio de Inmunobiología UIDCC-UMIEZ FES-Zaragoza UNAM, Ciudad de México, México. *E-mail: albertomon@yahoo.com

Development of cervical cancer (CC) is associated with mechanisms of immune suppression, including the expression of immunosuppressive molecules such as PD-L1. It is known that adenosine (Ado) by signaling on its receptors (A1R, A2AR, A2BR and A3R) can increase the immunosuppressive activity of tumor cells. In this study, the ability of Ado to induce PD-L1 expression in CC cells and its immunosuppressive effect on CD8+ cells were analyzed. For this, CaSki cells were cultured for 72h in the presence of Ado (1uM-1mM). PD-L1 expression was analyzed by flow cytometry. CD8+ T cells previously stimulated with anti-CD3/CD28/CD2 antibodies and IL-2 were co-cultured with paraformaldehyde-fixed tumor cells. The proliferation and expression of PD-1, CTLA-4, perforins, granzymes, and IFN-γ molecules were analyzed in CD8+ T cells. CC cells increased the expression of PD-L1 in a manner dependent on the Ado concentration, which was reversed by adding the selective inhibitor (ZM241385) of A2AR. CD8+ T cells showed a significant decrease in proliferation in direct relation to the proportion of CC cells, in addition to a significant increase in the expression of PD-1 and CTLA-4 and a decrease in the expression of granzymes, perforins and IFN-γ. The addition of anti-PD-L1 reversed these effects. It is concluded that Ado increases the tolerogenic capacity of CC cells through the increase in the expression of PD-L1, resulting in the generation of exhaust CD8+ T cells.

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Resumen corto

Effect of HPV-16 E1 protein on the regulation of the interferon-stimulated genes (ISGs) signaling pathway

Monroy-Mora, K.A. [1,2*], Lizano-Soberón, M. [1,3]

[1]Instituto Nacional de Cancerología, Ciudad de México, México; [2]Programa de Maestría y Doctorado en Ciencias Bioquímicas, UNAM, Ciudad de México, México ; [3]Instituto de Investigaciones Biomédicas, UNAM, Ciudad de México, México.
*E-mail: katiaamm20@gmail.com

Viruses have developed several mechanisms to evade the antiviral immune response. In the case of high-risk Human Papilloma Virus (HR-HPV), which cause around 5% of human cancers, it has been shown that E5, E6 and E7 oncoproteins are capable of modulating the signaling pathway of interferon-stimulated genes (ISGs). I In the present study, we evaluated the effect of the presence of the HPV 16 and 11 E1 proteins on the regulation of the ISGF3 complex components (STAT1, STAT2 and IRF9). HaCaT cells were transfected with the pCA control vector and with HPV16 or HPV11 E1 expressing plasmids. To stimulate ISGs signaling pathway, cells were co-transfected with 0.01ug of Poly I:C and collected 24 h after transfection. HPV E1 HA tagged proteins were ascertained by western blot using anti-HA. Once E1 expression was confirmed via mRNA or protein, the transcript or protein levels of the components of the ISGF3 complex were determined. The E1 protein of HPV-16, unlike E1 of HPV-11, significantly decreased the expression levels of mRNAs and STAT1, STAT2 and IRF-9 proteins, as well as IFNβ1 mRNA in HaCaT cells, in absence and presence of stimulus with Poly I:C. These results suggest that HPV HR- (high risk) and LR- (low risk) E1 proteins, in addition to being necessary for viral genome replication, could be involved in inhibiting the antiviral immune response at the initial stages of infection. Supported by CONACYT PRONAII-7-Virus and Cáncer.

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Resumen corto

Isolation and characterization of a promising anti-PD-1 antibody to treat cancer.

Montes-Luna, A. [1*], González-González, E. [1,2], Ramírez-Villedas, F. [1], Comparán-Alarcón, S. [1,2], Gómez-Castellano, K. [1], Álvarez-Fosado, T. [1], Godínez-Palma, S. [1], Elizarraras-Rodríguez, L. [1], Vázquez-Leyva, S. [1], Pérez-Tapia, S.M. [1,2] , Almagro, J. [1,3]

[1]Unidad de Desarrollo e Investigación en Bioterapeuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [2]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México.[3]Global Bio, Cambridge Massachusetts, United States.

Antibodies targeting checkpoint inhibitors have been shown to be a very effective therapy to treat cancer, being PD-1 (Programmed cell death protein 1) one of most successful targets to develop antibody-based drugs. PD-1 is expressed on the surface of T and B lymphocytes and transmits inhibitory signals when binds to its ligands PD-L1 and PD-L2 expressed on macrophages and dendritic cells. PD-L1/L2 are also highly expressed in several cancer cells resulting in immune evasion of tumor cells. Hence, blockade of the PD-1:PD-L1/L2 interaction by monoclonal antibodies unleashes the immune system to destroy cancer cells. In this work we used a fully synthetic phage display library to generate a panel of anti-PD-1 antibodies with diverse binding and functional profiles. After three rounds of panning in solution with recombinant PD-1 as a selector, 315 clones were tested for PD-1 binding. Out of these clones, 143 were specific for PD-1, with 60 being unique. Further characterization of this panel of PD-1 binders and conversion of the best performing clones to IgG4PE, resulted in an antibody called D9 that blocked PD-1:PD-L1/L2 interaction in ELISA and Junkat cells, and was not cross-reactive with CD28 family-related molecules. C9 also promoted expression of Interferon gamma in a mixed lymphocyte reaction co-culture assay comparable to FDA-approved anti-PD1 therapeutic antibodies Keytruda and Obdivo. Therefore, D9 seems to be a good lead candidate for development of an antibody-based drug targeting checkpoint inhibitors as a therapy to treat cancer.

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Resumen corto

Isolation and characterization of in vitro functional anti-PD-1 antibodies from ALTHEA 4:3 VH:VL Platinum Libraries™

Montes-Luna, A. [1*], González-González, E. [1,2], Ramírez-Villedas, F. [1], Comparán-Alarcón, S. [1,2], Gómez-Castellano, K. [1], Álvarez-Fosado, T. [1], Godínez-Palma, S. [1], Elizarraras-Rodríguez, L. [1], Vázquez-Leyva, S. [1], Pérez-Tapia, S.M. [1,2], Almagro, J. [1,3]

[1]Unidad de Desarrollo e Investigación en Bioterapeuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [2]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México.[3]GlobalBio, Cambridge Massachusetts, United States.

PD-1 (Programmed cell death protein 1) is expressed on the surface of T and B cells and has a role in down-regulating the immune system. It promotes self-tolerance by suppressing T cell inflammatory activity once coupled to its ligands PD-L1 and PD-L2, which are expressed on macrophages and dendritic cells. As PD-L1 and PD-L2 are also highly expressed in several cancer cells it results in tumor immune evasion. Thus, development of anti-PD1 antibodies blocking the PD-1:PD-L1 interaction has been shown to boost the immune system promoting the destruction of cancel cells. In this work, ALTHEA 4:3 VH:VL Platinum Libraries™, a set of semi-synthetic phage display libraries were used to generate a panel of anti-PD-1 antibodies with diverse binding, PD-1:PD-L1/PD-L2 blocking and functional profiles. After three rounds of solution panning againt recombinant PD-1, 88 clones were tested for PD-1 binding, yielding 13 positive single-chain variable fragments (scFvs), with five clones being unique. These unique clones were converted to human IgG4PE and assayed for blocking the PD-L1/PD-L2 interaction in ELISA and Junkat cells. One of the antibodies, called D38, was selected based on its performance in these assays. The in vitro functionality of D38 was assessed by expression of the interferon response in a mixed lymphocyte reaction co-culture. Importantly, a comparison with with FDA-approved therapeutic antibodies (Keytruda and Obdivo) showed a similar functional profile. to. These results demonstrate that general purpose libraries are a valuable source for obtaining functional anti-PD1 antibodies with a promising profile for cancer drug development.

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Resumen corto

Comparative analysis of five immunonutritional indexes in patients with Systemic Lupus Erythematosus: Across Sectional Study

Mora-Garcia, P.E. [1,2*], Ruiz-Ballesteros, A.I. [1,2], Meza-Meza, M.R. [1], Parra-Rojas, I. [1,3], Campos-López, B. [1,2], Pesqueda-Cendejas, K. [1,2], Rivera-Escoto, M. [1,2], Luquin, S. [2], Montoya-Buelna, M. [1,4], Cerpa-Cruz, S. [5], De la Cruz-Mosso, U. [1,2].

[1]Red de Inmunonutrición Y Genómica Nutricional en Las Enfermedades Autoinmunes, Centro Universitario de Ciencias de La Salud, Universidad de Guadalajara, 44340 Guadalajara, Jalisco, Mexico.[2]Instituto de Neurociencias Traslacionales, Departamento de Neurociencias, Centro Universitario de Ciencias de La Salud, Universidad de Guadalajara, 44340 Guadalajara, Jalisco, Mexico.[3]Laboratorio de Investigación en Obesidad Y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, 39087 Chilpancingo de los Bravo, Guerrero, Mexico.[4]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de La Salud, Universidad de Guadalajara, 44340 Guadalajara, Jalisco, Mexico.[5]Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, 44280 Guadalajara, Jalisco, Mexico

Immunonutritional status in systemic lupus erythematosus (SLE) could modulate the immune cells and its inflammatory mediators. Notably, the immunonutritional status of the SLE Mexican population has not been previously described. This study aimed to assess the relationship of immunonutritional status indexes with SLE manifestations. A cross-sectional study was conducted in 188 female SLE patients classified by the SLE ACR-1997 criteria. Clinical disease activity was evaluated by the Mex-SLEDAI index and the immunonutritional status with the CONUT, NRI, PNI, NLR, PLR, BLR, MLR, and ELR indexes. SLE patients presented a median age of 37 years. Active SLE patients had lower albumin serum levels than inactive SLE patients (3.8 *vs.* 4.04 mg/dL; $p<0.001$). Moreover, active SLE patients had a lower basophil count (0.06 *vs.* 0.08 1x10^3/µL; $p=0.01$), and lower A/G ratio (1.25 *vs.* 1.47; $p<0.01$), ELR (0.051 *vs.* 0.071; $p=0.04$), NRI (94.01 *vs.* 106.13; $p=0.01$) and PNI (46.1 *vs.* 49.6; $p<0.01$) scores compared to inactive SLE patients. According to Receiver Operating Characteristic (ROC) curves in which we observed that PNI index (AUC=0.62, 95% CI=0.53-0.71, $p<0.01$), Albumin (AUC=0.67, 95% CI=0.59-0.75, $p<0.001$), basophil count (AUC=0.66, 95% CI=0.54-0.77, $p=0.01$) ELR index (AUC=0.65, 95% CI=0.51-0.80, $p=0.04$), and albumin/globulin ratio (AUC=0.71, 95% CI=0.58-0.84, $p<0.01$) are adequate biomarkers to discriminate the clinical disease activity. Therefore, these indexes are adequate discriminators of SLE clinical disease activity, and could be complementary biomarkers to assess the SLE clinical disease activity.

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Resumen corto

The adjuvant RL2706 mixed with RBD from SARS-CoV-2 induced increased specific antibody responses in mice

Morales-González, C. [1], Torres-Flores, A. [1]*, Lozano-Cisneros, D. [1], García-Valeriano, M. [1], Rivera-Hernández, T. [1], Dubhe, B. [2], Karim, E.J. [2], Rivera-Castro, J.C. [2], Tonatiuh-Ramírez, O. [2], Palomares, L.A. [2], López-Macias, C. [1]

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI. Instituto Mexicano del Seguro Social (IMSS). Ciudad de México, México. [2]Instituto de Biotecnología, Universidad Nacional Autónoma de México.

Ciudad de México, México.

Several effective vaccines for SARS-CoV-2 have been developed and used in the population. However, current production capacity cannot meet global demand, thus novel vaccine platforms that can fill in the distribution gap needed to be further developed.

One option in the development and production of vaccines is the use of protein subunits. However, purified proteins are not efficient immunogens. Over time, numerous microbial components have been used as vaccine adjuvants. Our group has developed a new adjuvant formulation called RL2706 based on microbial components. RL2706 was mixed with SARS-CoV-2 RBD recombinant protein as prototype subunit vaccine anti-SARS-CoV-2. RL2706-RBD immunization of BALB/c induced an increase in the RBD specific IgG antibody response and neutralization in the sera from these mice compared to the sera of mice immunized with RBD alone.

In conclusion, RL2706 showed adjuvant effect in the antibody response induced by the RBD subunit experimental vaccine against COVID-19.

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Resumen corto

Identification of new potential T Cell activation molecules in human CD4 T cells

Morales-Martínez, M. [1], Hernandez-Hernandez, A. [2], Patino-Lopez, G. [1]*.

[1]Laboratorio de Investigación en Inmunología y Proteómica, Hospital Infantil de México, Fedrico Gómez, Ciudad de México, Mexico. [2]Department of Cell and Molecular Biology, Karolinska Institutet, Stockholm, Sweden. *E-mail: gpatino@himfg.edu.mx

T-cell activation is a central process of the adaptive immune response and is the result of the close communication between the Antigen Presenting Cell (APC) and the T lymphocyte. T-cell activation has been widely studied and is currently well understood, nevertheless with the use of new technologies like, microarray gene expression, whole exome sequencing, RNA-seq, etc., these biological pathways have been updated with the addition of several proteins, microRNAs or lncRNAs, complementing the protein interactome previously reported. In this work we aimed to identify new players in T cell activation, for this, we reviewed and analyzed results of microarray gene expression datasets reported in the public database GEO-NCBI. Using data from GSE136625, GSE50971, GSE13887, GSE11989 and GSE902 we performed different comparisons using R and GEO2R, to identify upregulated proteins upon T-cell activation that have no previous reports to participate in immune related functions, particularly in T-cell activation. Interestingly among many candidates we identified at least two lncRNAs with high expression upon T-cell activation that let us suggest could be involved in the regulation of T-cell activation. Further in vitro studies are warranted to confirm the proposed roles in T cell activation for the different candidates here reported. Funding: CONACYT grant #320456 from the Fondo Ciencia de Frontera 2022

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Resumen corto

Changes in B-cell subpopulations and expression IL-10R/IL-17R in rheumatoid arthritis: Association with cell differentiation and clinical activity

Morales-Núñez, J.J. [1]*, Muñoz-Valle, J.F. [1], García-Chagollán, M. [1], Cerpa-Cruz, S. [2], Martínez-Bonilla, G.E. [2], Medina-Rosales, V.M. [1], Díaz-Pérez, S.A. [1], Hernández-Bello, J. [1].

[1]Instituto de Investigación en Ciencias Biomédicas (IICB). Universidad de Guadalajara - Centro Universitario de Ciencias de la Salud, Guadalajara, Jalisco, México. [2]Servicio de Reumatología del Hospital Civil de Guadalajara "Fray Antonio Alcalde, Guadalajara, Jalisco, México. *E-mail: javier.morales@academicos.udg.mx

IL-10 and IL-17, as well as their receptors, can be key molecules in the activation and differentiation of subpopulations of B cells, which play a preponderant role in autoimmune and inflammatory pathologies such as rheumatoid arthritis (RA). Therefore, this study aimed to determine the association of IL-10R and IL-17R expression in B cell subpopulations with cell differentiation and clinical activity in patients with RA. We included 99 patients with RA classified based on their clinical activity (DAS28 index) and 25 control subjects (CS). Flow cytometry was used to determine the frequencies (%) of peripheral B cell subpopulations, the markers CD69, CD40, IL10R, and IL17R. We found that total B cells did not differ between patients and CS (p>0.05). However, memory B cells and pre-plasmablasts were observed to decrease (p<0.0001; p=0.0043, respectively) in RA compared to CS, while mature B cells were found to be increased in RA (p=0.0002). Among patients with RA, those with moderate activity had a higher percentage of B cells (p=0.0021). The $CD69^+$ marker was found to be increased (p<0.0001) and decreased $CD40^+$ (p<0.0001) in patients compared to CS. IL-10R and IL-17R were expressed more in plasmablasts (p<0.0001) than in other B cell subpopulations, but their expression did not differ by clinical activity. IL-17R expressed more in B cells than IL-10R (p<0.0001). In RA there are alterations in subpopulations of B cells. IL-10R and IL17RA may be associated with B cell differentiation due to their high expression in plasmablasts.

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Resumen corto

Immune organoids for the study of the germinal center reaction and antibody production

Moreno-Domínguez, S. [1]*, González-Sánchez, H.M. [2], Martínez-Barnetche, J. [1]

[1]Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México.
[2]CONACYT-Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México.
*E-mail: stephania.moreno@insp.edu.mx

Germinal centers (GCs) are microstructures within secondary lymphoid organs where antibody affinity for the antigen is improved, and B cells are activated, proliferate, and differentiate into memory and plasmatic cells. GCs form by an antigen- and T-cell-dependent process that involves somatic hypermutation (SHM) and affinity maturation of the B cell receptor. The main objective of this project is to generate a 3D model of human GCs *in vitro*, in which B cells undergo SHM and class switch, and will differentiate into plasmatic and memory cells, with the subsequent production of Abs in response to the stimulation with an antigen. In our preliminary experiments, human B cells obtained from peripheral blood were stimulated *in vitro* with an antigen (RBD of SARS-CoV-2) and a cytokines cocktail. Under these conditions, B cells proliferated and produced specific antibodies against RBD. A stimulation protocol based on a 3D culture of alginate beads revealed that B cell survival and specific antibody production increased in comparison with 2D culture. Now, some matrices will be evaluated to optimize the conditions of the 3D culture. GC morphology will be analyzed by confocal microscopy, B cell phenotype will be determined by FACS, and expression of transcriptional factors related to GC function will be assessed by qRT-PCR. Finally, specific antibodies will be identified by next-generation sequencing of the variable regions, and in silico evidence of SHM and antibody abundance will be generated, reflecting the function of the model.

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Resumen corto

Evaluation of Levels of CXCL9, CXCL10, and CXCL13 Chemokines in Serum, Saliva, and Tears in Primary Sjogren's Syndrome

Moreno-Eutimio, M.A. [1]*, Barbosa-Cobos, R.E. [2], Castillo-Ortiz, A.A. [2], Becerril-Mendoza, L. [2], Lugo-Zamudio, G. [2], Lima-Gómez, V.[2], Tzec-Pérez, A. [2], Soriano-Rivero, A.I. [1], Aguilar-Razo, K.J. [1], Vargas-Álvarez, C.E. [1], Pastelin-Palacios, R. [1]

[1]Facultad de Química, Universidad Nacional Autónoma de México (UNAM). Mexico City, Mexico. [2]Hospital Juárez de México, Mexico City, Mexico. E-mail: marioadan@quimica.unam.mx

Sjogren's Syndrome is an autoimmune disorder that damages the salivary and lacrimal glands, leading to dryness of the mouth and eyes. It can also affect other parts of the body, resulting in various clinical manifestations. Chemokines are important in the development of Sjogren's syndrome, as they regulate the movement and activation of immune cells in affected tissues. This study aimed to assess the levels of chemokines CXCL9, CXCL10, and CXCL13 in the serum of Sjogren's syndrome patients and correlate these levels with the severity of the disease. The study analyzed 86 patients diagnosed with pSS. The levels of CXCL9, CXCL10, and CXCL13 chemokines in serum, saliva, and tears were higher in the pSS group compared to healthy volunteers. The highest levels were found in serum, followed by saliva and tears. The chemokine levels were also compared between patients with different levels of disease activity as measured by the ESSDAI tool. The concentration of CXCL10 was higher in patients with higher ESSDAI scores, while CXCL13 levels were significantly higher in patients with higher ESSDAI scores in all three body fluids. Only the serum levels of CXCL13 showed a correlation with the concentration in saliva. In conclusion, individuals with pSS exhibit elevated levels of CXCL9, CXCL10, and CXCL13 chemokines in their serum, saliva, and tears. Furthermore, CXCL13 levels are higher in relation to disease activity, and there is a positive correlation between serum and salivary levels. Funding: PAPIIT-IN219121 and PAPIIT-IA208423.

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Resumen corto

Serum Thymic Stromal Lymphopoietin (TSLP) Levels in Atopic Dermatitis Patients: A Systematic Review and Meta-analysis

Moreno-Eutimio, M.A. [1]*, Zumaya-Pérez, L.C. [1], García-Reyes, M.M. [1,2], Rangel Castañeda, I.A. [1], Pastelin-Palacios, R. [1]

[1]Facultad de Química, Universidad Nacional Autónoma de México (UNAM). Mexico City, Mexico. [2]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional (IPN). Mexico City, Mexico. E-mail: marioadan@quimica.unam.mx

Thymic stromal lymphopoietin (TSLP) plays a critical role in the development of allergic responses, including atopic dermatitis (AD). This systematic review and meta-analysis aim to summarize quantitatively the levels of serum TSLP in AD patients. The study was prospectively registered in the PROSPERO database (ID=CRD42021242628). We conducted a comprehensive search of the PUBMED, SCOPUS, and Cochrane Library databases for original articles investigating serum TSLP in AD patients. Standardized mean differences (SMD) were used to summarize the differences in TSLP levels between AD patients and controls using a random effects model. Fourteen studies, comprising 1,032 AD patients and 416 controls, were included in the meta-analysis. The results demonstrated significantly higher TSLP levels in the AD group compared to the control group (SMD=2.21, 95% CI=1.37–3.06, p<0.001). Subgroup analysis based on geographical region, age, disease severity, TSLP determination method, sample size, and study quality revealed significantly elevated TSLP levels in European AD patients (SMD=3.48, 95% CI=1.75–5.21, p<0.0001), adult AD patients (SMD=4.10, 95% CI=2.00–6.21, p<0.0001), child AD patients (SMD=0.83, 95% CI=0.08–1.59, p=0.031), and across all severity groups (mild: SMD=1.15, 95% CI=0.14–2.16, p=0.025; moderate: SMD=2.48, 95% CI=0.33–4.62, p=0.024; severe: SMD=8.28, 95% CI=4.82–11.74, p=2.72e-6). Notably, adults exhibited higher serum TSLP levels compared to children with AD, and TSLP levels increased with AD severity. In conclusion, our meta-analysis demonstrates elevated circulating TSLP levels in patients with AD. Further studies are needed to explore the sources of heterogeneity. Funding: PAPIIT-IN219121 and PAPIIT-IA208423.

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Resumen corto

Influence of pathogen-derived signals on il-9 receptor expression in basophils

Moreno-Yllescas, C.L.A. [1]*, Ramos-Balderas, J.L. [1],
Licona-Limón, P. [1]

[1]Departamento de Biología Celular y del Desarrollo, Intituto de Fisiología Celular de la Universidad Nacional Autónoma de México, Ciudad de México, México.
E-mail: cmoreno@ifc.unam.mx

Basophils, which make up the smallest population of circulating leukocytes, play a crucial role in the innate immune response against helminth parasites, posing a significant health challenge in developing countries. Soil-transmitted helminthiasis affects 24% of the global population. Interleukin 9 (IL-9) is a vital cytokine in the response against helminth parasites. Previous research has observed a reduction in basophils in the spleen and lungs during the early assessment of the type 2 immune response against *Nippostrongylus brasiliensis* in a mouse model lacking IL-9. Subsequently, the expression of the messenger RNA that translates to the IL-9 receptor (IL-9R) was also identified in basophils. Based on our laboratory's prior findings, we have hypothesized that the expression of the IL-9R in basophils depends on signals derived from pathogens, as it is not induced in sterile inflammation or in vitro conditions with other cytokines. This suggests that basophils can recognize signals, such as those from various Toll-like receptors that are constitutively expressed in basophils and that this signals allows for IL-9R expression in these cells. By employing Myd88-deficient mice, which are incapable of signaling via Toll-like receptors, we have evaluated the importance of these receptors in the expression of IL-9R. Using fluorescence-activated cell sorting (FACS), we propose to purify basophils from in vivo and in vitro models, identify the receptor, and characterize its properties upon IL-9 stimulation, including proliferation, survival, degranulation, and migration.

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Resumen corto

Pathophysiological characterization of an autoimmune glomerulonephritis model in Brown Norway rats haplotype RT1n

Mundo-Franco, Z. [1]*, Cano-Europa, E. [1], Blas-Valdivia, V. [2], Rojas-Franco, P. [1], Londoño-Moreno, A. [1] y Franco-Colín, M. [1]

[1]Laboratorio de Metabolismo I, Departamento de Fisiología, Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Neurobiología, Departamento de Fisiología, Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, CDMX,México. E-mail: zmundof1500@alumno.ipn.mx

Systemic lupus erythematosus (SLE) is an immunological disorder characterized by the accumulation of autoantibodies and immune complexes that cause tissue damage and destruction because of the activation of a chronic inflammatory response. One of the most serious manifestations of SLE is glomerulonephritis (GNF) which represent a risk factor that increases the morbidity and mortality. The treatment of SLE involves; long periods and expensive drugs that produce adverse effects. The pathophysiological characterization of the model will allow an specific study of each stage in the evolution of the disease. In this work, the course of the disease was developed in animals of the Brown Norway strain by administering mercury chloride ($HgCl_2$) and the damage evolution 20 days. The following was evaluated: the oxide-reduction environment, markers of inflammation, oxidative stress, cell death and endoplasmic reticulum stress, the presence of immunoglobulins and deposition of autoimmune complexes in the kidney.

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Resumen corto

PD-L1 expression in neutrophils is increased when exposed to an elevated concentration of glucose

Muñiz-Buenrostro, A. [1]*, Arce-Mendoza, A.Y. [1], Salinas-Carmona, M.C. [1], Mejía-Torres, M.G. [1], López-López, N. [1], Montes-Zapata, E. [1], Huerta-Polina, J.A. , Castillo-Peña, L.I. , Espinoza Gamez, J.G. , Mata-Rico, H.C.

[1]Departamento de Inmunología, Facultad de Medicina, Universidad Autónoma de Nuevo León, Av. Gonzalitos #235 Col. Mitras Centro, C.P. 64460, Monterrey, Nuevo León, México.
E-mail: antonio.munizbn@uanl.edu.mx

Type 2 diabetes has a higher risk of developing bacterial infections. It has been studied that type 2 diabetes modifies the activation state of macrophages by increasing the expression of PD-L1 which promotes T cell exhaustion, so the objective of our study was to analyze if an elevated concentration of glucose increases the expression of PD-L1 in neutrophils. We isolated human neutrophils from venous blood of 3 healthy subjects. We cultured neutrophils with normal glucose concentration of 5 mmol and an elevated glucose concentration of 27 mmol during 3 hours. After the culture, neutrophils were evaluated with flow cytometry to detect the presence of PD-L1. PD-L1 expression was higher in neutrophils incubated with 27 mmol of glucose compared to 5 mmol of glucose (n=3, p <0.001). In conclusion, elevated glucose concentrations increase the expression of PD-L1 in neutrophils and this could be associated with the immunodeficiency in type 2 diabetes.

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Resumen corto

Extracellular proteins of mycobacterium tuberculosis stabilize HIF-1 alpha in human neutrophils

Muñiz-Buenrostro, A. [1]*, Arce-Mendoza, A.Y. [1], Salinas-Carmona, M.C. [1], Mejía-Torres, M.G. [1], López-López, N. [1], Montes-Zapata, E. [1], Huerta-Polina, J.A. [1]

[1]Departamento de Inmunología, Facultad de Medicina, Universidad Autónoma de Nuevo León, Av. Gonzalitos #235 Col. Mitras Centro, C.P. 64460, Monterrey, Nuevo León, México.
E-mail: antonio.munizbn@uanl.edu.mx

In has been studied that *Mycobacterium tuberculosis (Mtb)* protein, Early Secreted Antigenic Target 6-kDa protein (ESAT-6) stabilizes the Hypoxia Inducible Factor-1alpha (HIF-1 alpha) in THP-1 macrophages, so the objective of our study was to analyze if extracellular proteins of *Mtb* could stabilize HIF-1alpha in human neutrophils. We isolated human neutrophils from venous blood of 3 healthy subjects. *Mtb* H37Rv culture was filtered to obtain extracellular proteins. The proteins were precipitated, desalted and quantified with Bradford, after that we did an SDS-PAGE to observe the bands of the proteins. We cultured neutrophils with no stimulus, $CoCl_2$ and extracellular proteins of *Mtb* during 5 hours in normoxia. After the culture we did a immunocytochemistry and western blot to identify the presence of HIF-1 alpha. In the SDS-PAGE of the extracellular proteins of *Mtb* we obtained 4 proteins with the following weights: 62, 49, 38 and 6 kDa. We identified the presence of HIF-1alpha in neutrophils stimulated with CoCl2 and extracellular proteins of *Mtb* in the immunocytochemistry and western blot. HIF-1alpha was not stabilized in neutrophils that were incubated with no stimulus (n=3, p <0.001). In conclusion, extracellular proteins of *Mtb* stabilize HIF-1alpha in human neutrophils.

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Resumen corto

Effect of consumption of sucrose in the form of binge eating on CD25+ FoxP3+ and CD11c+ leukocytes of peripheral blood of rats.

Muñoz Camacho, A. A.[1, 2]*, Sandoval Herrera, V. [2], Rodríguez-Flores, A. [1]

[1]Departamento de Fisiología, laboratorio de Electrofisiología de la Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional. Unidad Profesional "Adolfo López Mateos". Ciudad de México, México. [2] Departamento de inmunología, laboratorio de Inmunología aplicada de la Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional. Prolongación de Carpio y pan de Ayala s/n, Zip 11340. Ciudad de México, México. E-mail: arodriguezfl@ipn.mx

Malnutrition is associated with metabolic disorders and non-transmissible diseases, this dietary imbalance is one of the significant factors for the development of inflammatory processes, affecting the functioning and regulation of biological systems including the immune. Therefore, this work seeks to determine if there is a relationship between the consumption of sucrose in the form of binge eating and the number of leukocytes CD25 + FoxP3 + and CD 11c + in peripheral blood of rats by flow cytometry. We worked with 36 male Wistar rats of 250 ± 5 g, and three groups were formed: normal diet (D), sucrose control (S) and experimental binge (B), with an n = 8. Group S was given a 10% sucrose solution *ad libitum* and group B was induced to binge on 10% sucrose solution for two hours every 24 hours for 25 days (Avena *et al*. 2008). The results show that the body weight of groups S and B, have a significant increase ($p = 0.017$) compared to group D and a significant decrease in the consumption of Chow food at 24 hours with a $p< 0.0001$. It was observed that rats with binge eating have an anxious behavior with a $p = 0.015$. Of the leukocyte populations, the most affected in group B were band neutrophils and monocytes and in S, monocytes and CD11c +. So the consumption of sucrose in the form of binge eating is a cellular immune disruptor.
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Resumen corto

Attenuated *Salmonella* expressing Cell-permeable Bax BH3 Peptide elicits Chemosensitization in a Murine Xenograft model of Human Non-Hodgkin´s Lymphoma

Muñoz-López, P. [1,2], Becerra-Báez, E.I. [1,3], Flores-Martínez, L.F. [1], García-Nava, Y.E. [1,4], Magaño-Bocanegra, K.J. [1,5], González-Franco, J.[1,6], Luria-Pérez, R. [1*]

[1]Unit of Investigative Research on Oncological Diseases, Children's Hospital of Mexico Federico Gomez, Mexico City, Mexico. [2]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, Mexico. [3]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [4]Faculty of Veterinary Medicine and Zootechnics, National Autonomous University of Mexico, Mexico City, Mexico [5]Department of Molecular Biomedicine, Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico City, Mexico. [6]Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México, México.
E-mail: rluria@himfg.edu.mx

The survival of patients with non-Hodgkin´s Lymphoma (NHL) has been demoted with the appearance of drug-resistant cancer cells leading to patient relapse. The overexpression of anti-apoptotic members of the Bcl-2 protein family, such as Bcl-XL, Bcl-2, and Mcl-1, can promote this drug resistance. We have recently shown that a cell-permeable Bax BH3 peptide may antagonize the anti-apoptotic activity of the Bcl-2 family proteins, and the delivery of this peptide by an attenuated *Salmonella enterica* strain SL3261 into the tumor microenvironment elicited an antitumor activity and extended survival in a murine xenograft model of human B NHL. In this work, we analyzed the feasibility of this recombinant attenuated Salmonella to induce Chemosensitización of this NHL murine xenograft model. Thus, *in vitro* assays were performed using previously reported recombinant attenuated *Salmonella enterica* expressing and releasing the cell-permeable Bax BH3 peptide to treat Ramos cells (a human B NHL cell line) in the presence or absence of Vincristine as chemotherapy. Results demonstrated that the recombinant bacterium significantly decreased the viability (measured by trypan blue assay), increased the apoptosis (measured by caspase-3 active), and induced successful chemosensitization of the Ramos cells. On *in vivo* assays, the intravenous administration of this recombinant Salmonella enhanced the antitumor activity and extended survival in a murine xenograft model of human B NHL in the presence of the chemotherapeutic agent. These results documented the feasibility of attenuated *Salmonella enterica* expressing cell-permeable Bax BH3 peptide as a potential treatment to improve patient outcomes with relapsed or refractory **NHL cells.**

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Resumen corto

An anti-Transferrin Receptor-1 Single-Chain Fragment Variable Recognizes Head and Neck Cancer cells for Antitumor purposes

Muñoz-López, P. [1,2], González-Franco, J. [1,3]*, Flores-Martínez, L.F. [1], Becerra-Báez, E.I. [1,4], García-Nava, Y.E. [1,5], Magaño-Bocanegra, K.J. [1,6], Ribas-Aparicio, R.M. [2], Luria-Pérez, R. [1]

[1]Unit of Investigative Research on Oncological Diseases, Children's Hospital of Mexico Federico Gomez, Mexico City, Mexico. [2]Departamento de Microbiología, Escuela Nacional de Ciencia Biológicas, Instituto Politécnico Nacional. Ciudad de México, México. [3]Escuela Superior de Medicina, Instituto Politécnico Nacional. Ciudad de México, México. [4]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas. Instituto Politécnico Nacional. Ciudad de México, México. [5]Faculty of Veterinary Medicine and Zootechnics, National Autonomous University of Mexico, Mexico City, Mexico. [6]Department of Molecular Biomedicine, Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico City, Mexico.
E-mail: gofrajo@live.com.mx

Head and neck cancer is a group of neoplasms among Mexico's frequent causes of cancer. Despite advances in treatments, the appearance of drug resistance represents a problem in eradicating tumor cells. Many molecules have been implicated in resistance to treatments, such as Transferrin receptor-1 (TfR-1), a molecule overexpressed in head and neck cancer cells, associated with many metabolic processes necessary for the growth and destruction of tumor cells. In this work, we propose to construct a single-chain Fragment variable (scFv) against TfR-1 to induce the death of these tumor cells through the iron deprivation mechanism and, at the same time to evaluate its feasibility as a delivery system of molecules with antitumor activities. Bioinformatics tools predicted an adequate three-dimensional structure of the anti-TfR-1 scFv, and using recombinant DNA technology, the plasmids that encode for the anti-TfR-1 scFv and controls were generated. Protein expression was evaluated by SDS-PAGE and Western Blot and purified by affinity chromatography, obtaining a protein of 68 kDa. The anti-TfR-1 scFv binding capacity to head and neck cells (FaDu) that overexpress TfR-1 was confirmed by flow cytometry. Treating FaDu cells with anti-TfR-1 scFv significantly reduced tumor cell viability (measured by MTT assay). These results documented the successful development and characterization of an anti-TfR-1 scFv that recognizes TfR-1 in head and neck tumor cells, an scFv with potential use as antitumor therapy, and also as a delivery system of cytotoxic molecules for cancer treatment.

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Resumen corto

Effect of the antioxidant system on NET formation induced by LPS; The roles of vitamins E & C, glutathione and N-acetyl-cysteine

Muñoz-Sánchez, G. [1]*, Valencia-Hernández, G. [1], Gámez, L.A. [1], Fafutis-Morris, M. [1,2], Del Toro-Arreola, S. [1], Delgado-Rizo, V. [1]

[1]Laboratorio de Inmunología, Departamento de Fisiología, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2] CIINDE con sede en el Instituto Dermatológico de Jalisco Dr. José Barba Rubio, Secretaría de Salud, Zapopan, Jalisco, México. [3]Instituto de Investigación en Ciencias Biomédicas, Departamento de Fisiología, Universidad de Guadalajara, Guadalajara, Jalisco, México.
E-mail: german.munoz2599@alumnos.udg.mx

Reactive oxygen species (ROS) eliminate pathogens during NET formation but can also damage the host. Humans normally contain vitamins E, C, and glutathione (GSH) in their bloodstream at concentrations of 30 µM, 100 µM, and 800 µM respectively. The chemical nature, redox potential, and localization of these antioxidants improve the cell's capacity to face ROS-induced damage. Neutrophils have high concentrations of vitamin C (1500 µM) capable of interacting with endogenous vitamin E and GSH, but during NET formation, these concentrations may be insufficient. Previous studies have shown that vitamin E, C, or N-acetyl cysteine (NAC) reduce NETs *in vitro*, but their combined effect remains unknown. Neutrophils were pre-loaded with vitamins E, C, GSH, and NAC alone or in combination (2 - 4 antioxidants) and NETs were induced with LPS. We evaluated NET formation, total antioxidant capacity (TAC), redox state of neutrophils, lipid peroxidation and ROS/NOS production. Our results show that vitamin E and C, GSH, and NAC induce a suppressive effect of NETs that is stronger when two or four antioxidants are combined. Additionally, neutrophils increase their TAC and reduce oxidative molecules. These results suggest that antioxidants are effective in controlling NET formation and avoid oxidative stress in human neutrophils *in vitro*.

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Resumen corto

Relationship between the cellular adaptive response of T-helper lymphocytes and dendritic cell phenotype in peripheral blood of uninfected HIV-exposed newborns

Nájera-Hernández, M.A. [1]*, Valeriano-Baena, R.G. [1], Bermejo-Haro, M.Y. [1,2], Camacho-Pacheco, R.T. [1,2], Brito-Pérez, Y. [1], Plazola-Camacho, N. [1], Figueroa-Damian, R. [1], Mancilla-Herrera, I. [1]

[1] Departamento de Infectología e Inmunología Perinatal, Instituto Nacional De Perinatología, Secretaría de Salud, Cuidad de México, CDMX, México. [2] Programa de posgrado en inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Cuidad de México, CDMX, México.
E-mail: mnajerah1600@alumno.ipn.mx

Due to perinatal care and antiretroviral therapy, vertical transmission has been reduced in HIV-infected pregnant women. Although they are absent from infection from the HIV virus, HIV-exposed uninfected infants (HEU) present a higher morbidity and mortality rate during their first year of life, compared to HIV-uninfected non-exposed infants (NHEU). Previously, we have reported reduced percentages of differentiated Th lymphocytes in peripheral blood. However, it is not known whether myeloid dendritic cells (mDCs), plasmacytoid dendritic cells (pDC), and the serum cytokine environment who support the Th differentiation could also be altered. The objective of this work was to evaluate the percentages of Th lymphocytes, mDC, pDC, the concentration of plasma cytokines, and their interrelationships in HEU and NHEU newborns. Using multiparametric analysis by flow cytometry we analyzed the phenotype of DCs, Th cells and quantified cytokine concentrations in blood from 15 HEU and 4 NHEU newborns. We observed that the expression of CD80 and CD86 in mDCs and pDCs has a positive correlation with the concentration of cytokines, meanwhile it has a negative correlation with Th1, Th1/Th17, Th2 and Th17 phenotypes. Hence the expression of CD86 in mDCs correlates positively with Treg in HEU newborns. These findings lend support that DCs in HEU newborns promote a preferentially immunomodulatory environment over effector responses, generating an immune imbalance that could explain the increased vulnerability of these newborns to infectious diseases during their first year of life.

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Resumen corto

The MGL1 receptor plays a critical role in mediating colorectal cancer malignancy

Nieto-Yañez, O. [1], Rodríguez, T. [1], Juárez-Avelar, I. [1], Andrade-Meza, A. [1,2], Ortiz-Robles, C. [1], Flores, A. [1], Terrazas, L.I. [3,4], Rodriguez-Sosa, M. [1]*

[1]Innate Immunity Laboratory, Biomedicine Research Unit (UBIMED), Facultad de Estudios Superiores Iztacala (FES-Iztacala), Universidad Nacional Autónoma de México (UNAM), Tlalnepantla, Estado de México, México. [2]Programa de Doctorado en Ciencias Biomédicas, UNAM, Mexico City 04510, Mexico. [3]Immunoparasitology Laboratory, UBIMED, FES-Iztacala, UNAM, Tlalnepantla Estado de México, México. [4]National Health Laboratory, FES-Iztacala, UNAM, Tlalnepantla, Estado de México, México. E-mail: rodriguezm@unam.mx

The macrophage receptor C-galactose lectin (MGL1) recognizes abnormal glycosylation patterns present in malignant colorectal cancer cells with high affinity. To determine the role of MGL1 in colitis-associated colon cancer (CAC), dextran sulfate sodium salt (DSS) was administrated to mice that lacked MGL1 (Mgl1-/-) and the wild-type (WT) littermates. Mgl1-/- mice showed significatively less damage to the colonic structure, as well as a smaller number of tumors compared to WT mice after CAC induction. Mgl1-/- mice displayed higher number of CD8+ lymphocytes and a smaller number of suppressor myeloid cells than WT mice in spleen and blood. In addition, tumor cells from Mgl1-/- mice had less activation of ERK (Extracellular-Signal-Regulated Kinase) signaling cascade pathway compared to WT mice. Taken together these findings suggest that MGL1 plays an important role in the development of CAC. Importantly, MGL could be a potential therapeutic target in CAC.

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Resumen corto

Inhibition of the P450 aromatase enzyme increases cytotoxic T lymphocytes and TNF-α in a murine model of malaria

Nolasco-Pérez, T J [1]*, Salazar-Castañón, V.H. [1],
Legorreta-Herrera, M. [1]

1Laboratorio de Inmunología Molecular. Unidad de Investigación Multidisciplinaria. Facultad de Estudios Superiores Zaragoza, UNAM. Batalla 5 de mayo, Esq. Fuerte de Loreto, Iztapalapa. Ciudad de México, México. CP. 09230. E-mail: teresyta.qfb@gmail.com

Malaria is the deadliest parasitic disease in the world. The severity of Plasmodium infection as well as mortality is higher in men than in women. Testosterone contributes to this sexual dimorphism due to its immunosuppressive effect on the immune response. $CD3^+CD8^+$ cytotoxic T lymphocytes (CTL) promote parasite elimination. However, it is not known whether testosterone modulates CTL activity. Testosterone is synthesized from cholesterol and converted to oestrogen by the P450 aromatase enzyme (P450arom). In this work, to investigate the effects of testosterone on CTLs in malaria, we used CBA/Ca mice that we administered and/or inhibited P450arom in vivo with letrozole (to avoid oestrogen interference) and infected all mice with *P. berghei* ANKA. From day 3 post infection (PI) to day 8 PI parasitaemia was determined and on day 8 PI all mice were sacrificed. Spleen and plasma were removed. Cells from the spleen were stained with PE-anti-$CD8^+$ and quantified by flow cytometry. The plasma obtained was mixed with capture beads from the CBA Th1/Th2/Th17 kit and the concentration of TNF-α and IFN-γ was quantified by flow cytometry. Co-administration of letrozole and testosterone raised testosterone concentration and increased parasitaemia. In addition, androgens increased CTL number and TNF-α concentration, but did not change IFN-γ concentration. These results suggest that TNF-α promotes CTL proliferation due to interaction with its receptor TNRF and not by increasing IFN-γ. Probably, TNRF receptor activation promotes CTL cytotoxicity through FAS/FASL and TRAIL interaction. This work was supported by the PAPIIT IN228620. The authors are beneficiary from the Becas Nacionales CONACyT and Posdoctorales DGAPA-UNAM.

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Resumen corto

Determination of tryptophan and kynurenine in plasma of active, recovered and vaccinated individuals against SARS-CoV-2.

Nungaray Anguiano, E.J. [1*] Méndez-Frausto, G. [2], Oropeza-Valdez, J.J. [3], Romo-García, M.F. [2], García- López, D.A. [4], Lopez-Hernandez, Y. [4], Godina González, S. [1], Galván Tejada, C..E. [5], Navarro Solís, O. [1], Martínez-Orozco, R.A. [1], Bollain-y Goitia de la Rosa, J.J. [6], González-Curiel, I.E. [1*]

[1]Maestría en Ciencia y Tecnología Química, Unidad Académica de Ciencias Químicas, Universidad Autónoma de Zacatecas, Zacatecas,Zac. [2]Laboratorio de Inmunotoxicología, Unidad Académica de Ciencias Químicas, Universidad Autónoma de Zacatecas, Zacatecas,Zac. [3]Laboratorio de Biología en Sistemas.Instituto de Medicina Genómica. CDMX, México. [4]Laboratorio de Metabolómica y Proteómica, Unidad Académica de Ciencias Biológicas. Universidad Autónoma de Zacatecas, Zacatecas,Zac. [5]Unidad Académica de Ingeniería Eléctrica, Universidad Autónoma de Zacatecas, Zacatecas,Zac. [6]Laboratorio de Biología Molecular e Inmunología. Unidad Académica de Ciencias Biológicas. Universidad Autónoma de Zacatecas, Zacatecas,Zac.
E-mail: irmacuriel@uaz.edu.mx, 32134310@uaz.edu.mx

COVID-19 is the disease caused by SARS-CoV-2, the coronavirus that emerged in December 2019. This disease characterizes by a metabolic imbalance which contributes to a progression in seriousness and duration of itself. Tryptophan (TRP) and Quinurenine (KYN) are Metabolites with an essential role in the immunological process of disease. Determine TRP and NYK by UPLC-MS among different disease stages on vaccinated subjects. Intensities of TRP and KYN were determined on the plasma of subjects classified into 4 groups: Control (n=20), Actives COVID-19 (n=20), Recovered COVID-19 (n=32), Vaccinated(n=22). Extraction of TRP and KYN was performed on liquid phase with acetonitrile and resuspended on MQ water plus formic acid. As an internal standard, Tryptophan indol-D5 (10µg/ml) was added to samples and were analyzed on UPLC-MS equipment. For statistical analysis Shapiro-wilk test was performed, followed by descriptive statistics and one-way ANOVA for each metabolite. Intensities obtained between groups Control (TRP: 63.70 (246.2) and KYN: 44.05±22.94), Actives (TRP: 58.45(246.4) and KYN: 32.36±10.34)), Recovered (TRP: 93.93±65.83 and KYN:43.13±11.96) and Vaccinated (TRP: 83.53±54.56 and KYN:26.65±11.96) didn't show significative statistical differences. Neither changes statistically significant ton relation KYN/TRP upon the 4 groups (Control: 0.3400(3.46), Actives: 0.3343(1.822), recovered: 0.2968(1.975) and Vaccinated: 0.2458±0.1788) were found. No alteration was observed in TRP or KYN levels among the different disease stages and on Vaccinated. This suggests the existence of other immune metabolites intrinsic to COVID-19 pathogenesis.

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Resumen corto

Do thymic epithelial progenitor cells really exist in the epithelial compartment of the postnatal thymus? On the way to understand thymus regeneration

Ocampo Godinez, J.M.[1]*, Vergara Lope Núñez, J.A. [1], González Quiroz, J.L. [2], Villagomez Olea, G.[1], García Latorre, E. [2], Alvarez-Perez, M.A. [1]

[1]Laboratorio de Bioingeniería de Tejidos, Departamento de Estudios de Posgrado e Investigación, Universidad Nacional Autónoma de Mexico, Mexico City, Mexico. [2]Laboratorio de Inmunoquímica I, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico. E-mail: moisesoagj@gmail.com

Thymus regeneration is relevant for its potential to treat immunodeficiencies and to induce xenotransplant tolerance. To explain the regeneration of thymic epithelial cells (TECs) in the postnatal life, some groups have proposed the existence of thymic epithelial progenitor cells (TEPCs). However, recent single-cell RNA sequencing analysis (scRNA-seq) have not been able to confirm their presence in the epithelial compartment. Instead, these studies have found transit-amplifying thymic epithelial cells (TAC-TECs). The present work aimed to characterize several proliferative ki67^{+}TECs and ki67^{+}Lgr5^{+} dual positive cells (DPCs) in all thymic epithelial compartments to explain part of the regeneration model of the postnatal thymus. We validated the existence of these cells with a bioinformatic scRNA-seq reanalysis. Moreover, we also found that integrins CD11b and podoplanin (PDPN) are highly expressed in most proliferative cells. Our results support the existence of TAC-TECs and also suggest that mature TECs from all thymic epithelium compartments can proliferate to self-renew, enhancing their proliferative capacity with the expression of CD11b and PDPN. However, our findings do not support the existence of TEPCs in the epithelial compartment of the postnatal thymus. These findings significantly change the understanding of how TECs are regenerated in the postnatal life, breaking the dogma that they cannot longer proliferate and demonstrate that is not necessary TEPCs to explain the regeneration of the thymic epithelium in postnatal life. Future studies should integrate the model of TAC-TECs, proliferative TECs and DPCs to regenerate functional thymi with potential clinical applications.

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Resumen corto

HMGB1 is released during ACPA-positive serum-NET induction and correlates with disease stage and severity in RA

Ochoa-Gonzalez, F. L. [1,4,5] , Fernandez-Ruiz, J. C. [1,6], Bastian, Y. [2], Zapata-Zuñiga, M. [3], Lopez, J. A. [4,5], Enciso-Moreno, J. A. [1], Castañeda-Delgado, J. E.[1,2].

[1]Unidad de Investigación Biomédica de Zacatecas, IMSS, Zacatecas, México.[2]Cátedras-CONACyT-Unidad de Investigación Biomédica de Zacatecas-IMSS, Zacatecas, México. [3]Hospital Rural # 51, IMSS, Villanueva, Zacatecas, México; Facultad de Medicina Humana y Ciencias de la Salud, Universidad Autónoma de Zacatecas, Zacatecas, México.[4]Doctorado en Ciencias Básicas, Universidad Autónoma de Zacatecas, Zacatecas, México. [5]Laboratorio de microRNAs y Cáncer, Unidad Académica de Ciencias Biológicas, Universidad Autónoma de Zacatecas, Av. Preparatoria S/N, Zacatecas 98066, México. [6]Universidad Autónoma de San Luis Potosí, San Luis Potosí, México.

Rheumatoid arthritis (RA) is a chronic, systemic inflammatory disease that primarily affects the peripheral synovial joints leading to cartilage destruction, bone erosion, and joint deformity. Synovial inflammation is characterized by leukocyte infiltration the most abundant are neutrophils, during their activation they increase the production of reactive oxygen species, thereby releasing intracellular calcium activating enzymes that ultimately lead to the formation of neutrophil extracellular traps (NETs). During release of NETs, damage-associated molecular patterns (DAMPs) including HMGB1 (High mobility group box 1). A nuclear protein that acts as alarmin in the nuclear space, increasing the inflammatory response. We evaluated the dynamics of HMGB1 during the formation of NETs induced with serum from patients with RA and to evaluate its relationship with several markers of disease activity characteristic of the inflammatory process in RA. HMGB1 is released into the extracellular space during the induction of NETs with serum from patients with RA, patients with RA show an increase in the relative expression of HMGB1 and it is associated with the clinical characteristics of patients with RA.

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Resumen corto

HSA-SMX-NO hapten model for the study of hipersensitivity reactions

Ordoñez-Rodriguez, A.M. *[1], Gómez-Castro, C. Z. [2], Castrejón-Flores, J. L. [1]

[1]PPCTV.UPIBI-IPN. Av. Acueducto, La Laguna Ticomán, Gustavo A. Madero, 07340 Ciudad de México, CDMX [2]UAEH.Km. 4.5, Pachuca -Tulancingo, 42184, Mineral de la Reforma, Hgo.
alma.ordonez.rod@gmail.com

Drug hypersensitivity reactions are originated when a drug activates the immune system, it is an important health problem because it can lead to life-threatening diseases. Antibiotics among other therapeutic agents have a high incidence of developing drug hypersensitivity reactions, where 6 % of the adult population might presence a type of allergic reaction to sulfamethoxazole (SMX). The metabolite sulfamethoxazole nitroso (SMX-NO), generated by the oxidation reactions of the parent drug, is believed to be the final antigen responsible to modify proteins, such as albumin (HSA). Together conformed an hapten, which can break immunological tolerance. Nonetheless, crystallographic resolved structures of the hapten had not been reported. Therefore, the aim of the following investigation is to generate a computational model of the modified albumin based upon *in vitro* and *in vivo* experimental mass spectrometry data by the using of computational tools including molecular dynamics, modelling and docking. We successfully simulate the hapten with different lysine modifications, Lys-199 (Hapten A) and Lys-137 (Hapten B). These models will help understanding the chemical mechanism involved in haptenization as well as find new treatments to help in hypersensitivity reactions.

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Resumen corto

Establishment of the quantification and purification of circulating colorectal cancer tumor cells

Oregon, R. [*1,2], Montesinos, J. J. [1], Mayani H. [1], Vadillo E. [1]

1Unidad de Investigación Médica en Enfermedades Oncológicas, Hospital de Oncología, Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, CDMX, México. 2Facultad de Estudios Superiores Zaragoza, Universidad Nacional Autónoma de México, UNAM, México.
reynaoregon.qfb@gmail.com

In colorectal cancer (CRC) almost 90% of mortality is currently associated with metastasis. From a clinical point of view, it is essential to develop and establish techniques that help predicting the outcome of patients with CRC and other neoplasms. The quantification of circulating tumor cells (CTC) is a test that helps in the early detection and evaluation of the response to treatment in CRC. In this project, CTC quantification and purification methods were standardized for application in CRC. Quantification of CRC cells in peripheral blood was performed by spectral flow cytometry. Purification of CTC was carried out by the pressurized peripheral blood filtration technique. Establishment of the methods indicated that spectral flow cytometry is effective and sensitive for detecting CTC in numbers less than 10 cells per mL of peripheral blood; the filtration technique is not sensitive enough for CTC quantification, but it is efficient for their isolation and culture.

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Resumen corto

Establishment of a model for Hepatitis E Virus infection *in vitro* to support the study of antivirals

Orozco-Córdoba, J. *[1], Abarca-Magaña, J. C.[1], Reyes-Rico, M. [1], Domínguez-Romero, A. [1], Du Pont, G. [1], Calderon, A. [1], Lamoyi, E. [1], Fierro, N. A. [1]

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad Universitaria, CDMX, México.
orozcocordobajavier@gmail.com

Despite Hepatitis E Virus (HEV) is the major cause of acute hepatitis in the world, its study remains limited. The systems available for HEV propagation are inefficient and poorly reproducible. These systems are crucial for describing virus biology and evaluating antivirals. An antiviral role for bilirubin (BR) has been proposed in Hepatitis C Virus and Herpes Virus infections. Moreover, we recently reported that Conjugated Bilirubin (CBR) regulates the immune function during Hepatitis A Virus infection. The mechanisms related to the effect of BR in modulating the immune response and how this metabolite exerts an antiviral effect are still unclear. A specific interaction between BR and the aryl hydrocarbon receptor (AhR) has been proposed. AhR is expressed in a variety of tissues, and it has been suggested to modulate inflammatory processes. Thus, it is plausible that during viral hepatitis an interaction between CBR and AhR occurs, resulting in CBR effects. Herein, a culture system for HEV was standardized; this system is based on an A549-derived cell line (A549/D3) susceptible to HEV infection and an A549-derived cell line (A549/N5) persistently infected with HEV. A constitutive AhR expression was found in A549/D3, and it was upregulated by CBR incubation in a dose-response manner as evaluated by flow cytometry and fluorescence microscopy. Additionally, CBR cytotoxicity and HEV propagation were evaluated by MTT and RT-PCR assays respectively. Based on our results, the use of this cell lines constitutes a reliable model for determining the CBR antiviral effect during HEV infection.
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Resumen corto

Pathogenic Th17 cells generation in EAE is modulated by the transforming growth factor receptor III (Betaglycan)

Ortega-Francisco, S. *[2,3], Duesman, S. [1], Olguin-Alor, R. [3], Acevedo-Dominguez, N. [2], Sestero, C. [6], Chellappan, R. [4], De Sarno, P. [5], Yusuf, N. [1], Salgado-Lopez, A. [2], Segundo-Liberato, M. [2,3], Montes de Oca-Lagunas, S. [2], Raman, C. [1], Soldevila, G. [2,3]

[1]Department of Dermatology, [4]Department of Pathology, [5]Department of Biology, University of Alabama at Birmingham, United States; University of Alabama at Birmingham, Alabama, USA. [2] Department of Immunology. [3] National Laboratory of Flow Cytometry Biomedical Research Institute, UNAM,Mexico City, Mexico. [6]Department of Biology, Chemistry, Mathematics and Computer Science, University of Montevallo, Alabama, USA. *amyrisortega@gmail.com

The Transforming Growth Factor receptor III (TβRIII) is a co-receptor of the TGF-β super family ligands that is upregulated during T cell activation; however, its function in mature T cells remains unclear. As TβRIII genomic deletion results in perinatal mortality, we developed a conditional knock-out mouse with restricted TβRIII deletion in mature T cells (*Tgfbr3$^{fl/fl}$.dLCKCre or* TβRIII$^{-/-}$*)*. We used a mouse model of autoimmunity to evaluate the role of TβRIII on Th1/Th17-mediated EAE. Our results showed that TβRIII$^{-/-}$ mice developed more severe disease after immunization with MOG_{35-55}, compared to wild-type littermates, which was associated with increased numbers of CNS infiltrating IFNγ^{+} CD4^{+} T cells and T cells co-expressing IFNγ and IL-17 (IFNγ^{+}/IL-17^{+}), but not IL-17 alone. This led us to speculate that TβRIII might be involved in regulating the conversion of encephalitogenic Th17 cells to Th17 coexpressing IL-17 and IFNγ. To directly address this, we generated *in vivo* MOG specific encephalitogenic Th17 and Th1 cells from wild type and TβRIII null mice and passively transferred them into naïve mice. Remarkably, TβRIII $^{-/-}$ Th17 cells induced a more severe EAE, with an earlier onset, than those from TβRIII $^{+/+}$ mice, in accordance with the enhanced production of IFNγ observed after Th17 but not Th1-skewed restimulation of *in vivo* primed TβRIII$^{-/-}$ CD4+ T cells. Altogether, our data indicate that TβRIII is a coreceptor that functions as a key checkpoint in controlling the pathogenicity of autoreactive T cells in neuroinflammation probably through regulating plasticity of Th17 T cells into pathogenic Th1 cells.

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Resumen corto

PD-1 and Helios expression in Treg and Th17-like Treg cells

Ortega-Mejía, I. [1,2]*, Ortega-Tapia, G. [1,2], Gómez-Mosqueira, R. [1,2], Bernal-Alferes, B. [1,2], García-Latorre, E. [1], Domínguez-López, M. L. [1], Romero-López, J. P. [1,2].

1Laboratorio de Inmunoquímica 1, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, IPN. 2Laboratorio de Patogénesis Molecular, Edificio A4, Facultad de Estudios Superiores Iztacala IMSS.
Contacto: itzayannaortega@gmail.com

This article examines the expression of two proteins, Helios and PD-1, in different types of T cells, specifically Treg cells and Th17-like Treg cells. Treg cells play a crucial role in regulating the immune response, while Th17 cells are known to promote inflammation. The differentiation of these subtypes depends on the presence of various cytokines during the immune synapse process. Recent studies have suggested that Treg cells can acquire characteristics of the Th17 lineage, resulting in a Treg/Th17 phenotype that has been linked to psoriasis. However, the mechanism behind this conversion is still unclear.

The aim of this study was to evaluate the expression of Helios and PD-1 in Treg cells that produce IL-17, a cytokine associated with the Th17 lineage. Blood samples were collected from 15 healthy individuals and 3 patients with psoriasis. The samples were analyzed using multiparameter flow cytometry to identify Treg, Th17, and Treg/Th17 cells and to assess the expression of Foxp3, IL-17, Helios, and PD-1.

The results showed that all three types of T cells were present in both healthy individuals and patients with psoriasis. There was a significant difference in the percentage of Helios+ cells between Treg and Treg/Th17 cells in both healthy individuals and patients. Similarly, the analysis of median fluorescence intensity revealed a significant difference in the expression of Helios between Treg and Treg/Th17 cells in both groups.

These findings suggest that the expression of Helios and PD-1 may be involved in the differentiation of Treg and Th17-like Treg cells, which could have implications for the development and treatment of inflammatory diseases such as psoriasis. Further studies are needed to fully understand the mechanisms involved in this process.

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Resumen corto

Molecular and cellular mechanisms implicated in the pathogenesis of psoriasis

Ortega-Rocha, E. M. *[1,2], Santos-Carmona, S. V. [2,3], Lemini-López, A. [4], Pérez-Koldenkova, V. [5], Hernández-Herrera, P. [7], Domínguez-Hüttinger, E. [6], Bonifaz, L.C. [2].

[1]Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, CDMX, México. [3]Facultad de Química, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [4]Servicio de Dermatología, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, IMSS. [5]Laboratorio Nacional de Microscopía Avanzada, Centro Médico Nacional Siglo XXI, IMSS. [6]Departamento de Biología Molecular y Biotecnología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [7]Laboratorio Nacional de Microscopía Avanzada, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México.
elizabeth13mor@gmail.com

Psoriasis is an inflammatory skin disease characterized by hyperproliferation of keratinocytes which causes the formation of red scaly plaques. The inflammatory response of the disease has been mainly attributed to Th17 cells and their associated cytokines however to understand the pathogenesis of the disease it is important to evaluate different components and its interaction to have a cellular and molecular signature related to the prognosis and treatment election. In this work, we evaluated the interaction of epidermal barrier, the microbiota, and the immune response mediated by Th17 cells related to the disease activity. These components were evaluated by immunofluorescences on skin biopsies of psoriasis´ patients. We found that tight junctions like claudin-1 and occludin have an aberrant distribution in lesioned skin of patients with high severity indexes (PASI). The aberrant distribution of these proteins was related to the presence of enterotoxin B of Staphylococcus aureus (SEB) in the epidermis and dermis of biopsies. We found that patients with SEB localized on the dermis had higher PASI which could contribute to the inflammatory response of the skin. We also evaluated the expansion of TCRvβ17 clones on lesioned skin and found that the percentage of CD4 TCRvβ17 cells correlated with the severity of the disease. Taken together, our results suggest a relation between tight junctions, SEB and CD4 TCRvβ17 cells contributing to severity of psoriasis.

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Resumen corto

Identification and characterization of α4β7+ T lymphocytes in psoriasis in an animal model

Ortega-Tapia, G. T. [1,2], Romero-López, N. *[1,2], Estrada-Aguilar, L. G. [3], Casasola-Vargas, J. C. [4], García-Romo, G. S. [5], Reyes-Maldonado, E. [6], Rivas-Hernández, N. [7], Prieto-Chávez, J. L. [8], Salinas-Lara, C. [9], Sánchez-Garibay, C. [9], Domínguez-López, M. L. [2], Romero-López, J. P. [1,2]

[1]Laboratorio de Patogénesis Molecular, Red MEDICI, Carrera de Médico Cirujano, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México. [2]Laboratorio de Inmunoquímica. Posgrado en Ciencias Biológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [3]Departamento de Dermatología, Hospital Regional "Lic. Adolfo López Mateos", ISSSTE, Ciudad de México, CDMX, México .[4]Departamento de Reumatología, Hospital General de México "Dr. Eduardo Liceaga", Ciudad de México, CDMX, México.[5]Laboratorio de Inmunología, Unidad de Morfología y Función, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México.[6]Departamento de Morfología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [7]Departamento de Parasitología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [8].Laboratorio de Citometría, Centro de Instrumentos - CIS IMSS, Ciudad de México, CDMX, México. [9]Departamento de Neuropatología, Instituto Nacional de Neurología y Neurocirugía "Dr. Manuel Velazco Suárez", Ciudad de México, CDMX, México. nayerola@gmail.com.

T lymphocytes and intestinal inflammation play an important role in the pathogenesis of psoriasis. In patients with spondyloarthritis, we have demonstrated a high frequency of gut-activated γδ T cells through the expression of α4β7 integrin. Considering the similarity in the pathogenesis of psoriasis and spondyloarthritis, we aimed to evaluate the expression of α4β7 integrin in T lymphocytes from patients with psoriasis and in a murine model. Blood and skin samples were collected from 10 patients with psoriasis, these were analyzed by flow cytometry to determine the frequency of α4β7 integrin-positive T and γδ T cells. In addition, these cells' frequency was identified in the skin and blood of mice with imiquimod-induced psoriasis, characterizing histologically the presence of cutaneous, intestinal, and joint inflammation. In patients, the percentages of αβ T lymphocytes in blood were found to be increased (p=0.0072) while those of T γδ were found to be decreased (p=0.0072). T γδ α4β7+ lymphocytes presented increased expression of IL 22 (p=0.0400). In mice, αβ T lymphocytes were found to be increased in the skin (p=0.0173), whereas T γδ, were found to be decreased (p=0.0357), but with high α4β7 integrin expression (p=0.0357). In blood, we observed increased α4β7 integrin expression in total T and αβ T lymphocytes. By histology, we observed the correct induction of the model and congestion of blood vessels accompanied by marked edema at the large intestine's submucosal, muscular, and serosal levels. Acknowledgments: This project was funded by grant PAPIIT-UNAM IA206822 and SIP-IPN 20210213, SIP20211581.

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Resumen corto

Application of data science for the identification of immunogenic T-cell epitopes from the whole genome of *Giardia lamblia*

Ortega-Tirado, D. [1]*, Velazquez-Valdez, C.A. [2], Garzon-Lizarraga, T.M. [1], Lopez-Romero, G. C. [1], Velazquez-Contreras, C.A. [1]

1Departamento de Ciencias Químico-Biológicas, Universidad de Sonora, Hermosillo, Sonora, México. 2Departamento de Matemáticas, Universidad de Sonora, Hermosillo, Sonora, México
david.ortega@unison.mx

Giardia lamblia is the etiological agent of giardiasis. This parasite is classified into eight genotypes, named assemblages A-H. Assembles A and B infect humans. Nowadays, there is no vaccine against human giardiasis so the study of new immunogenic antigens remains pivotal. Recently, bioinformatics has proven to be a useful and reliable tool to identify immunogenic antigens. In this work, we performed an Immunoinformatic analysis of the whole genome of the parasite to identify immunogenic T-cell epitopes recognized by murine MHC-II molecules. The whole FASTA sequences of the genome of assemblage A were taken from GiardiaDB (https://giardiadb.org/giardiadb/app) and submitted to NetMHCII 2.3 of the IEDB (http://tools.iedb.org/mhcii/). Data science was applied to perform a faster and more complete analysis of all the epitopes derived from assemblage A genome. For this, a programming code was built using Python 3.9 in order to interact with the API of IEDB and submit the FASTA sequences all at once. Also, this code allowed to concentrate all the data from analysis. Until now, around $1.78x10^5$ epitopes from the whole genome of assemblage A have been identified. Therefore, we continue applying data science to establish the association between these data and biological features to observe if the predicted epitopes belong to proteins located in Giardia's trophozoite, cysts or the secretome. This analysis will contribute to the discovery of all the possible immunogenic antigens of Giardia and highlights how data science can be applied in the development of a vaccine against giardiasis.

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Resumen corto

Determination of autophagy and apoptosis in SiHa and HeLa cells treated with IL-2 and anti-CD95

Ortiz-Garrido, I. [1], Romero-Hernández, C.B. [1]*, Gutiérrez-Hoya, A. [1-2], Soto-Cruz, M. I. [1]

[1] Molecular Oncology Laboratory, Cell Differentiation and Cancer Research Unit, FES Zaragoza, National University of Mexico, Batalla 5 de Mayo s/n Col. Ejército de Oriente, Mexico City 09230, Mexico. [2] Cátedra CONACYT, CONACYT, Avenida Insurgentes Sur 1582, Col. Crédito Constructor Del. Benito Juárez, Mexico City 03940, Mexico.

IL-2 has shown to have a pleiotropic role in cervical tumor cells, inducing or inhibiting their proliferation. In addition, it has been used as immunotherapy against cervical cancer, as well as other cancers. On the other hand, CD95, a well-known death-inducing receptor in abnormal cells, may play an opposite role in tumor cells promoting survival processes. Therefore, in the present work the role of IL-2 (10 and 100 UI/mL), anti-CD95 antibodies (10, 20, 25, 100, 200 and 400 ng/mL) and treatments together were evaluated on proliferation, apoptosis, and autophagy in cervical cancer cells. The determinations were performed by crystal violet, flow cytometry and confocal microscopy. We found that IL-2 induces or inhibits proliferation in dose dependent manner. Cervical tumor cells express CD95 and its ligand; treatment with anti-CD95 promotes cell proliferation. The doses used of IL-2 and anti-CD95 do not induce apoptosis, but simultaneous treatment IL-2 and CD95 promotes accumulation of LC3B fluorescent foci, i.e, autophagosomes, structures inherent in the autophagic process. Our results demonstrate the pleiotropic role in cervical cancer cells, 100 UI negatively regulates proliferation, while 10 UI induces the opposite. Also, that the expression of CD95 and its ligand play a pro survival role. Besides, LC3B protein accumulation through IL-2 stimulation, and followed by CD95 is related to increased cell proliferation and as a possible autophagy-mediated cytoprotective process.

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Resumen corto

MIF induces macrophage polarization toward the proinflammatory-M1 phenotype

Ortiz-Robles, C.D. *[1], Andrade-Meza, U.A. [1], Juárez-Avelar, I. [1], Calderón-Aranda, E. [2], Rodríguez-Sosa, M. [1]

[1]Laboratorio de Inmunidad Innata, Unidad de Investigación en Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México (UNAM); Tlanepantla, Edo. Méx. [2]Departamento de Toxicología, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. christianortiz@cinvestav.mx

Macrophage migration inhibitory factor (MIF) is a pleiotropic cytokine that was initially recognized to increase macrophage proinflammatory cytokines production, such as TNF-α, IL1β, and IL-6, however, increasing evidence shows that MIF also influences important processes for the maintenance of cellular homeostases, such as the promotion of cell survival, antioxidant signaling, and wound repair. Therefore, it has not been described in detail whether MIF influences macrophage polarization towards the M1 (proinflammatory) or M2 (reparative) phenotype. This study aimed to clarify the function of MIF on the phagocytic capacity and its influence to induce the expression of molecules that characterize the M1 and M2 macrophage phenotypes. Here, we employ bone marrow-derived macrophages (BMDM) from wild-type (Wt) and MIF knockout (Mif-/-) mice differentiated with M-CSF, these were unpolarized, polarized toward M1 (LPS+IFN-γ) or M2 (IL-4 +IL-13), and stimulated with recombinant MIF (r) for 72 h to assess IL-10 and TNF-α secretion, nitric oxide (NO.-) production, arginase activity, and phagocytosis. rMIF increased the TNF-α secretion, the number of phagocytic cells and enhances the phagocytosis capacity in non-polarized macrophages. MIF increased the TNF-α secretion and NO.- production without affecting IL-10 secretion, arginase activity, and phagocytosis in M1 macrophages. While MIF did not modify any parameter evaluated in M2 macrophages. These results confirmed that MIF favors the macrophage polarization towards the M1 phenotype, importantly MIF does not modify the M2 phenotype.

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Resumen corto

Salivary pro-inflammatory biomarkers of periodontal disease severity

Ortiz-Rosas, X. [1,2], Sartillo-Mendoza, L.G. [1,3], Herrera-Barrios, M.T. [1], González, Y. [1], Espinosa-Sosa, A.B.[4], Carrasco-Rueda, C.A.[4], Vinitzky-Brener, I. [4] Juárez, E. [1]*

[1]Departamento de Investigación en Microbiología, INER, CDMX, México. [2]Facultad de Ciencias, UNAM, CDMX, México. [3]Facultad de medicina, BUAP, Puebla, México. [4]Servicio de Estomatología INER, CDMX, México.
*ejuarez@iner.gob.mx

Periodontal diseases are highly prevalent in Mexico. Periodontitis is defined by the pathologic loss of the periodontal ligament and alveolar bone following chronic inflammation resulting from interactions between pathogens and destructive immune responses. Biomarkers are needed for diagnosis, severity assessment, and treatment success evaluation in periodontal diseases. However, some metabolites may be altered in the presence of comorbidities. In this study, we evaluated the salivary levels of markers of inflammation (PGE2, LTB4, IL-8), return to homeostasis (Mar1, RvD1, LXA4, 15-epi-LXA4), and tissue damage (nucleosomes), and the presence of neutrophils in oral lavage in subjects with gingivitis, periodontitis, and periodontally healthy controls regardless of any comorbidities. All the metabolites were measured by ELISA, and the percentage of neutrophils was assessed by enumerating myeloperoxidase+ cells in cell preparations.

We found high levels of LTB4, Mar1, LXA4, 15-epi-LXA4, nucleosomes in saliva, and a high percentage of neutrophils in the oral lavage of patients with gingivitis and periodontitis. Furthermore, levels of PGE2, LTB4, Mar1, IL-8, nucleosomes, and neutrophil counts were higher in patients with periodontitis, suggesting their role in discriminating the severity of the disease. These preliminary results suggest a potential link between these biomarkers' levels in the local site and the development of periodontitis. Further studies are warranted to confirm the results because salivary biomarkers may help evaluate the disease progression, follow the response to treatment, and determine a relationship with respiratory and metabolic diseases.

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Resumen corto

MIF promotes periodontal disease associated to pregnancy in a murine model

Ortiz-Sánchez, B. J. *[1,2], Ramírez-Palomino, M. M. [1,2], Juárez-Avelar, I. [2], Rodríguez-Sosa, M. [2]

[1]Dental Surgeon Career, Facultad de Estudios Superiores Iztacala (FES-Iztacala), Universidad Nacional Autónoma de México (UNAM). Tlalnepantla, Estado de México, México. [2]Innate Immunity Laboratory, Biomedicine Research Unit (UBIMED), FES-Iztacala, UNAM. Tlalnepantla, Estado de México, México. b.ortiz@unam.mx

Periodontal disease (PD) is a chronic inflammatory disease, which is favored by oral biofilm, affecting 23% of women in reproductive age, and it increases up to 56% in pregnant women. It's been controversial the relationship between the development of PD and inflammatory mediators in pregnant women. Macrophage migration inhibitory factor (MIF) is a proinflammatory cytokine, which is expressed in periodontal tissues, and is overexpressed in PD and in pregnancy. In this work we evaluated in a murine model of pregestational PD in BALB/c females WT and MIF-/- mice, histological changes and histometric analysis of the clinical attachment loss (CAL), relative expression of metalloproteinase (MMP)-2 and -13 by immunofluorescence and the relative expression of *mif, tnf-α, ifn-γ* and *il-17* by qPCR. We found elevated levels of MMP-13, *mif, tnf-α*. Theses correlated with tissue destruction and increased depth of the CAL in PGPD WT mice compared with control. Importantly we found over expression of MMP-2 and -13 and *il-17*, abated levels of *tnf-α, ifn-γ* and a severe tissue remodeling and no CAL modification in PGPD *Mif-/-* mice. These results suggest MIF plays an important role in exacerbating the inflammatory pathology of preexisting periodontitis. The absence of MIF down regulates inflammatory transcripts and decreases insertion loss in PD. Funding: COMECYT FICDTEM-2021-072 and PAPIIT-UNAM IN-217021

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Resumen corto

Differential inhibition of FcεRI-dependent degranulation and cytokine synthesis in mast cells by cannabinoid receptors

*Osorio-Pérez, R.M. [1], Cruz-Martín del Campo, S.L. [1], González-Espinosa, C. [1].

[1] Departamento de Farmacobiología, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (Cinvestav, IPN). Calzada de los Tenorios 235, Col. Granjas Coapa, Ciudad de México, México, 14330. E-mail: cgonzal@cinvestav.mx

Mast cells (MC) are essential effectors in Type I hypersensitivity (allergic) reactions. Due to their location, MC sense potential hazardous antigens and allergens, initiating inflammatory reactions. In the sensitization phase, the high affinity IgE receptor (FcεRI) attaches binds immunoglobulin E (IgE). Subsequently, the formation of FcεRI/IgE/Ag aggregates causes the synthesis of cytokines, lipid mediators, and the release of proinflammatory components. Several mechanisms of negative control of MC activation have been described. Among them, the activation of cannabinoid receptors (CBR) has been proposed, although molecular mechanisms are not fully described and effects of cannabinoids on MC activation cannot be consistently replicated. To evaluate the participation of CBR in the modulation of MC activation, we used primary cultures of bone marrow-derived mast cells (BMMCs) generated from C57BL6/J mice. We found that the sensitization process with monomeric IgE modifies the intracellular location of CBR and that those receptors are desensitized, since a pre-treatment with inverse CBR agonists allows the cannabinoid-mediated inhibition of degranulation. CBR activation also inhibited FcεRI-dependent cytokine synthesis. This work provides information about the non-redundant actions of distinct CBR in MC responses and shows that activation state of CBR influences the study of the endocannabinoid system in BMMCs.

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Resumen corto

High expression of inhibitory markers on CD8+ T cells from patients with SARS-CoV-2 infection

Osuna-Espinoza, K. Y. [1]*, Mejía-Torres, M. [1], Camacho-Ortiz, A. [2], Perez-Alba, E. [2], Salinas-Carmona, M. C. [1], Rosas-Taraco, A. G. [1]

[1] Departamento de Inmunología, Facultad de Medicina, Universidad Autónoma de Nuevo León. Monterrey, N.L. México. [2] Departamento de Infectología. Hospital Universitario "Dr. José Eleuterio González". Monterrey, N.L. México.
kosunaez@uanl.edu.mx

During viral infections, cytotoxic lymphocytes such as CD8+ and NK play an important role in virus clearance. In the course of the current pandemic of COVID-19, the immunologic response to viral infections gains a main interest. Several protocols have been developed to understand the role of these cells in SARS-CoV-2 infection. Despite the extensive evidence, the functional status of cytotoxic cells has remained a controversial area of interest. Here, we provide a detailed comparative analysis of population counts (leukocytes, lymphocytes, NK, lymphocytes B, lymphocytes T) and the activation markers granzyme B, TIM3, LAG3, and PD1 by means of flow cytometry, in peripheral blood from COVID-19 patients and healthy participants. No significant differences were observed in absolute counts of cell populations and percentage of CD8+/Granzyme B+ cells between the control group and COVID-19 patients *(P>0.05)*. Higher expression of inhibition markers was observed (TIM3, LAG3, and PD1) in COVID-19 patients compared with the control group *(P<0.05)*. In conclusion, we provided evidence that the CD8+ cells of COVID-19 patients showed increased expression of cell markers related to exhaustion, an inhibitory functional state in lymphocytes associated with pathology.

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Resumen corto

Non-Natural Sweeteners And Its Implications On Metabolic Syndrome.

Pacheco-Ramírez, E.G. *, Torres-Canizal, A.,
Serafín-López, J., Moreno-Altamirano, M.M.B.

[1]Laboratorio de Inmunorregulación, y Laboratorio de Inmunología celular e Inmunopatogénesis, Departamento de Inmunología. Instituto Politécnico Nacional-ENCB. UST. CDMX. México.
*E-mail: drpachecoe@gmail.com

Up to date, population have modified their diet by increasing the intake of non- natural sweeteners (NNS) to consume less calories to lose weight. Scientific data supporting the safety of consuming NNS is insufficient. Recent studies show that intake of these sweeteners induce to gut microbiota dysbiosis, neuronal disorders, type 2 diabetes mellitus and metabolic alterations. The aim of this study was to analyse if NNS such as sucralose, aspartame and acesulfame K have a role in the metabolic syndrome. Methods. Five groups of four male Wistar rats were collocated in cages. The sweeteners were added to their daily drinking water. The weight, cholesterol, insulin triglycerides, ROS, and glucose cell intake, were registered before the treatment every 3 weeks for 3 months. Results. After the statistical analysis, no differences were observed between the groups with different sweeteners in insulin or triglycerides levels. The group of rats consuming only water or sucralose had less increase on their body weight. Rats consuming aspartame developed a slightly anxiety and demanded to drink more water than those drinking other sweeteners. Interestingly, rats drinking sucrose were the ones with highest weight but drank less water and showed less anxiety. When ROS and Glucose intake of glucose on the cell population were analysed, there was a differential concentration dependent of every sweetener. Conclusion. There is a need to continuing studying NNS, to understand their role in development of metabolic syndrome, including the analysis on oxidative stress in the cellular system.

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Resumen corto

Evaluation of probiotics on metabolic syndrome and their effectiveness for the prevention of acute lung injury secondary to endotoxic shock.

Pacheco-Ramírez, E.P.*, Mussot-Castro, M.E., Serafín-López, J.

Laboratorio de Inmunología celular e inmunopatogénesis, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México.
*E-mail: drpachecoe@gmail.com

Acute-lung-injury (ALI) and acute-respiratory-distress-syndrome (ARDS) are caused by sepsis, characterized by an exaggerated release of inflammatory cytokines, epithelial damage, and multiple-organ-damage. Metabolic syndrome (MetS) is a cluster of physiological abnormalities that increases the risk of developing sepsis and ALI/ARDS. Probiotics are live microorganisms that have beneficial effects when consumed. A probiotic, Lactobacillus rhamnosus (LGG) influences the regulation of metabolic diseases and immune response.

We evaluated if LGG administration in a murine model of MetS prevents lung damage caused by endotoxic shock.

We use C57BL/6 mice high-fat-diet fed to induce MetS. We measured weight, glucose tolerance curve, glycemia, triglycerides and cholesterol. LGG was administered orally daily after MetS was established. Biochemical parameters were measured before sacrificing the mice in week18. Liver and adipose tissue were histologically analyzed, and qPCR was used to determine IL-6, arginase-1, inducible nitric-oxide-synthase, and leptin receptor in the liver. To induce endotoxic shock, MetS mice were given intravenous lipopolysaccharides (LPS). After 24h, bronchoalveolar lavage, lung, liver, and adipose tissue were obtained and IL-10, TNFa, and oxidative-stress molecules were measured using ELISA and colorimetric reactions.

Dietary LGG decreased clinical parameters and oxidative-stress in MetS; and histologically reduced non-alcoholic-fatty-liver disease. LGG ingestion reduced lung damage and improved clinical score in MetS mice with endotoxic shock.

LGG ingestion in the murine model of MetS improved biochemical parameters and diminish the presence of steatosis. LGG ingestion in mice with endotoxic shock improved clinical parameters and prevented lung parenchymal damage, which could be important in reducing sepsis mortality in people with MetS.

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Resumen corto

Genomic organization and transcriptional analysis of t-cell receptor *locus* in *Ambystoma mexicanum.*

Pacheco-Olvera, D.L.*[1,2], Saint Remy-Hernández, S.[1,2], Godoy-Lozano ,E.E.[3], Téllez-Sosa, J.M.[3], Martínez-Barnetche, J.[3+], López-Macías, C.[2*]

[1]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional. Ciudad de México, México. [2] Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Ciudad de México, México [3]. Centro de Investigación sobre enfermedades infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México.
*Corresponding authors diana.laura.pacheco@gmail.com

T and B cells possess a wide range of receptors that allows virtually unlimited antigenic recognition capable of activating the adaptive immune response against very specific determinants of the pathogen through the clonal expansion process. T lymphocytes are fundamental to the adaptive immune system of all jawed vertebrates and can be classified into two main lineages according to the T cell receptor (TCR) they use. *Ambystoma mexicanum*, is a research model for the study of tissue regeneration. This work aimed to characterize *A. mexicanum* T-cell receptor *loci* and compare them with other tetrapods. Using the genome sequence of the axolotl (V6), we have mapped, characterized, and compared T-cell receptor *loci* using other species reference sequences. The expression of the TCR sequences was analyzed by means of transcriptome mapping obtained from NCBI/SRA. . The TRA-TRD (TCR) clusters were mapped in chr13p and the TRB cluster in chr3p. Only one TRDV segment and no TRG *locus* was found, indicating that although the observed architecture of the TCR *loci* of *A. mexicanum* is like other vertebrates ,its combinatorial diversity is highly restricted.

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Resumen corto

Effect of two mycobacterial proteins on macrophages activation during *Mycobacterium tuberculosis* infection

Paredes-González, I.S.[1]*, Ramos-Espinosa, O.[1], López-Torres, M.O.[1], Mendoza-Trujillo, M.[1], Barrera-Rosales, A.[1], E., Hernández-Pando, R.[1]

[1]División de Patología Experimental, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán. Tlalpan, Ciudad de México, México. [2]Departamento de Inmunología, Instituto de Ciencias Biomédicas, UNAM. Ciudad Universitaria, Coyoacán, CDMX, México.
*Email: iris_selene142@hotmail.com

During the early and progressive (late) stages of murine experimental pulmonary tuberculosis, the differential activation of macrophages contributes to disease development by controlling bacterial growth and immune regulation. Mycobacterial proteins P27 and PE_PGRS33 can target the mitochondria of macrophages. This study aims to evaluate the effect of both proteins in macrophage activation during mycobacterial infection. We assess both proteins for mitochondrial oxygen consumption, and morphological changes, as well as bactericide activity, production of metabolites, cytokines, and activation markers in infected MQs. The cell line MH-S was used for all the experiments. We show that P27 and PE_PGRS33 proteins modified mitochondrial dynamics, oxygen consumption, bacilli growth, cytokine production, and some genes that contribute to macrophage alternative activation and mycobacterial intracellular survival. Our findings showed that these bacterial proteins partially contribute to promoting M2 differentiation by altering mitochondrial metabolic activity.

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[1]División de Patología Experimental, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán. Tlalpan, Ciudad de México, México.[2]Departamento de Inmunología, Instituto de Ciencias Biomédicas, UNAM. Ciudad Universitaria, Coyoacán, CDMX, México.
*Email: iris_selene142@hotmail.com

During the early and progressive (late) stages of murine experimental pulmonary tuberculosis, the differential activation of macrophages contributes to disease development by controlling bacterial growth and immune regulation. Mycobacterial proteins P27 and PE_PGRS33 can target the mitochondria of macrophages. This study aims to evaluate the effect of both proteins in macrophage activation during mycobacterial infection. We assess both proteins for mitochondrial oxygen consumption, and morphological changes, as well as bactericide activity, production of metabolites, cytokines, and activation markers in infected MQs. The cell line MH-S was used for all the experiments. We show that P27 and PE_PGRS33 proteins modified mitochondrial dynamics, oxygen consumption, bacilli growth, cytokine production, and some genes that contribute to macrophage alternative activation and mycobacterial intracellular survival. Our findings showed that these bacterial proteins partially contribute to promoting M2 differentiation by altering mitochondrial metabolic activity.

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Resumen corto

Innate immune response of the keratinocyte in infection by the fungus *Sporothrix schenckii*

Paredes-Rojas, A.[1, 2], Palma-Ramos, A.[2], Castrillón-Rivera, L. E.[2], Mendoza-Pérez, F.[2], Navarro-González, M. Del C.[3], Arenas-Guzmán, R.[4], Castañeda-Sánchez, J. I.[2], Luna-Herrera, J.

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City 11340, Mexico.[2]Departamento de Sistemas Biológicos, Universidad Autónoma Metropolitana Unidad Xochimilco, Mexico City 04960, Mexico. [3]Laboratorio de Investigación en Enfermedades Reumáticas, Instituto Nacional de Enfermedades Respiratorias "Ismael Cosío Villegas", Mexico City 14080, Mexico.[4]Sección de Micología, Hospital General "Dr. Manuel Gea González", Mexico City 14080, Mexico.

Sporotrichosis is a fungal infection caused by traumatic skin inoculation of material contaminated with the fungus *Sporothrix schenckii*, which is part of the *Sporothrix* spp. complex. In the control of the infection, the participation of various cell lines has been described, however, the response of the keratinocytes during this infection is little known. In this work we used the HaCaT cell line of human keratinocytes that were infected with conidia and yeast-like cells of *Sporothrix schenckii.* Modifications in the cytoskeleton and the expression of innate response molecules were evaluated. Both phases of the fungus induced changes in the actin cytoskeleton, formation of membrane protrusions, and loss of stress fibers in the keratinocyte. On the other hand, the overexpression of surface receptors: MR, TLR6, CR3 and TLR2. In addition, it was shown that conidia and yeasts induced the production of high levels of chemokines: MCP-1 and IL-8 and of proinflammatory cytokines: IFN-α, IFN-γ and IL-6. During infection, keratinocytes participate by inducing an inflammatory response (Paredes-Rojas *et al*.).

References

Paredes-Rojas, A.; Palma-Ramos, A.; Castrillón-Rivera, L.E.; Mendoza-Pérez, F.; Navarro-González, M.D.C.; Arenas-Guzmán, R.; Castañeda-Sánchez, J.I.; Luna-Herrera, J. Keratinocyte response to infection with Sporothrix schenckii. *J. Fungi* 2022, *8*, 437.

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Resumen corto

Biosensor for physical-chemical cellular variations as predictors of inflammasome activation by metabolic inflammatory signals

Pastrana-Peralta, P.[1], Villaseñor-Toledo, T.[1], Camacho-Concha, N.[1], Cuevas-Velazquez, C.L.[2], Pérez-Martínez, L.[1], Pedraza-Alva, G.[1]

[1]Laboratorio de Neuroinmunobiología/Departamento de Medicina Molecular y Bioprocesos, Instituto de Biotecnología, UNAM. Cuernavaca, Morelos, 62210 México. [2]Departamento de Bioquímica, Facultad de Quîmica, UNAM, Ciudad de México, 04510 México.
*E-mail: gustavo@ibt.unam.mx

Nucleotide-binding oligomerization domain-like receptors (NLRPs) are intracellular proteins involved in detecting pathogen-associated molecular patterns (PAMPs) and danger-associated molecular patterns (DAMPs) that are released during cellular stress or damage. Adipocyte stress resulting from caloric excess leads to a chronic inflammatory process in the adipose tissue that instigates insulin resistance and diabetes. The NLRP3 receptor in repose to lipid excess or oxidative stress forms a multiprotein structure called inflammasome leading to caspase-1 activation and inflammation. Although several studies suggest that physical-chemical changes in the cell resulting from the ion release (K efflux) preceding inflammasome formation are important for NLRP3 inflammasome activation the molecular mechanisms underlying inflammasome assembly in a single perinuclear structure are still obscure.

The recent development of biosensors to monitor cellular physical-chemical changes triggered by environmental cues allows us to evaluate whether metabolic stress signals triggering NLRP3 inflammasome assembly and activation involve physical-chemical changes. Additionally, given that the SED1 sensor is sensitive to macromolecular crowding its use will let us know whether molecular crowding occurs perinuclearly during inflammasome assembly. Here we will describe the activation of the SED1 sensor in mouse and human macrophages exposed to different signals leading to NLRP3 inflammasome activation.

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Resumen corto

A bioinformatic analysis to define intrinsically disordered regions in the NLRP family of receptors and its role in inflammasome activation

Pastrana-Peralta, P.[1]*., Ramírez-Nava, B.T[2]., Covarrubias, A.A[2]., Cuevas-Velazquez, C.L[3]., Pérez-Martínez, L[1]., Pedraza-Alva,G.[1]

[1]Laboratorio de Neuroinmunobiología/Departamento de Medicina Molecular y Bioprocesos, [2]Departamento de Biología Molecular de Plantas, Instituto de Biotecnología, UNAM. Cuernavaca, Morelos, 62210 México. [3]Departamento de Bioquímica, Facultad de Quîmica, UNAM, Ciudad de México, 04510 México.
*E-mail:pamela.pastrana@ibt.unam.mx

NLRPs (nucleotide-binding oligomerization domain-like receptors) are a family of intracellular proteins that play a role in the innate immune system. They are involved in detecting pathogen-associated molecular patterns (PAMPs) and danger-associated molecular patterns (DAMPs) that are released during cellular stress or damage. Upon activation, NLRPs, through protein-protein interactions, form a multiprotein structure called inflammasome leading to caspase-1 activation and inflammation. Despite inflammasome's relevance in immune response the molecular mechanism regulating its formation and activation are not totally understood. However, several studies suggest that physical-chemical changes in the cell resulting from the ion release (K efflux) preceding inflammasome formation might play a key role.

Intrinsically disordered regions (IDRs) are regions within proteins that lack a fixed 3D structure but can still carry out important functions. IDRs are present in many proteins, and their flexible nature allows them to interact with multiple binding partners and adopt different conformations, which can be important for regulating protein functions in shaping the cellular response to external or internal cues promoting cellular stress by abrupt physical-chemical changes including osmotic and pH modifications.

Although NLRP pyrin domains have structural flexibility allowing conformational changes, fold stability, and dimerization no IDRs have been formally identified in the NLRP family of receptors.

The ongoing study aims to characterize IDRs and discover conserved regions within the IDRs of NLRP receptors. The results obtained will determine whether IDRs could play a relevant role during inflammasome assembly and activation allowing hypothesis-driven research to uncover the molecular mechanism underlying the onset of inflammation.

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Resumen corto

Supramolecular nanoassemblies for the capture of antibodies in tuberculosis diagnosis

Patiño-Cárdenas, J.*[1], López-Marín, L.M.[1]

[1]Laboratorio de Nanobio-óptica, Centro de Física Aplicada y Tecnología Avanzada de la Universidad Nacional Autónoma de México, Juriquilla, Querétaro, México.
*E-mail: juanpatino@fata.unam.mx

Tuberculosis (TB) is the leading cause of death due to a single infectious agent. Early detection of the disease is essential for the application of timely treatment, and essential to control its spread. Therefore, the development of new diagnostic methods for TB that do not require specialized equipment and personnel and that are low cost is a necessity. Immunodiagnosis is one of the most valuable options. It is known that among the most abundant and specific surpluses of Mycobacterium tuberculosis are glycans. Of these, the diacyl trehalose glycolipid (DAT) has been identified as one of the best antigens for the diagnosis of tuberculosis; however, its lipophilic nature has limited its exploitation. In this work, a colloidal construction, stable in an aqueous medium, capable of exploiting the DAT as a tool for the capture antibodies associated with TB, was designed. The DAT antigen was obtained from an organic extract of mycobacterial cells, and characterized by chemical reactivity, chromatographic behavior, and mass spectrometry. Using a mixture of phosphatidylcholine and dodecanethiol, DAT was biomimetically deployed in unilamellar liposomes. The supramolecular structures obtained were characterized by transmission electron microscopy. These liposomal constructs were easily immobilized on metal surfaces with the potential to generate plasmonic and/or conductometric signals. Likewise, these nanosystems can capture anti-DAT antibodies. Exploration of a method capable of transducing the signal of the reaction-antibody reaction is currently underway.

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Resumen corto

Histological and hematological evaluation of tumor cell infiltrate in lymphoid and metastatic tissues in breast cancer murine model treated whit GK-1

Patiño-Chávez, O.P.*, Fragoso-González, G.C.,
Sciutto-Conde, E.L.

Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. *E-mail: osirisjair@hotmail.com

Brest cancer continues to have the highest prevalence and mortality among women worldwide. Currently, the main treatments against triple-negative breast cancer focus on a combination of radiotherapy, surgical intervention and systemic chemotherapy. However, this therapeutic approach has brought little improvement in the management of metastatic disease. Immunotherapy has positioned as an important treatment option, since it stimulates the patient's own immune system to destroy tumor cells, demonstrating its clinical potential, improving the outcome of cancer patients. Recently, it has been shown that treatment with immunomodulator peptide GK-1 in murine breast cancer model, reduces tumor growth, metastatic burden and significantly increases survival. This project proposes to characterize the effects of immunotherapy with GK-1 in a 4T1 model of murine breast cancer, on the progression of metastatic lung disease, leukemoid reaction and splenomegaly. Mice bearing 4T1 breast tumor were treated weekly whit GK-1 (100 µg) for 28 days; lungs and draining lymph nodes were dissected to evaluate macro and micro metastases, hematological samples were taken to identify changes in leukemoid reaction (paraneoplastic myelopoiesis), spleens were weighed to assess splenomegaly. We demonstrate that GK-1 treatment significantly reduces the number and progression macro and micro metastases in pleura and lung parenchyma, GK-1 also retards the development of leukemoid reaction and reduce splenomegaly severity compared to untreated mice. Additionally, the treatment significantly reduced tumor growth rate and weight of primary tumor. These findings corroborate GK-1 peptide effectiveness in treatment of neoplastic and metastatic disease generated by 4T1 triple-negative breast cancer murine model.

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Resumen corto

Babesia vogeli rhoptry-associated protein 1 (RAP-1) contains B-cell epitopes that elicit a humoral immune response.

Pavón-Rocha, A.J.*[1,2], Hernández-Silva, D.J.[2], Gómez-Soto, J.G.[3], Rubio-Venegas, Y.[3], Mosqueda, J.J.[1]

[1]Maestría en Salud y Producción Animal Sustentable, Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro.[2]Laboratorio de Inmunología y Vacunas, Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro.[3]Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro.
*E-mail: aldo.pavon@uaq.mx

Babesia vogeli is the species that causes canine babesiosis with the largest worldwide distribution, including Mexico. *Babesia* parasites secrete proteins through their organelles located in the apical complex in order to achieve successful cell invasion. Rhoptry associated protein 1 (RAP-1) is one of the secreted, immunogenic proteins, which have been characterized in several *Babesia* species, but not in *B. vogeli*. For this purpose, the nucleotide sequence corresponding to this gene was isolated by cloning and sequencing. Then, the transcription of the *rap-1* gene was demonstrated in the intraerythrocytic stages of *B. vogeli* by RT-PCR, followed by the identification of two B-cell epitopes from the predicted RAP-1 amino acid sequence using the BCEpred, ABCpred and IEDB programs. An immunization assay was performed in New Zealand rabbits with synthetic peptides containing these predicted B-cell epitopes. The results showed that the immunized animals generated specific antibodies tested by indirect ELISA. In addition, indirect immunofluorescence (IFI) showed that the generated antibodies recognize the native protein in the parasite and it is localized in the apical complex. With these results we conclude that selected *B. vogeli* RAP-1 B-cell epitopes are immunogenic and can be further evaluated as vaccine or diagnostic antigen candidates for control measures against canine babesiosis caused by *B. vogeli*.

Funding

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Resumen corto

Evaluación de la actividad enzimática y expresión de NAT1 y NAT2 en linfocitos T de pacientes con Diabetes Mellitus tipo 2 con sobrepeso u obesidad

Paz-Rodriguez, V.A.*[1], Coronado-Sánchez, L.G.[2], Rosso-Rojas, M.S.[2], Turiján-Espinoza, E.[2], Martínez-Leija, M.E.[1,2], Rivera-López, E.[3], Milán-Segovia, R.[2], Monsiváis-Urenda, A.[1], Portales-Pérez DP.[1,2]

[1]Centro de Investigación en Ciencias de la Salud y Biomedicina, Universidad Autónoma de San Luis Potosí, México. [2]Facultad de Ciencias Químicas, Universidad Autónoma de San Luis Potosí, México.3Hospital Central "Dr. Ignacio Morones Prieto", San Luis Potosí, México.
*E-mail: dportale@uaslp.mx

Chronic low-grade inflammation from lymphocyte infiltration, cytokine synthesis, and decreased regulatory T cells is characteristic of type 2 diabetes mellitus and obesity. The cytosolic enzymes N-Acetyl Transferases 1 and 2 (NATs) are involved in insulin resistance, which transfer an acetyl group from acetyl-CoA to a xenobiotic substrate. The enzymatic activity of NATs is regulated at the genetic and epigenetic levels and by deacetylase enzymes such as sirtuins. The function of these enzymes and their regulation by SIRT1 in metabolic diseases such as DM2 associated with overweight and obesity are unknown. The expression of NAT1, NAT2, and SIRT1 of CD3+ T lymphocytes from overweight and obese patients with DM2 was evaluated by flow cytometry and the enzymatic activity of NATs by cell culture and HPLC analysis. High levels of NAT2-positive cells (p=0.0005) and decreased enzymatic activity (p=0.0024) were found in patients with DM2 compared to the control group. Sirtuin inhibition with nicotinamide showed an increase in NAT2 activity (p=<0.0001), while using a SIRT1 agonist (SRT1720), decreased activity was observed in both groups (p=<0.001). In contrast, a regulatory effect by SIRT1 on NAT1 was not observed. This would indicate that the sirtuin-NATs axis would be involved in the pathological process of DM2, so future study strategies will be the search for therapeutic targets in the modulation of sirtuins.

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Resumen corto

Level of knowledge of HPV associated with sexual risk behavior in patients of UMF No.16 Queretaro, Qro.

Peña-Ramirez, D.*, Reyes Chavez, P. D.

Coordinación Clínica de Educación e Investigación en Salud, Ciudad de Queretaro, Qro, México.

Sexual behavior is considered as a set of attitudes that tend to stimulate personal and couple eroticism, risky sexual behavior are practices that endanger the health of the individual; The knowledge according to the Spanish royal academy is to have a notion of something; Likewise, there is an increase in the number of infections of the Human Papilloma Virus, the level of knowledge they have of this disease is low and therefore they have risky sexual behavior.To determine the sexual risk behavior associated with the level of knowledge of HPV in patients of the UMF No. 16 of Querétaro. Observational, comparative cross-sectional study, male and female beneficiaries between the ages of 18 and 35, from UMF No. 16; the sample size was calculated using the formula for two proportions with a total of 82 patients for each group. Non-probability sampling for convenience. According to the sociodemogafrican characteristics, the female gender has very good knowledge of 76.8%, the higher the level of schooling, the better knowledge 55.2% (p= 0.331); The female gender has a high risk of sexual behavior 74.1% compared to the male gender 25.9% (p=0.425). It was identified that there is no association between risky sexual behavior and the level of knowledge of HPV (p=0.681) , There is an association between the level of schooling with the level of low-risk sexual behavior at the undergraduate level with 50% compared to high school with a high risk of 55.6% (p=0.017).There is no association between risky sexual behavior and HPV knowledge level.

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Resumen corto

Dopaminergic agonists and L-DOPA used to treat Parkinson's disease, induce dopamine receptor expression on immune cells

Pérez-Figueroa, E.[1*], Guevara-Salinas, A.[1], Álvarez–Luquín, D.[1], Netzahualcoyotzi-Piedra, C.[2], Adalid-Peralta, L.[1]

[1]Unidad Periférica para el Estudio de la Neuroinflamación en Patologías Neurológicas del Instituto de Investigaciones Biomédicas de la UNAM en el Instituto Nacional de Neurología y Neurocirugía, Insurgentes Sur 3877, Col. La Fama, Ciudad de México 14269, México.[2]Instituto Nacional de Neurología y Neurocirugía, Insurgentes Sur 3877, Col. La Fama, Ciudad de México 14269, México.

Dopamine is a catecholamine found predominantly in the central nervous system. It also acts as a regulator of immune function as cells of the immune system express receptors for dopamine and other dopamine-related proteins, which enables them to actively respond to this neurotransmitter. Thus, it is essential for neuroimmune communication, which suggests that dopaminergic immunoregulation is crucial for a proper immune function. In Parkinson's disease (PD) dopamine is diminished due to the loss of dopamine-producing neurons. This is meant to be compensated by the administration of dopaminergic agonists and/or drugs such as levodopa (L-DOPA), which improve the availability of dopamine in the brain.

The consequences of dopamine stimulation on immune cells are collectively called the dopaminergic effect. These include metabolic changes, cytokine release and, importantly, variation in the proportion of the sub-populations expressing the different dopamine receptors (DRs). Thus, our interest is to study the effects of dopaminergic agonists (pramipexole and rotigotine) and drugs used for the treatment of PD (L-DOPA) on the expression of the DRs in immune cells. Particularly in CD3+, CD19+ and CD11c+ lymphocyte sub-populations from healthy donors.

Our results show that pramipexole stimulation increased the proportion of CD3+ and CD11c+ cells expressing the DRD2. While dopamine and L-DOPA increased the proportion of CD11c+ and CD19+ cells expressing the DRD5 receptor. These data suggest that common pharmacological treatments for PD play a regulatory role in the expression of DRs.

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Resumen corto

Targeting of E5 protein of human papillomavirus 16 to dendritic cells delay tumor growth and survival in a murine model

Pérez-Morales, A.C*.[1,2], Badillo-Godínez, O.[3], Quiroz-Medina, B. [1,4], Gama-García, G.J.[1,5], Pedroza-Saavedra, A.[1], Bonifaz-Alfonzo, L.[6], Esquivel-Guadarrama, F.[7], Gutiérrez-Xicotencatl, L[1].

[1] Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México. [2] Facultad de Ciencias, UAEM, Cuernavaca, Morelos, México. [3] Uppsala University, Uppsala, Sweden. [4] Escuela de Salud Pública de México, Cuernavaca, Morelos, México. [5] Facultad de Biología, UAEM, Cuernavaca, Morelos, México. [6] Hospital de Especialidades, Centro Médico Nacional siglo XXI, IMSS, México. [7] Facultad de Medicina, UAEM, Cuernavaca, Morelos, México. *E-mail:acpmiaw@gmail.com

The HPV16 E5 oncoprotein evade the immune response by inhibiting antigen presentation by MHCI and MHCII. Targeting of antigens to dendritic cells (DCs) via DEC-205 stimulates a specific T cell response. Previously, we evaluated the therapeutic targeting of HPV16-E5 to DEC-205 in a murine tumor model, observing a 75% increase in survival and 70% elimination of tumors in mice, generated by a memory immune response. However, 30% of mice escape therapeutic treatment and it is known that E5 is expressed early in lesions; we set out to determine the type of immune response generated by prophylactic targeting of HPV16-E5 to DCs in a murine tumor model. Anti-DEC205:E5 was generated by chemical cross-linking and its activity evaluated by Western-blot. Balb/c mice were immunized at days 0 and 21 with 5 µg of anti-DEC-205:E5, 16E5 alone, Isotype:16E5, anti-DEC-205:OVA or PBS and 40 days later inoculated with BMK16-myc tumor cell line. The anti-tumor effect was evaluated by tumor measurement and survival analysis. Prophylactic vaccination with anti-DEC-205:16E5 was more efficient in delaying tumor growth for up to 88 days after tumor challenge compared to the other groups, which was 30 days. In addition, 70% of mice anti-DEC-205:16E5 vaccinated were tumor-free for up to 100 days and the survival of those mice that maintained tumor growth increased for up to 80 days. The data suggest that targeting of 16E5 to DC by prophylactic vaccination increases protection against HPV-associated tumors.
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Key Words: Targeting, DEC-205, Dendritic Cells, E5 HPV-16, Tumor.

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Resumen corto

Molecular analysis of communication pathways between species in a host-parasite model: *Nippostrongylus brasiliensis* and *Mus musculus*

Pérez-Rivera, E.[1*], Flores, L.J.[1], Ramos-Balderas, J.L.[1], Peralta-Alvarez, C.A.[2], Poot-Hernández, A.C.[2], Licona-Limón, P.[1]

[1]Departamento de Biología Celular y del Desarrollo, [2]Unidad de Bioinformática y manejo de la información, Instituto de Fisiología Celular, Ciudad de México, México
*E-mail: ericperezrivera1996@gmail.com

Helminth infections can cause problems for both human health and the livestock industry. *Nippostrongylus brasiliensis* is a type of nematode that can infect rats, mice, and other rodents. During its life cycle, it travels through different organs and undergoes larval changes. It begins its infection in the skin at the L3 larval stage, moves to the lung (L4), and finally to the small intestine (L5), where it lays eggs that are excreted to begin the cycle again. *N. brasiliensis* has evolved to manipulate the host's immune system using the products it secretes/excretes. The aim of this work is to identify a candidate within these products that is necessary for its parasitism and to characterize it in the parasite-host interaction model of *Nippostrongylus brasiliensis* - *Mus musculus*. RNA was extracted from skin (1h pi), lung (2d pi), and small intestine (5d pi) of infected mice and the data was analyzed to identify the most highly expressed genes in each larval stage. Six possible candidates were selected, all from the SCP-TAPS family (Sperm-coating protein/Tpx-1/Ag5/PR-1/Sc7) to be analyzed using bioinformatic tools to predict their possible functions. One of the candidates (SCP2) had high sequence identity and structure superposition with a well-studied protein called Na-Asp-2, which is capable of recruiting neutrophils and monocytes. SCP2 was found to have a palmitate-binding cavity and a caveolin-binding motif, which are important for lipid binding. Based on these analyses, it is concluded that SCP2 may play a role in lipid binding and the recruitment of neutrophils and monocytes.

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Resumen corto

The Translationally Controlled Tumor Protein (TCTP) of *Babesia bovis* induces neutralizing antibodies and participates in the establishment of an acute infection

Pérez-Almeida, C.Q. [1,2]*, Hernández-Silva, D.J. [1], Hernández-Arvizu, E.E. [1], Velasco-Elizondo, M.A. [1], Gómez-Soto, J.G. [3], Vega y Murgía, C.A. [3], Dávila-Montero, U.M. [3], Asada, M. [4], Kawazu, S.I. [4], Mosqueda, J. [1]

[1]Immunology and Vaccines Laboratory, Natural Sciences College, Autonomous University of Querétaro, México. [2]PhD program in production sciences and animal health, Faculty of Veterinary Medicine and Animal Husbandry, National Autonomous University of México. [3]Natural Sciences College, Autonomous University of Querétaro, México. [4]National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Inada, Obihiro, Japan.
*E-mail: chyntiaq@gmail.com

Babesia bovis is a protozoan causing bovine babesiosis. It has been postulated that, in Apicomplexa parasites, the Translationally Controlled Tumor Protein (TCTP) interferes with the immune response, by blocking the interaction of host TCTP with its receptor, preventing the activation and proliferation of B-cell lymphocytes. The aim of this work was to analyze *B. bovis* TCTP activity as an immunogen against an acute *B. bovis* infection. In the present project, the complete *tctp* gene was amplified and sequenced in *B. bovis* isolates; 1the gene and the predicted protein sequences were highly conserved. Expression was confirmed by WB and confocal microscopy. Peptides containing predicted B-cell epitopes were predicted, synthesized, and used in immunization assays, demonstrating their immunogenic capacity by inducing specific antibodies. Cattle were immunized with the mix of TCTP peptides then, they were challenged with a virulent strain of *B. bovis.* Clinical signs and parasitemia were monitored for 15 days. Less severe clinical signs were observed in immunized animals compared with controls. A lower amount of total antibodies was observed in the serum of animals in the control group after challenge, indicating an interference of *B. bovis* TCTP in the bovine immune response. A neutralization assay was carried out using *in vitro* cultured *B. bovis*, a percentage inhibition of 32-34% was observed using sera from immunized cattle. It is concluded that *B. bovis* has a *tctp* gen that is expressed in intraerythrocytic stages. The protein contains peptides with conserved B-cell epitopes, which induce neutralizing antibodies in immunized animals. Anti-TCTP antibodies help reduce the clinical signs and improve the humoral immune response of infected cattle.

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Resumen corto

Evaluation of the expression of the membrane molecules PD-L1, PD-L2, and CD163 in monocyte subpopulations as predictors of 28-day mortality in patients with sepsis

Pérez-Dimas, G. [1,3], Flores-Mejía, R. [1], Arriaga-Pizano, L. [4], Prieto-Chávez, J.L. [4], Rodríguez-Cortés, O. [1], León-Pedroza, J.I. [2,5*]

[1]Laboratorio de Inflamación y Obesidad, Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, IPN. Ciudad de México, México. [2]Servicio de Urgencias, Hospital General de México. Ciudad de México, México. [3]Servicio de Medicina Interna, Hospital General de México. Ciudad de México, México. [4]Laboratorio de Citometría de Flujo, Centro de Instrumentos, Coordinación de Investigación en Salud, Hospital de Especialidades del Centro Médico Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, México.[5]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, IPN. Ciudad de México, México.

Sepsis is a life-threatening organ dysfunction caused by a dysregulated host response to infection. In 2017, sepsis caused 11 million deaths worldwide. Monocytes have stood out in the study of sepsis. Three subpopulations of monocytes have been described: classic (MC), intermediate (MI), and non-classic (MNC). PD-L1/PD-L2 are related to cell exhaustion and CD163 is associated with inflammatory processes, these molecules have shown utility in the prognosis of mortality in sepsis. Blood samples were obtained from patients with a diagnosis of sepsis in their first 72h of admission. Membrane staining for flow cytometry was performed for CD11b, CD14, CD16, PD-L1, PD-L2, and CD163. Patients were followed up for 28 days to know their clinical outcome. Twenty-eight patients were included, nineteen were survivors and nine were non-survivors. The non-survivors had a higher MFI of PD-L2 in MI (p=0.044). The MFI of PD-L2 in MI was a test with good prognostic potential (p=0.044, AUC 0.740), and an MFI of 139.5 was selected as a cut-off point with a sensitivity of 77.8% and specificity of 73.7%. Patients with MFI of PD-L2 in MI greater than 139.5 had an HR =6.364 (p=0.022) of not surviving. In CD14+ monocytes, finding a higher MFI of PD-L1 in non-surviving patients (p=0.005), and a ROC curve was performed (p=0.005, AUC 0.836) revealing that it was the best prognostic test compared to MFI of PD-L2. Conclusion the MFI of PD-L1 in CD14+ monocytes and PD-L2 of MI increased significantly in patients with sepsis who did not survive compared to survivors. Acknowledgment SIP: 20221202, 20231249 and SIP2023201.

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Resumen corto

Evaluation of humoral response directed against PRSS Virus peptides derived from GP5 membrane protein

Perez-Duran, F. *, Calderón-Rico, F., Bravo-Patiño, A., Cortés Vieyra, R. Nuñez-Anita, R.E.

Facultad de Medicina Veterinaria y Zootecnia, Universidad Michoacana de San Nicolás de Hidalgo, Tarímbaro, Michoacán. México. *E-mail: 0618713G@umich.mx

Porcine reproductive and respiratory syndrome virus (PRRSV) is a pathogen that affect swine industry. Efficacy of vaccines against PRRSV is targeted against homologous strains. Nevertheless, the safety of commercial vaccines is limited, because vaccine virus can revert to pathogenic state. Accumulating data have indicated that peptides or epitopes play essential roles in adaptive immunity and can be sufficient to trigger humoral immunity. In this work, two synthetic peptides, immunodominant B epitopes, denominated GP5-B and GP5-B3 were inoculated separately in pigs. Twenty-eight piglets at 28 days of age, were randomly separated (N=7 per group). From immunized pig's blood serum, the anti-peptide IgG´s were measured by ELISA assays at 21 and 42 days after immunization (dpi). The immunoreactivity of GP5-B and GP5-B3 peptides were tested using serum from vaccinated pigs with vaccine (Ingelvac PRRS MLV®), at 42 dpi. Mononuclear cells (PMBC) were isolated from peripheral blood and B lymphocytes were phenotyped by Flow cytometry. Results, both peptides induced anti-peptide IgG´s statistically different from vehicle and control group. Only GP5-B peptide induced significantly increased IgG´s at 21 and 42 dpi, while GP5-B3 peptide only induced the increased IgG´s at 21 dpi, without significant changes at 42 dpi. Both peptides showed cross reactivity against antibodies from vaccinated pigs. Analysis of B cells subpopulations showed that GP5-B and GP5-B3 peptides induced antibody-secreting effectors cells (LB CD2+/CD21+) and both peptides induced trained B cells (CD2-/CD21+). Therefore, both peptides that include B cell epitopes were sufficient to elicit humoral responses mediated by antibodies and B cells. Funding: CONACyT (A1-S-43236; INFR: 2015-255010; Fomento a la infraestructura científica 2021-317189). Scholarship FPD Beca Nacional CONACYT 2020.

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Resumen corto

CD38 correlates with an immunosuppressive Treg phenotype in Lupus-prone mice

Pérez-Lara, J.C. [1,7*], Espinosa, E. [2], Santos-Argumedo, L. [1], Romero-Ramírez, H. [1], López-Herrera, G. [3], García-García, F. [4], Sandoval-Montes, C. [5], Ortiz-Navarrete, V. [1], Flores-Muñoz, M. [6], Rodríguez-Alba, J.C. [7]

[1]Departamento de Biomedicina Molecular, CINVESTAV, Ciudad de México, CDMX, México. [2]Laboratorio de Inmunología Integrativa, Instituto Nacional de Enfermedades Respiratorias, Ciudad de México, CDMX, México. [3]Unidad de Investigación en Inmunodeficiencias, Instituto Nacional de Pediatría-SSa, CDMX, México. [4]Laboratorio de Biología del Sueño, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, Veracruz, Mexico. [5]Laboratorio de Inmunología, Escuela Nacional de Ciencias Biológicas, IPN, Ciudad de México, Mexico. [6]Laboratorio de Medicina Traslacional, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, Mexico. [7]Unidad de Citometría de Flujo, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, Mexico.
*E-mail: jocelyn1908@hotmail.com

CD38 is a transmembrane glycoprotein expressed by T-cells. It has been reported that patients with systemic lupus erythematosus (SLE) showed increased CD38+CD25+ T-cells correlating with immune activation and clinical signs. Contrariwise, CD38 deficiency in murine models has shown enhanced autoimmunity development. Recent studies have suggested that CD38+ regulatory T-cells are more suppressive than CD38− regulatory T-cells. Thus, we have suggested that CD38 overexpression in SLE patients could play a role in regulating immune activation cells instead of enhancing it. The aim of our work was to assess CD38 protein function in the immune regulation of a SLE murine model, through its expression by splenic regulatory T (Treg) cells. This study found a correlation between CD38 with FoxP3 expression and immunosuppressive molecules in T-cells from lupus-prone mice. Additionally, lupus-prone mice showed a decreased proportion of CD38+ Treg cells regarding wild-type mice (WT). Furthermore, CD38 is required for immunosuppressive molecules expression and expansion in Treg. Finally, we demonstrated an increased ratio of IFN-γ/IL-10 secretion in CD38-/- splenocytes. Altogether, our data suggest that CD38 represents an element in maintaining activated and proliferative Treg cells. Funding: CONACYT-CF 2015 Grant No. 214.

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Resumen corto

Identification of Non-Replicating Persistent Salmonella in B cells during *in vitro* and *in vivo* Infections

Pérez-Lara, J.C. [1*], Velázquez-Valdez, D.Z. [1,2], Cruz-Cruz, A.D. [3], Ortiz-Navarrete, V. [1]

[1]Departamento de Biomedicina Molecular. CINVESTAV, Ciudad de México, CDMX, México. [2]Doctorado en Ciencias de la Producción y Salud animal en la Universidad Nacional Autónoma de México, Facultad de Medicina Veterinaria y Zootecnia, Ciudad de México, CDMX, México. [3]Programa de Maestría del Departamento de Biología Celular, CINVESTAV and Departamento de Microbiología Univesidad Estatal de Ohio. *E-mail: jocelyn1908@hotmail.com

Salmonella enterica serovar Typhimurium (S. Typhimurium) is a Gram-negative bacterium that cause systemic infection in mice, like the typhoid fever caused by S. enterica serovar Typhi in humans. Within populations of many bacterial species, there is a small group of bacteria that do not replicate and are tolerant to multiple antibiotics, known as persisters. A quiescent state is a characteristic of these persistent bacteria by which they avoid being controlled and eliminated by the host cells, permitting chronic infections. We have previously published that S. Typhimurium remains within B cells from the bone marrow and spleen 60 days after infection. Thus, we conducted experiments to study the dynamics of Salmonella replication in infected B cells using the fluorescence dilution (FD) technique. At different time points after infection, we identified a high percentage of non-replicating persistent Salmonella bacteria in B cells from bone marrow and spleen in both *in vitro* and *in vivo* infections. In contrast, there are almost no persistent bacteria within Salmonella-infected macrophages. These results demonstrate that B cells are the niche of Salmonella during chronic infection.
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Resumen corto

Effect of STAT6 inhibition as a new strategy to promote the induction of potent and stable regulatory T cells that can be used as therapy during colitis-associated colon cancer.

Pérez-Noriega, F.A. *, Olarte-Arroyo, R.D., Correa-Pérez, M.F., León-Cabrera, S.A.

Laboratorio de inmunología tumoral, UBIMED, FES-I, Universidad Nacional Autónoma de México, Estado de México, México.
*E-mail: pereznoriegaf@gmail.com

Colorectal cancer (CRC) is one of the main neoplasms with the highest mortality and incidence worldwide and inflammatory bowel disease has been shown to promote the oncogenesis of CCR associated with colitis (CAC). It has been analyzed that the development of tumors, the aggressiveness of the disease and therefore the local and systemic inflammatory state is lower in STAT6 KO mice than in WT mice model CAC and this has been correlated with an increase in regulatory T cells in the early stages of develop CAC. Therefore, we set out to analyze the differentiation and functional properties of Treg cells generated during inhibition of STAT6 with AS1517499 and provide the necessary information to determine its usefulness as a therapeutic tool in the context of CAC. To do this, we induced CD4 + lymphocytes towards iTregs in the presence / absence of the specific inhibitor of STAT6, AS1517499, measured the degree of differentiation and suppressive capacity of these cells and transferred them intravenously to BALB / c mice in a model with AOM / DSS. We observed that inhibiting STAT6 improves the phenotypic stability of iTregs and its suppressive capacity and that these cells when transferred improve the disease status of CAC in the in vivo model.

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Resumen corto

LRBA is important for a proper NF-κB activation in B cells driven by BCR signalling

Pérez-Pérez, D. [1,2*], Flores-Hermenegildo, J.M. [3], Romero-Ramírez, H. [3], Rodríguez-Alba, J.C. [4], Kilimann, M. [5], Santos-Argumedo, L. [3], López-Herrera, G. [3]

[1]Doctorado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Coyoacán, CDMX, México. [2]Unidad de Investigación en Inmunodeficiencias, Instituto Nacional de Pediatría, Coyoacán, CDMX, México. [3]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del IPN, Gustavo A Madero, CDMX, México. [4]Unidad de Citometría de Flujo, Universidad Veracruzana, Jalapa, Veracruz, México. [5]Department of Molecular Neurobiology, Max Planck Institute for Experimental Medicine, D-37075, Göttingen, Germany.
*E-mail: dan.pez1515@gmail.com

Lipopolysaccharide-Responsive Beige-like anchor (LRBA) is a scaffolding protein whose deficiency is associated with an inborn error of immunity similar to common variable immunodeficiency. Patients with LRBA deficiency have a heterogeneous clinical presentation that includes hypogammaglobulinemia, reduction of B cells and T regulatory cells, recurrent infections, and autoimmune diseases. Studies have demonstrated the importance of LRBA in the recycling of CTLA-4 on Treg cells, however, its action on B cells remains unknown. This work aims to identify the function of Lrba in B-cell receptor (BCR) signaling.

Mice deficient of Lrba (Lrba-/-) have higher numbers of Trasitional 1 B cells on the spleen; it shows reduced B cell proliferation and increased apoptosis, in response to activation B through BCR crosslinking. Immunoblot and confocal microscopy revealed an increased activation of p50, p65, and IκBα (components of the canonical pathway of NF-κB) in Lrba-/- B cells under basal conditions. Preliminary co-immunoprecipitation assays suggest an interaction between Lrba and components of B cell signaling: PLC-γ, p65, and ERK2. Those results suggest the participation of Lrba in BCR signaling regulation.

Finally, cytometry analysis has shown reduced levels of membrane and cytoplasmic IgM in Lrba-/- B cells, hence Lrba could be important for the recycling of BCR, not only CTLA-4 in T regulatory cells. Lasted studies are focused on the physiological importance of those findings.

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Resumen corto

Anti-protein citrullination humoral immunity and PAD/AD homologous enzymes in human microbiota

Pérez-Pérez, E. [1*], Nieto Torres, E. [2], Bollain y Goytia, J.J. [1], Delgadillo Ruíz, L. [1], Mauricio Basurto, D.L. [1] Avalos Díaz, E. [1], Herrera Esparza, R. [1]

[1]Department of Immunology and Molecular Biology, Academic Unit of Biological Sciences. [2]General Physician Degree, Academic Unit of Human Medicine and CS. Autonomous University of Zacatecas. 1Boulevard de la Revolución Mexicana s/n Colonia Tierra y Libertad, 98615, Guadalupe Zacatecas, Mexico. Campus SXXI, Building 3, 98160 Zacatecas, Zacatecas, Mexico.
*Email: perezperez@uaz.edu.mx

Introduction: The human microbiota lives in balance with man. Persistent dysbiosis over time can lead to chronic and inflammatory diseases. Rheumatoid arthritis (RA) is associated with a greater presence of PADI as well as its citrullinated targets that are the targets of ACPAs. Bacterial PAD enzymes have been described in P. gingivalis, implying a pathogenic infection in the etiology of RA. **Objective:** To determine the humoral immunity of ACPA sera against the expression of citrullinated proteins and PAD/AD homologues in human microbiota. **Material and Methods:** Observational, cross-sectional, comparative and analytical study. Protein extracts of 21 microbial strains isolated from clinical and food samples, identified through the Viteck Bio-Mériux equipment, were obtained. The measurement of humoral immunity and the expression of citrullinated proteins and PAD/AD homologues was performed by Western blot using ACPA sera, control sera, and polyclonal antibodies (pAbs) anti-PADI2, anti-PADI4, anti-citrulline from invitrogen. The analysis was performed using the ImageLab program. Non-parametric statistics were used; the Mann Whitney U test and the Kruskal Wallis test were used. All with a significance of p=<0.05. **Results:** The presence of citrullinated proteins and PAD/AD homologues was detected in 9 opportunistic bacteria, but not in probiotic bacteria or yeast. Said proteins are recognized by ACPA sera. **Conclusions:** The results open the opportunity to explore the possible clinical implications of bacterial citrullinated proteins and PAD/AD homologous enzymes suggesting a molecular link between bacterial dysbiosis and RA pathogenesis.

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[1]Department of Immunology and Molecular Biology, Academic Unit of Biological Sciences. [2]General Physician Degree, Academic Unit of Human Medicine and CS. Autonomous University of Zacatecas. 1Boulevard de la Revolución Mexicana s/n Colonia Tierra y Libertad, 98615, Guadalupe Zacatecas, Mexico. Campus SXXI, Building 3, 98160 Zacatecas, Zacatecas, Mexico. *Email: perezperez@uaz.edu.mx

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Resumen corto

Evaluation of a multi-epitope HIV-1 vaccine displayed in parvovirus B19 Virus-like particles.

Pérez-Saucedo, D.G.*, Ruiz-Cruz, A.A., Moreno-Fierros, L.

Facultad de Estudios Superiores Iztacala, UBIMED Laboratorio 9 Inmunidad de Mucosas, Estado de México, Tlalnepantla de Baz, Av. de los Barrios 1.

The development of an effective HIV-1 vaccine has been hindered by the rapid mutation rate and antigenic diversity of the virus. Correlates of protection from clinical trials and rational vaccine design enables the development of novel antigen and carrier platforms targeting conserved sites of vulnerability. Virus-like particles (VLPs) allow the display and delivery of relevant epitopes, as well as increasing the immunogenicity of the construct. In this work, we designed and evaluated chimeric VLPs based on the B19 parvovirus, deploying multiple HIV-1 epitopes recognized by neutralizing antibodies and assessing humoral and cellular responses in immunized C57bl/6 female mice. Dynamic Light Scattering was used to characterize chimeric VLPs, mice sera and vaginal lavages were assayed by ELISA for whole-VLP and specific peptide binding activity, lymphocyte proliferation and IFNg production was measured using flow cytometry. Significant antibody responses against whole-VLPs were detected, as well as the epitopes corresponding to the CD4bs, V3 loop and several MPER super-site epitopes contained in the chimeric VLPs were observed in sera of mice immunized via the sub-cutaneous route, while the intra-muscular route displayed more discrete antibody titers. Anti-VLP antibodies were detected in vaginal lavages, however epitope-specific responses were not observed. Mice that received a *prime-boost* immunization scheme achieved higher titers of epitope-specific antibodies, with a distinct binding profile. In conclusion, chimeric HIV-VLPs have demonstrated to be an effective antigen system capable of inducing specific antibodies and cellular memory responses, particularly when administered via the sub-cutaneous route.

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Resumen corto

Evaluation of vaccine efficacy in cattle of Chitinase peptides with conserved B-cell epitopes predicted by *in silico* analysis against *Rhipicephalus microplus*

Pérez-Soria, M.M.E. *, López-Díaz, D.G. [1], Mosqueda, J.

Laboratorio de Inmunología y Vacunas. Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro. Av. de las Ciencias S/N, Delegación, 76230 Juriquilla, Santiago de Querétaro, Querétaro, México. *E-mail: marty_76080@yahoo.com

R. microplus ticks are hematophagous ectoparasites that economically impact livestock farming worldwide. The use of chemicals for its control results in resistance to acaricides and environmental contamination. An alternative is immunological control, based on the identification of tick antigens that generate immunological protection in cattle. The developed vaccines are based on the Bm86 antigen, which present variable efficacy, due to allelic variations in the Bm86 gene in ticks from different geographical areas. It is possible to identify conserved tick antigens in order to develop a vaccine that generates antibodies. The objective was to identify and evaluate peptides with conserved B-cell epitopes of *R. microplus* chitinase. Sequence analysis of this protein was performed using bioinformatics tools. For multiple alignment, three sequences were used, one corresponding to Querétaro state, another was the Media Joya strain, and the reference strain was JAC58962.1. The fragment used was 1311 bp, of which 890 bp were amplified. An average percentage of identity of 99.32% and similarity of 99.84% was observed. Four protein peptides containing the B epitopes conserved in *R. microplus* were selected. The peptides immunogenicity was evaluated by inoculating cattle with the peptides synthesized in the MAP-8. The antibody response was significant after the second immunization, in one peptide (chitinase 3) the response stood the same and slightly increased after every boost and had an efficacy of 71%, in addition significantly reducing the weight, oviposition and fertility of engorged ticks. Therefore, chitinase peptide may be an excellent vaccine candidate against *R. microplus*.

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Resumen corto

Effect of naringenin on the production ofcytokines stimulated with the RBD domain of the SARS-CoV-2 virus

Pérez-Torres, C. [1]*, Baltierra-Uribe, S.L. [1], Castrejón-Jiménez, N.S. [2], Flores-Jaramillo, M.E. [3], García-Pérez, B.E. [1]

[1]Laboratorio de Microbiología general, Departamento de Microbiología, Posgrado en Ciencias en Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [2]Área Académica de Medicina Veterinaria y Zootecnia, Instituto de Ciencias Agropecuarias-Universidad Autónoma del Estado de Hidalgo, Hidalgo, México. [3]Laboratorio de Polímeros, Departamento de Ingeniería Bioquimica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México.
*E-mail: chris_copernicium@hotmail.com

Severe COVID-19 patients generally present a deregulated inflammatory process, which, in principle, starts from the infection mediated by the interaction of the RBD domain of the Spike protein of the SARS-CoV-2 virus, with the ACE2 receptor of host cells. On the other hand, several studies suggest that naringenin has broad antiviral and anti-inflammatory effects in different pathologies, as well as neutralizing the proteins involved in infection by this virus. The present work evaluated the ability of naringenin to regulate the expression of IL-1β, IL-6, TNF-α and MCP-1 in an inflammation model induced by the RBD domain and LPS in BEAS-2B and THP-1 cells under three different conditions, before the stimulation with the RBD domain, after the stimulation and at the same time, this by means of a panel of multiplex cytokines. The results showed that the RBD domain alone was not able to increase the basal production of these cytokines in both models. However, when naringenin was tested after LPS stimulation, it was observed that this compound was able to return the increased levels of all cytokines to near normal, although naringenin also increased cytokine production in THP-1 cells under basal conditions. These results together suggest that the cell models used do not respond with an increase in cytokine production to the RBD domain of the S protein of the SARS-CoV-2 virus and that naringenin has an anti-inflammatory role independent of its ability to inhibit the interaction RBD domain-receptor ACE2.

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Resumen corto

Acute lung injury is prevented by monocyte locomotion inhibitory factor in experimental severe malaria mouse model

Pérez-Vega, M.J. [1,2*], Corral-Ruiz, G.M. [1,2], Galán-Salinas, A. [1,2], Silva-García, R. [3], Horta-Montaño, V. [1], Mancilla-Herrera, I [4], Barrios-Payán, J. [5], Fabila-Castillo, L. [1], Hernández-Pando, R. [5], Sánchez-Torres, L. E. [1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [2]Posgrado en Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México. [3]Unidad de Investigación Médica en Inmunología, Hospital de Pediatría, CMN-Siglo XXI, IMSS, Ciudad de México, México. [4]Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología, Ciudad de México, México. [5]Sección de Patología Experimental, Departamento de Patología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, México. *E-mail: jackelineperezvega@gmail.com

Acute lung injury (ALI) caused by severe malaria (SM) is triggered by a dysregulated immune response towards the infection with *Plasmodium parasites*. Postmortem human lung samples show diffuse alveolar damage (DAD), the presence of CD8 cells, neutrophils, and increased expression of ICAM-1. Infection of C57BL/6 mice with P. berghei ANKA (PbA) recapitulates a wide range of SM manifestations, including ALI. In the SM mouse model, lungs present DAD, CD8 cells in the parenchyma and tissular expression of IFN-γ, TNF-α, ICAM and VCAM, then, the use of immunomodulatory agents has been proposed to prevent SM consequences. The monocyte locomotion inhibitory factor (MLIF) is a pentapeptide isolated from axenic cultures of *Entamoeba hystolitica* with immunomodulatory properties. Thus, we evaluated if the MLIF treatment prevented SM induced ALI. We observed that the peptide prevented SM manifestations without a parasiticidal effect, indicating that its protective effect was related to modifications in the immune response. Furthermore, peripheral seric proinflammatory cytokines levels, CD8 cells and neutrophil proportions were more elevated in treated mice. Regarding pulmonary injury, the MLIF administration prevented DAD, CD8 and neutrophil presence into the tissue and downregulated IFN-γ, TNF-α, and ICAM while VCAM expression was abrogated. These results indicate that the MLIF treatment downregulated adhesion molecule expression which impeded cell migration and proinflammatory cytokine tissular production, resulting in the prevention of ALI and SM. Our findings represent a potential novel strategy to avoid this complication in various events where a dysregulated immune response triggers ALI.

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Resumen corto

Association of c.+677 C>T (rs1801133) and c.+1298 A>C (rs1801131) *MTHFR* genetic variants with cardiometabolic and disease risk in systemic lupus erythematosus patients

Pesqueda-Cendejas, K. [1,2], Parra-Rojas, I. [1,3], Campos-López, B. [1,2], E. Mora-García, P. [1,2], Ruiz-Ballesteros, A.I. [1,2], Rivera-Escoto, M. [1,2], Luquin, S. [2], Vizmanos, B. [1,4], Montoya-Buelna, M. [1,5], Meza-Meza, M. R. [1,2], Cerpa-Cruz, S. [6], De la Cruz-Mosso, U. [1,2]*

[1]Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes; Departamento de Neurociencias, Centro Universitario de Ciencias de la Salud; Universidad de Guadalajara; Guadalajara Jalisco 44340, Mexico. [2]Instituto de Neurociencias Traslacionales, Departamento de Neurociencias, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [3]Laboratorio de Investigación en Obesidad y Diabetes; Facultad de Ciencias Químico-Biológicas; Universidad Autónoma de Guerrero; Chilpancingo de los Bravo; Guerrero 39087, Mexico. [4]Laboratorio de evaluación del estado Nutricio, Departamento de Clínicas de la Reproducción Humana, Crecimiento y Desarrollo Infantil, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [5]Laboratorio de Inmunología; Departamento de Fisiología; Centro Universitario de Ciencias de la Salud; Universidad de Guadalajara; Guadalajara Jalisco 44340, Mexico. [6]Departamento de Reumatología; O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde; Guadalajara, Jalisco 44280, Mexico.
*E-mail: ulises_cdm@hotmail.com; ulises.mosso@academicos.udg.mx

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease. Environmental and genetic factors have been related to SLE onset and progression. Particularly, *MTHFR* genetic variants could modify the methylenetetrahydrofolate reductase (MTHFR) enzyme activity and subsequently alter folic acid and homocysteine levels contributing to cardiometabolic and SLE susceptibility risk.

Determine the association of the c.+677 C>T (rs1801133) and c.+1298 A>C (rs1801131) *MTHFR* genetic variants with cardiometabolic risk and clinical disease variables in SLE patients. A case-control study was conducted on 394 unrelated Mexican-mestizo women: 198 with SLE according to the 1997 SLE-ACR criteria and 196 control subjects (CS). Folic acid and homocysteine levels were evaluated by immunoassays. Genotyping of *MTHFR* genetic variants was carried out by allelic discrimination.

No significant differences were found for folic acid (p=0.15) and homocysteine levels (p=0.59) between groups. According to the CC c.+677 *MTHFR* genotype, this was associated to low cardiovascular risk by Castelli index (OR=0.42; CI:0.18-0.94; p=0.03) in SLE patients. The TC (OR=1.3; CI=1.02-1.8; p=0.03) and TA (OR=1.6; CI=1.1-2.5; p<0.01) haplotypes of c.+677 C>T and c.+1298 *MTHFR* were associated with SLE susceptibility, while CC *MTHFR* haplotype (OR=0.5; CI=0.3-0.8; p=0.01) was found as protector factor for the disease.

In conclusion, the CC c.+677 MTHFR genotype is a protector factor for cardiometabolic risk and the TC and TA c.+677 C>T plus c.+1298 A>C MTHFR haplotypes are associated with SLE risk in Mexican-mestizo SLE patients.

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Resumen corto

Analysis of fucosylation in Alpha 1-acid glycoprotein (AGP) as a breast cancer marker

Quevedo-Razo, A.G. [1 2]*, Téllez-Araiza, M. [2], García-Ortiz, L. [3], Hernández-Figueroa, L. [4], Bázan-Perkins, B. [2], López- González, J.S. [5]

[1]Universidad Nacional Autónoma de México. [2]Departamento de Inmunofarmacología, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas CDMX, México. [3]Centro Médico Nacional "20 de noviembre" ISSSTE. [4]Laboratorio Clínico, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas CDMX, México. [5]Departamento de cáncer pulmonar Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas CDMX, México. *E-mail: angelquevedo1307@gmail.com

Breast cancer (BCA) is one of the main causes of death in the world, and the first in adult Mexican women due in part to the expensive and late diagnosis. Alpha 1-acid glycoprotein (AGP) is an immunomodulatory and acute phase serum protein produced by the liver and some imme cells. AGP is highly glycosilated (45%) and has been found increased in cancer and other diseases. Recent studies have related AGP carbohydrate structure as a biomarker for certain diseases. Here we analyzed the presence of fucose as a posttranlational modification of AGP in serum samples of patients with BCA and compared to healthy individuals. Fucose detection of the external carbohydrate branches of AGP for each sample was determided by ELISA-lectin assay with AAL-*Aleuria aurantia* lectin wich is specific for linked alpha 1,6 fucose. Protein concentration was performed by nephelometry. We found increased expression of AGP in BCA vs healthy individuals as previously reported. In addition, fucosylation of AGP was also increased and higher fucosylation correlates with higher AGP serum values. Our results suggest measurement of AGP fucosylation as a low cost test for BCA.

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[1]Universidad Nacional Autónoma de México, [2]*Departamento de Inmunofarmacología, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas CDMX, México,* [3]*Centro Médico Nacional "20 de noviembre" ISSSTE,* [4]*Departamento Laboratorio Clínico, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas CDMX, México.* [5]*Departamento de cáncer pulmonar Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas CDMX, México. *E-mail:* angelquevedo1307@gmail.com

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Resumen corto

Dengue virus nonstructural protein 1 (NS1) modifies mosquitoes' intestinal epithelium architecture.

Quezada-Ruiz, E. [1,2]*, Silva-Olivares, A. [1], Betanzos, A. [1], Lanz-Mendoza, H. [2], Ludert, J.E. [1]

[1]Departamento de Infectómica y Patogénesis Molecular, Centro de Investigación y de Estudios Avanzados del IPN, Ciudad de México, CDMX. [2]Centro de Investigaciones sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Secretaría de Salud, Cuernavaca, Morelos, México. *E-mail: edgar.quezada@cinvestav.mx

Dengue is a viral infection transmitted by the bite of female mosquitoes of the *Aedes aegypti* and *A. albopictus* species. It is an RNA-enveloped virus composed of structural and non-structural proteins involved in the replicative virus cycle. Dengue virus nonstructural protein 1 (NS1) is the only nonstructural protein that is continuously secreted by infected cells. NS1 has been associated with the pathogenesis of the disease, as it can alter endothelial homeostasis by several mechanisms, thus favoring the spread of the infection to the target tissue. When the mosquito feeds, it ingests the virus and the NS1 protein. It is known that NS1 decreases the antiviral response in the vectors; however, it is not known if this protein can alter other factors that help in the spread of the virus. In this work, we sought to determine the modifications caused by the NS1 protein of DENV in the intestinal epithelium of the *Aedes aegypti* mosquito. The change in intestinal permeability was evaluated through a colorimetric assay, increasing in the presence of NS1 protein. In addition, the localization of proteins involved in cell-to-cell binding was evaluated through immunofluorescence assays, observing a change in their localization with NS1 present. Finally, by RT-PCR, virus dissemination in different mosquito tissues was verified. The NS1 protein likely participates in disseminating the Dengue virus through modifying factors that are part of the homeostasis of the intestinal epithelium of the mosquito. I received a fellowship from CONACyT 2023-CVU.927706.

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Resumen corto

Preview therapy with corticosteroids in severe COVID-19 hospitalized patients and longer stay between SARS-CoV-2 variants

Ramírez, C.O. [1*], Ceja-Gálvez, H.R. [1], Arellano-Arteaga, K.J. [2], Miramoentes-Luna, E. [2], Muñoz-Valle, J.F. [1]

[1]Instituto de Investigación en Ciencias Biomédicas, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México.[2]Servicio de Medicina Interna, Hospital Civil de Guadalajara Dr. Juan I. Menchaca, Guadalajara, Jalisco, México.
*E-mail: cristian.hernandez3703@alumnos.udg.mx

The COVID-19 is an infectious disease caused by the SARS-CoV-2 virus that can range in severity from mild symptoms to severe illness or even death. Severe COVID-19 is characterized by pneumonia, acute respiratory distress syndrome, multiple organ failure and other complications. The Delta and Omicron variants are strains of SARS-CoV-2 virus that have mutated and become more transmissible than the wild variant. The Recovery Trial in 2021 established that for patients hospitalized with Covid-19, the use of dexamethasone resulted in lower 28-day mortality among those who were receiving either invasive mechanical ventilation or oxygen alone. However, dexamethasone is not recommended for use in patients with mild or moderate COVID-19. The aim of the study was determining the relationship between the use of preview corticosteroid and hospital stay in severe COVID-19. We collected samples at the time of admission of the patient to the internal medicine service; a nasooropharyngeal was used for a molecular determination of SARS-CoV-2 RNA and sequencing and blood sample was used to determine clinical parameters. COVID-GRAM as a risk scale for progression was determined in all the patients. We evaluated 86 patients hospitalized in the Internal Medicine Department of the Nuevo Hospital Civil de Guadalajara “Dr. Juan I. Menchaca”, of which 10 were negative for PCR and were discarded. Of the 76 patients, 48 men (51.6%) and 28 women (48.4%) were classified by age groups 20-40, 40-60 and >60 years. We determined the SARS-CoV-2 variant, 39 Delta and 22 Omicron, and were correlated for age groups, where a high age was associated with longer hospitalization (63.7 age in Omicron and 53.6 age in Delta, *p=0.01*). The hospitalized preview use of corticosteroid was associated with high risk by COVID-GRAM and longer hospitalization (OR 3.5, IC 95% 1.2-10.86).The use of a preview corticosteroid therapy produce a longer stay between patients, associated with age and COVID-GRAM risk between SARS-CoV-2 variants in hospitalized patients with COVID-19.

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Resumen corto

Development of ELISA for the quantification of bovine IFNγ for the diagnosis of bovine tuberculosis in Mexico using monospecific polyclonal antibodies

Ramírez-Andoney, V. [1,2*], Autrán-Martínez, M. [2],
Gayosso-Vázquez, A. [1], Pintor-Ríos, J.P. [1], Alonso-Morales, R. [1]

[1]Laboratorio de Genética Molecular. Departamento de Genética y Bioestadística. Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Laboratorio de Inmunología Veterinaria. Facultad de estudios Superiores Cuautitlán. Campo 4. Universidad Nacional Autónoma de México, Estado de México, México. *E-mail: vianny102@hotmail.com

The use of a test that identifies cattle affected with tuberculosis is essential for its control-eradication. The use of ELISA to quantify IFNγ in several countries has been successful in identifying infected individuals, eliminating them leading to the disease control. However, in Mexico the commercial tests available are imported and expensive, which limits its use. Based on this need, a capture ELISA system was developed and analytically validated that determines IFNγ levels using monospecific polyclonal antibodies against bovine IFNγ. The specific antibodies were produced by immunizing with a genetic vaccine expressing the bovine IFNγ gene in guinea pigs and rabbits. IgGs were purified and used to determine the sensitivity of the test to identify the minimum detectable IFNγ concentration. For this, recombinant IFNg expressed in E. coli was employed as positive control. The titration of rabbit and cuyo IgG's allowed us to estimate their optimal concentration to standardize the quantification of IFNγ. With this test we were able to detect a range of 200ng to 12ng of IFNγ with high level of repeatability. These results shows to have developed a sensitive and reproducible analytical system at low cost, that when validated, could be used effectively in the control and eradication of bovine tuberculosis in Mexico.

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Resumen corto

Immune response with the use of nanoparticles with tumor lysates and CpGs

Ramírez-Cortes, A. [1,2*], Piñón-Zarate, G. [1], Yañez-Jarquín, K. [1], Téllez-Hernández, B. [1], Herrera-Enríquez, M. [1], Castell-Rodríguez, A. [1]

[1]Laboratorio de Inmunoterapia e Ingeniería de Tejidos, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2] Universidad de la Salud, Ciudad de México, CDMX, México. *E-mail: ariel_rc_dios@comunidad.unam.mx

Melanoma has increased its incidence in the last five years. Therapies have been used to reactivate the immune response. One of the options that has been taken up the most is the use of vaccines with nanomaterials. This study aimed to evaluate the antitumor response with the use of nanoparticles with tumor antigens and CpGs. Chitosan nanospheres were made by the simple emulsion technique, which were later added CpGs on their surface, their shape was evaluated by scanning electron microscopy. C57BL/6 mice were immunized with one hundred micrograms of nanoparticles, seven days later they were inoculated with melanoma cells, to assess the immune response, tumor size and lymphocyte filtration in the tumor stroma were evaluated. To evaluate the effect, 4 groups were made, one with only the chitosan nanospheres, another with the nanospheres plus antigens, nanospheres with CpGs, and another with all the elements. It was observed that the group of chitosan and chitosan with CpGs had a greater decrease in tumor size, as well as greater survival in mice. The use of nanoparticles is an option to consider in the future as an adjuvant treatment. It is important to evaluate which molecules can guarantee the delivery of nanoparticles to conventional dendritic cells, which have the main role in activating the antitumor immune response.

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Resumen corto

Immunomodulatory effect of antimicrobial peptide LL-37 and their derivate FK-13 in human monocytes stimulated with *Trichomonas vaginalis*

Ramírez-Ledesma, M.G. [1*], Ávila-Muro, E.E. [1], Alva-Murillo, P.N. [1].

[1]División de Ciencias Naturales y Exactas, Universidad de Guanajuato, Lascarían de Retana No.5, C.P. 36000, Guanajuato, México. *E-mail: mg.ramirezledesma@ugto.mx

Trichomoniasis, a sexually transmitted infection, induces large recruitment of immune cells, the first line of cellular defense in the human genitourinary tract. Immune cells contribute to defense through effector molecules, such as reactive oxygen species, hydrolytic enzymes, and antimicrobial peptides (AMP), among others. The AMP are small molecules, generally positively charged, and have multiple functions, either as an immunomodulator or as a microbicide. LL-37 is the only human cathelicidin, and smaller derivatives peptides (FK-13) have been reported which may have different activities compared to LL-37. The aim of this project was to evaluate the immunomodulatory effect of the peptides LL-37 and its derivate FK-13 on the human monocytic cell line U937 during the interaction with *Trichomonas vaginalis* (Tv). For this, the U937 cells were stimulated with Tv and the peptides (2.5-10 µM) for 3 h, then the nitric oxide production and the relative gene expression of the chemokine IL-8 were measured by Griess reaction and ΔΔCT method, respectively. Tv induces the production of nitric oxide in U937 cells and when LL-37 or FK-13 peptides are added, this production decreases. The parasite also increases the expression of IL-8 in U937, when the LL-37 peptide is added it increases this expression, but FK-13 decreases it. Our results suggest that LL-37 contributes to the creation of a pro-inflammatory environment in U937 cells interacting with Tv; meanwhile, FK-13 decreases pro-inflammatory markers.

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Resumen corto

Immunologic and epigenetic modulation of *Trichomonas vaginalis* lipophosphoglycan in prostate epithelium

Ramírez-Leyva, J.A. [1], Palomera-Sánchez, Z. [2], Alva-Murillo, P.N. [1]

[1]Departamento de Biología, División de Ciencias Naturales y Exactas, Universidad de Guanajuato, Guanajuato, Guanajuato. [2]Instituto de Investigaciones Sobre los Recursos Naturales, Universidad de San Nicolás de Hidalgo, Morelia, Michoacán. *E-mail: ja.ramirezleyva@ugto.mx

Trichomoniasis is the curable non-viral sexually transmitted disease with the highest number of cases in the world and is caused by the parasite *Trichomonas vaginalis*. If trichomoniasis is not diagnosed on time in infected men and, therefore, is not adequately treated, the parasite can colonize the prostate, generating a moderate and chronic inflammatory state, In this sense, the study of the modification of the epigenetic marks of the host by the pathogen can help to understand the host-pathogen interaction, particularly with a focus on the modulation of the host's immune response. Therefore, there could be a close link between the proinflammatory state and the epigenetic response of the host in the human urogenital tract. In this work we were able to purify an lipophosphoglycan (LPG) product of ~100-60 KDa from *T.vaganialis* and we found that at concentrations of 62.5-250 µg/mL of LPG it is not cytotoxic in prostate epithelium. Additionally, we were able to establish a condition that allows us to stimulate the prostate epithelium, without the genetic material of *T. vaginalis* interfering with epigenetic marks of the host.

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Resumen corto

Evaluation of the immunosuppressive capacity by mesenchymal stromal cells from cervical cancer on dendritic cells.

Ramírez-Menes, K.Q. [1]*, Cortes-Morales, V.A. [1], Bonifaz-Alfonzo, L. [2], Rocha-Zavaleta, L. [3], Mayani, H. [4], Montesinos, J.J. [1]

[1]Laboratorio de Células Troncales Mesenquimales, Unidad de Investigación Médica en Enfermedades Oncológicas, Hospital de Oncología, CMN SXXI, IMSS, Ciudad de México, México. [2]Unidad de Investigación Médica en Inmunoquímica, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, México. [3]Departamento de Biología Molecular y Biotecnología, Instituto de Investigaciones Biomédicas, UNAM, Ciudad de México, México. [4]Laboratorio de Células Troncales Hematopoyéticas, Unidad de Investigación Médica en Enfermedades Oncológicas, Centro Médico Nacional Siglo XXI, IMSS, Ciudad de México, México.
*E-mail: keytzal@gmail.com

In Mexico, cervical cancer (CeCa) is the second in incidence and is the second cause of death from cancer in female malignancy. It has been suggested that mesenchymal stromal cells (MSCs) are part of the tumor microenvironment and could have an immune protective capacity in tumors. We previously demonstrated the presence of MSCs in CeCa-MSCs, and their participation in protecting neoplastic cells from the cytotoxic activity of T and NK lymphocytes, also they can help to promote M2 macrophage polarization. Dendritic cells (DCs) are professional antigen presenting cells, critical for the development of the primary immune response. It has been shown that bone marrow-derived MSCs (BM-MSCs) modulate the differentiation, maturation and antigen presentation capacity of DCs, but to date, it is unknown if MSCs have an immunosuppressive effect towards DCs in the tumor microenvironment. In the present study, we compared the immunosuppressive capacity of MSCs from normal cervix (NC-MSCs) and CaCu-MSCs on DCs derived from monocytes (moDCs) in terms of differentiation, maturation, phagocytosis, ability to induce proliferation of T lymphocytes and generate regulatory T cells (Treg). As control, MO-MSCs were used, which have been documented for their immunosuppressive potential towards moDCs. Our in vitro results indicates that CaCu-MSC and CN-MSC have a similar capacity to decrease the differentiation and maturation of DCs. Both types of cervical MSCs increased the capacity for phagocytosis, decreased the capacity of DCs to induce proliferation in T lymphocytes, and also improved the capacity of DCs to generate Tregs.

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Resumen corto

In vitro assessment of a novel vNAR against TGF-β as a potential therapeutic molecule in renal fibrosis

Ramírez-Ronzón, L.A. [1*], Kú-Centurión, M.J. [1],
Lugo-Fabres, P.H. [2], Camacho-Villegas, T.A. [2]

[1]Unidad de Biotecnología Médica y Farmacéutica, Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco (CIATEJ), Guadalajara, Jalisco, México. [2]CONACYT - Unidad de Biotecnología Médica y Farmacéutica, Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco (CIATEJ), Guadalajara, Jalisco, México.
*E-mail: luramirez_al@ciatej.edu.mx.

Renal fibrosis is the final pathological process of chronic kidney disease (CKD), affecting around 12% of the Mexican population. It is characterized by the excessive deposition of extracellular matrix (ECM) in response to a trigger or injury that disrupts the physiological architecture and leads to kidney failure. Transforming Growth Factor β (TGF-β) is a cytokine considered the master regulator of fibrosis due to its signaling role in fibroblast proliferation, ECM production, and epithelial cell death. Neutralizing this cytokine with conventional IgG antibodies in CKD pre-clinical models has shown promising results. However, undesirable secondary effects have been associated with IgG size (150 kDa) or immunogenicity. In response, the novel antigen receptor (vNAR) variable domain represents an alternative given that it is the smallest naturally occurring antibody domain with antigen recognition capability. Recently, a vNAR against the three human isoforms of TGF-β has been produced in our research group, but it was only assessed *in silico*. In this work, we produced and evaluated the capacity of the vNAR anti-TGF-β to modulate cytokine production in HEK293 cells stimulated with $CoCl_2$. We performed RT-PCR to detect pro-fibrotic genes and Western Blot to evaluate TGF-β concentration in culture medium in HEK293 fibrotic cells. We found distinct gene transcription and reduced cytokine concentration in cells treated with the vNAR. The results show that the vNAR anti-TGF-β could be a therapeutic strategy for renal fibrosis.

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Resumen corto

Phenotypic and epigenetic changes of metabolically differentiated macrophages in response to infection with Zika virus and the SARS-CoV-2 S protein

Ramírez-Segovia, S.G. [1,2]*, Castillo-Martín del Campo, C.G. [1,3], Rivas-Santiago, B.T. [6], Comas-García, M. [4,5], Monsiváis-Urenda, A.E. [1,2]

[1]School of Medicine, Autonomous University of San Luis Potosi, San Luis Potosi, San Luis Potosi, Mexico. [2]Molecular and Translational Medicine Division, Research Center of Health Sciences and Biomedicine, San Luis Potosi, San Luis Potosi, Mexico. [3]Neural Stem Cell Laboratory, Coordination for the Innovation and Application of Science and Technology, San Luis Potosi, San Luis Potosi, Mexico. [4]School of Sciences, Autonomous University of San Luis Potosi, San Luis Potosi, San Luis Potosi, Mexico. [5]High-Resolution Microscopy Division, Research Center of Health Sciences and Biomedicine, San Luis Potosi, San Luis Potosi, Mexico. [6]Biomedical Research Unit-Zacatecas, Mexican Institute for Social Security, Zacatecas, Zacatecas, Mexico. *E-mail: luizza_017@hotmail.com

Macrophages are phagocytes that are part of innate immunity. Components in the microenvironment play important roles in macrophage polarization and function. Stimulation with pathogen-associated molecular patterns or damage-associated molecular patterns induces the activation of macrophages with proinflammatory function (M1) and high concentrations of glucose, insulin and palmitate induce a metabolically activated (MMe) phenotype with dual function (pro and anti-inflammatory). Some stimuli such as oxLDL and palmitate, present in patients with dyslipidemia, train monocytes and macrophages to respond in an altered manner to second stimuli (same or different). So far it is unknown whether dyslipidemia influences the response of MMe macrophages to microbial stimuli, which is why the aim of this study is to compare the phenotypic and epigenetic changes of MMe macrophages from patients with dyslipidemia and healthy subjects in response to viral stimuli. We isolated monocytes from venous blood from healthy subjects and differentiated them into MMe macrophages. We infected MMe macrophages with Zika virus particles and assessed the permissibility to infection by qRT-PCR and light microscopy. We found that MMe macrophages become infected 48 hours after challenge, although the level of infection is lower compared to a positive control; likewise, we observed the formation of multiple vesicles in the cytoplasm at 48 and 72 hours after infection. The results suggest that the control of the infection was due to the phagocytic activity of macrophages and the antiviral effect of type I IFN, and that endoplasmic reticulum stress was possibly induced in infected cells.

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Resumen corto

Generation of knock out cell lines by CRISPR/Cas9 to evaluate the TGF- β signaling pathway.

Ramírez-Vélez, C.I. [1], de la Cruz, A. [1,2], Rubio, R.M. [1], Barroso-Zuppa, M. [1,3], Madera-Salcedo, I.K. [1], Rosetti, F. [1], Crispín, J.C. [1,3]

[1]Departamento de Inmunología y Reumatología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, CDMX. [2]Plan de Estudios combinados en Medicina PECEM, Facultad de medicina, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México [3]Escuela de Medicina y Ciencias de la Salud, Tecnológico de Monterrey, Ciudad de México, CDMX, México.
*E-mail: claurmzv93@outlook.com

Transforming growth factor-β (TGF-β) is an anti-inflammatory cytokine involved in various cellular processes, including the differentiation of regulatory T cells (Tregs). Mammals possess three genes that encode three TGF-β isoforms (TGF-β1, TGF-β2, and TGF-β3). All three signal through the same heterodimeric receptor comprised of TGF-βRI and TGF-βRII. However, each isoform conveys different responses, as the phenotype associated with deletion of individual isoforms is different in mice. Here, we present the generation of a set of Jurkat cells genetically edited to lack individual genes from the TGF- β signaling pathway. This tool will allow us to identify the differences in the signaling pathways triggered by each isoform.

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Resumen corto

Identification of signaling proteins involved in CD13-mediated cell adhesion

Ramos-Mexicano, K.E. [1*], Ortega-Soto, E. [1]

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.
*E-mail: keniaramos@iibiomedicas.unam.mx

Aminopeptidase N, or CD13, is a cell membrane ectopeptidase highly expressed in myeloid cells. In recent years it has been shown that independently of its peptidase activity, CD13 can activate signal transduction pathways that mediate effector functions such as phagocytosis and cell adhesion. These functions have been observed upon cross-linking to membranal CD13 using viral ligands, antibody-coated particles, or antibody alone, which induces intracellular signaling events such as increased intracellular calcium and activation of SRC, PI3K, ERK, and FAK kinases. The cytoplasmic domain of CD13 consists of 9 amino acids, of which only Tyrosine 6 phosphorylation is involved in the early signaling events induced by CD13 crosslinking. Although CD13 has been shown to be a receptor capable of initiating signaling events, it is currently unknown which intracellular proteins interact with the cytoplasmic domain of CD13 that could be part of the signaling pathway involved in cell adhesion. In this work we analyzed CD13 co-immunoprecipitates by liquid chromatography coupled to mass spectrometry (LC-MS) and were able to identify 12 proteins that interact with CD13, of which HSP27 protein is functionally related to processes such as cell adhesion, cell migration and invasion. HSP27, a heat shock protein, is present in specialized structures such as anchoring adhesion and focal adhesion. This interaction was validated by western blot and confocal microscopy. This finding opens the possibility of the involvement of heat shock proteins in CD13-mediated cell adhesion and that the small intracellular domain of CD13 could involve an unconventional signaling pathway.

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Resumen corto

Drug repositioning of GPR15 inhibitors by docking identifies effects on cell migration by a beta-arrestin 1 / 2 mediated and Ca^{2+} Independent manner

Rangel, Y.A. [1,2*], Macias-Pérez, M.E. [1], Lara-Ramírez, E. [1], Zarazúa-Guzmán, S. [2], Portales-Pérez, D.P. [2], Rivas-Santiago, B. [1], Castañeda-Delgado, J.E. [3]

[1]Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México. [2]Posgrado en Ciencias Farmacobiológicas, Facultad de Ciencias Químicas, Universidad Autónoma de San Luis Potosí, San Luis Potosí, México. [3]Cátedras CONACyT Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México.
*E-mail: yamily.anahy@gmail.com

Chemokines stimulate chemotaxis by binding to G protein-coupled receptors (GPCRs). GPR15/BOB is a chemokine receptor involved in inflammatory diseases. GPR15L is the ligand for GPR15 and is a chemokine expressed in various epithelia. Our group identified GPR15 antagonists by pharmacological repositioning, but their effect on the blockade of this receptor is unknown. The identification of GPR15 inhibitors could be important to treat inflammatory diseases. To evaluate *in vitro* potential GPR15 inhibitors: ZINC537931, ZINC1542146 and ZINC1530788 identified by *in silico* assays and characterize the molcular signaling. Docking was used to identify potential binders, cytotoxicity of drugs was evaluated through propidium iodide (PI) by flow cytometry. Receptor activation was measured with calcium assays with the fluo-4 AM indicator by flow cytometry. The effect of drugs on GPR15-mediated migration was assessed by a Transwell chamber migration assay. GPR15 is expressed in PMN and PBMC of healthy subjects. Viability assays show that only ZINC537931 [100 µM] was found to be cytotoxic. We were unable to detect calcium entry by GPR15L stimulation, compared to the A23187 control. The drugs showed an induction of calcium signal, suggesting an agonistic affect. GPR15 is expressed in both PBMC and PMN. The mechanism of migration induced by GPR15L is mediated by arrestin and independent of calcium.

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Resumen corto

IFN- γ (+874 T/A, rs2430561) polymorphism expression in Mexican population infected with SARS-CoV-2

Rangel-Ramírez, V.V. [1*], Huerta-García, A.P. [1], Pérez-Urizar, J.T. [2], Lee-Rangel, H.A. [1,3]

[1]Centro de Biociencias de la Universidad Autónoma de San Luis Potosí, [2]Facultad de Ciencias Químicas de la Universidad Autónoma de San Luis Potosí, [3]Facultad de Agronomía y Veterinaria de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, México.
*E-mail: dvero.rangel@gmail.com

Coronavirus disease (COVID-19) is the clinical syndrome associated with SARS-CoV-2 infection. SARS-CoV 2 is reported to be transmitted between humans through direct contact, aerosol droplets, fecal–oral route, and intermediate fomites from both symptomatic and asymptomatic patients during the incubation period. Cytokines such as Interferon (IFN)-γ are important in the antiviral response. In this regard, polymorphisms in IFNs become relevant in the context of the infection of SARC-CoV-2. The objectives of this study are to determine the frequency of the IFN-γ (+874 T/A, rs2430561) polymorphism in Mexican Individuals and to understand the relevance of the IFN-γ expression in the different polymorphisms in regards to the infection by SARS-CoV-2; clinical characteristics will also be analyzed. The method for genotyping IFN-γ polymorphism will be the ARMS-PCR technique and qPCR for gene expression. We hypothesize that SAR-CoV-2 can induce DNA damage which can affect the expression of IFN-γ. So far, we do not observe any difference regarding the IFN-γ (+874 T/A, rs2430561) polymorphism in SARS-CoV-2+ individuals (n=100) when compared with the control group (n=103). Regarding the clinical characteristics of the SARS-CoV-2 group we do observe differences between the symptoms analyzed when compared AT and T genotypes. IFN-γ +874A allele has been previously reported to be associated with infectious diseases such as tuberculosis and hepatitis B virus infection, therefore, a larger number of individuals is being included for both groups to assess the potential role of the IFN-γ gene (+874) polymorphisms and its expression in the context of the infection by SARS-CoV-2.

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Resumen corto

Study of the percentage of methylation of IFNG and IL10 genes in a pediatric group with obesity submitted to multidisciplinary intervention.

Rechy-Ahumada, M. [1,2*], Romero-Nava, R. [1], Giacoman-Martínez, A. [2], Flores-Mejía, R. [1], Huang, F. [2], Rodríguez-Cortés, O. [1]

[1]Laboratorio de Inflamación y Obesidad, Escuela Superior de Medicina del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de Farmacología, Hospital Infantil de México "Federico Gómez", Ciudad de México, CDMX, México.
*E-mail: miguel.rechy.93@gmail.com

Obesity is characterized by chronic low-grade inflammation associated with excessive fat accumulation. One of the causes of the increase in prevalence is childhood obesity, children with obesity have a high probability of persisting with the disease in adulthood, currently in Mexico, childhood prevalence is close to 20%. DNA methylation is a process associated with gene silencing and phenotypic expression. In the thin adipose tissue, there is an anti-inflammatory phenotype with the presence of cells such as Treg lymphocytes, which secrete IL-10, but in obesity, there is a proinflammatory phenotype, with the presence of cells such as Th1 lymphocytes that secrete IFN-γ. Many inflammatory parameters are associated with obesity in adults, but this association with childhood obesity is unknown. The aim of this study was to evaluate the change in the percentage of methylation in the promoter sites of the IFNG and IL10 genes before and after a multidisciplinary weight reduction therapy in a group of children and adolescents with obesity. The results show that the intervention generates favorable changes such as a reduction in BMI and LDL, furthermore, the therapy diminishes the percentage of methylation at the IL10 promoter site. These data suggest that weight reduction intervention in obesity may influence gene expression towards an anti-inflammatory phenotype.

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Resumen corto

Genomic organization and transcriptional analysis of immunoglobulin *locus* in *Ambystoma mexicanum.*

Remy-Hernández, S. [1, 3]*, Godoy-Lozano, E.E. [2] ,
Pacheco-Olvera, D.L. [1, 3], Téllez-Sosa, J.M. [2],
López-Macías, C. [3+], Martínez-Barnetche, J. [2+]

[1]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional. Ciudad de México, México.[1]. [2]Centro de Investigación sobre enfermedades infecciosas Instituto Nacional de Salud Pública A, Cuernavaca, Morelos, México. [3]Unidad de Investigación Médica en Inmunoquímica. UMAE Hospital de Especialidades Centro Médico Nacional Siglo XXI. Ciudad de México, México.

+Correponding Authors *E-mail: stephstremy2691@gmail.com

Ambystoma mexicanum is a research model for the study of tissue regeneration. This process is carried out in an environment with the presence of multiple potentially pathogenic agents so there must be an important regulation of the inflammatory response while maintaining the ability to generate immunity. This study aimed to characterize and compare with other organisms the immunoglobulin *loci* of the axolotl. Using the genome sequence of the *A. mexicanum* (V6), axolotl Ig sequences and reference sequences from other vertebrates such as human, *Xenopus tropicalis*, *Danio rerio* (zebrafish), and eight tetrapod reference genomes. Gene models were further curated using *A. mexicanum* spleen transcriptomic data. Heavy chain, lambda, sigma, and the surrogate light chain *loci* were identified, which share the same architecture as the other vertebrates studied. No *kappa locus* was found. More than half of IGHV genes are pseudogenes as well as IGHF. Furthermore, there is no clan I IGHV genes. An intergenic size restriction in the IGHM and V gene cluster was found, suggesting local size evolutionary constraints, likely imposed by high transcriptional demand for certain Ig genes as well as V(D)J recombination. This work is a first step to determine whether the observed pseudogenization compromises the potential repertoire diversity and to study the antibody response of axolotl.

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Resumen corto

Neutrophil infiltration in peri-implantitis and presence of β-lactamase genes in peri-implant bacteria

Reséndiz-Jaramillo, C. [1]*, Palacios-Castañon, Y. [2]*, Saldívar-Salas, S. [3], Zermeño-Loredo, M.T. [3], Bañuelos-Hernández, B. [2], Santiago-Martínez, M.P. [3] Secundino, I. [1,2]

[1]Universidad La Salle Bajío, Facultad de Odontología, León Guanajuato, México. [2]Universidad La Salle Bajío, Escuela de Veterinaria, León Guanajuato, México.[3]Universidad La Salle Bajío, Facultad de Odontología. Posgrado en Prostodoncia e Implantología, León, Guanajuato, México.
E-mail: isecundino@lasallebajio.edu.mx

Peri-implant mucositis is a reversible inflammatory lesion of the mucosa surrounding a dental implant without the loss of supporting alveolar bone. If inflammation is not abrogated, bacteria will accumulate around the dental implant, causing loss of supporting bone in a process known as peri-implantitis. While the incidence of peri-implant mucositis is 30.7%, the incidence of peri-implantitis is 9.6%. The primary etiological factor of peri-implant diseases is bacterial biofilm accumulation to implant that elicited chronic inflammatory response. Here, we present an 82 years-old female patient with peri-implant mucositis at implant in region 45 and peri-implantitis at implant in region 46. The patient was systemically healthy and was not taking any medication. Her medical history revealed moderate periodontitis affecting the mobility in her upper teeth. Clinical examination of implant #45 showed significant plaque accumulation; implant #46 had swelling, bleeding upon probing with suppuration, probing depth of ≥6 mm, and bone loss. We found a predominant infiltrate of neutrophils CD15+CD66+ with elevated expression of CD11b and CD64 in peri-implant tissue from implant #46 (peri-implantitis). In contrast, no leucocyte recruitment was observed in implant #45 (mucositis). Anaerobic facultative Gram-negative bacteria were isolated from implant #46, which elaborated higher biofilm levels compared with bacteria recovered from implant #45. Remarkably, bacteria isolated from both implants had plasmids that harboured the genes bla_{CfxA} and bla_{TEM} which encode to β-lactamases. To our knowledge, this is the first report of peri-implant bacteria that carry antibiotic-resistance genes to β-lactam antibiotics in plasmids.

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Resumen corto

Alterations in the mitochondria of CD8+ T lymphocytes from patients with lung cancer

Reyes, A.C. [1], Romero-Garcia, S., Mora-Orozco, A. M. [1], Sandoval-Martinez, R. [1], Castro-Flores, D. A. [1], Rumbo-Nava, U [2], Prado-Garcia, H. [1*]

[1]Laboratorio de Onco-Inmunobiología, Instituto Nacional de Enfermedades Respiratorias "Ismael Cosío Villegas", Ciudad de México, México. [2]Clínica de Neumo-Oncología, Instituto Nacional de Enfermedades Respiratorias "Ismael Cosío Villegas", Ciudad de México, México.
E-mail: hpradog@yahoo.com

CD8+ T cells have metabolic changes after activation that require functional mitochondria. In patients with lung cancer, CD8+ T cells that infiltrate the pleural compartment have alterations in their activation and effector functions that could be due to defects in the mitochondria. The goal of this study was to identify mitochondrial alterations in CD8+ T cells that infiltrate the pleura in lung cancer patients. RT-qPCR analysis showed that CD8+ T cells presented a deregulated expression of molecules associated with mitochondrial dynamics. The amount of ROS in memory CD8+ T cells from malignant effusions was higher compared with the corresponding subset from peripheral blood cells in lung cancer patients, as evidenced by flow cytometry. However, by stimulating via CD3/CD28, the production of ROS increased in the peripheral blood CD8+ T cells memory cells of cancer patients and healthy subjects, but not in the memory CD8+ T cells from pleural effusions. The effector subset from the pleural effusion presented a reduced proportion of cells with high mitochondrial membrane potential compared to the corresponding subpopulation from blood. After stimulation via CD3, memory TCD8+ cells (CD45RA–CD27+) from healthy subjects, but not from cancer patients, increased their mitochondrial mass and mitochondrial membrane potential. Our results suggest that the tumor environment in malignant pleural effusions induces alterations in the functionality of CD8+ T lymphocytes that can compromise antitumor function.

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Resumen corto

Vitamin C promotes a stable phenotype and demethylated TSDR *Foxp3 of in vitro* expanded *allospecific iTregs*

Reyes-Barrientos, J.E. [1,2]*, Álvarez-Salazar, E.K. [1,2], Cortés-Hernández, A. [1,2], Arteaga-Cruz, S. [1,2], Martínez-Iturbe, I.I. [1,2], Morales-Buenrostro, L.E. [3], Alberú-Gómez, J.M. [4], Soldevila, G. [1,2]

[1]Department of Immunology and [2]The National Laboratory of Flow Cytometry, Biomedical Research Institute, National Autonomous University of Mexico, Mexico City, Mexico. [3]Department of Nephrology and Mineral Metabolism, National Institute of Medical Sciences and Nutrition Salvador Zubirán, Mexico City, Mexico. [4]School of Medicine and Health Sciences, Monterrey Institute of Technology., Mexico City, Mexico.

The limited use of induced Foxp3+ regulatory T cells (iTregs) in immunotherapy is attributable to its phenotypic instability due to the epigenetic status of specific loci which include the hypermethylation of the TSDR *Foxp3 loci*. In this context, vitamin C has been shown to induce demethylation of this region by Tet enzyme activation, obtaining a more stable phenotypically and functionally Treg population. We have previously shown that allospecific iTregs can be efficiently expanded *in vitro* with a suppressive phenotype and function. However, our expanded cells showed an increased TSDR methylation. In this work we evaluated the effect of vitamin C in the generation and expansion of Allo-specific regulatory T cells to evaluate their phenotype and epigenetic status in the presence of proinflammatory cytokines.

Allospecific induced Tregs were obtained from co-cultured between Monocytes-derived Dendritic cells and Naive T cells. After 3 weeks of expansion, Vitamin C-iTregs showed higher Foxp3 levels in comparison to cells expanded in control media, also the expression of T-bet, RORγT transcription factors and intracellular production of IFN-γ and IL-17 inflammatory cytokines were significantly reduced. Surprisingly, these results were unaffected by the addition of external pro-inflammatory cytokine into the cell culture. In addition, methylation of the TSDR region was lower in presence of Vitamin C than control culture (30% vs 80%). In conclusion, Vitamin C-allospecific iTregs showed a stable phenotype in presence of proinflammatory cytokines and an increased demethylation in TSDR region, which is related with a superior stability, making them optimal candidates in immunotherapy for tolerance induction in transplanted patients.

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Resumen corto

Presumed lectin-like activity in the mucus of a phylogenetically basal invertebrate, the marine anemone *Exaiptasia diaphana*

Rivera Ortega, J. [1,2]*, Sánchez-Salgado, J.L. [3], Pereyra, M.A. [3], Pascual-Jiménez, C. [4], Zenteno, E. [3], Thomé, P. [2]

[1]Posgrado en Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Ciudad de México, México. [2]Laboratorio de Microbiología Molecular, Unidad Académica de Sistemas Arrecifales Puerto Morelos, Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Quintana Roo, México. [3]Departamento de bioquímica, Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, México. [4] Unidad Multidisciplinaria de Docencia e Investigación, Facultad de Ciencias, Universidad Nacional Autónoma de México, Sisal, México. E-mail: jacq.rior@gmail.com

Anemones and corals are marine invertebrates covered by mucus that present active immune molecules and other antimicrobial properties. The anemone *Exaiptasia diaphana* is a model organism for studying reef-building corals. Coral reef, a highly biodiverse marine ecosystem, is threatened by climate change and several diseases. Since mucus has immune properties, this work aimed to determine if mucus performed a lectin-like activity. Healthy anemones were cultivated in two treatments (n= 12): Filtered Sea Water (FSW, 0.22 µm) and sterile Artificial Sea Water (ASW). We determined the hemagglutination activity (HA) of pooled anemones' mucus using native A+ and O+ human erythrocytes, with or without $CaCl_2$ [5Mm] and with or without trypsinized erythrocytes [1mg/mL]. Native A+ erythrocytes showed the highest HA (HAU= 2,346.6). A+ erythrocytes showed 1.15 times high HA in native and $CaCl_2$ conditions, in FSW and ASW treatments, except in trypsinized O+, where the HA was 2 times higher than A+. $CaCl_2$ showed lower HA compared with native and trypsinized A+ and O+ erythrocytes (4.8 and 2.4 times, respectively, in the FSW treatment). Finally, FSW had the highest HA in native, $CaCl_2$ and trypsin A+ and O+ erythrocytes (52, 10 and 33 times, respectively). *Exaiptasia diaphana* mucus showed high HA in A+ except in trypsinized O+ erythrocytes, and $CaCl_2$ was the condition with the lowest HA. Moreover, the mucus from FSW anemones had the highest HA which could mean that there are immune elicitors in the FSW that were not discarded with the filter. JRO thanks Dr C Guluarte for her recommendations and E Segura-Perez for the anemone husbandry.

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Resumen corto

Impact of the pharmacist on the rational use of medicines

Rivera-Bañuelos, J.H. [1], Mancilla-Villeda, M.P. [1],
Abundes-Recilla, P. [2]*, Mondragón-Guillen, M.J. [2],
Álvarez-Cortes, V.E. [2]

[1]Facultad de Medicina/ Universidad Nacional Autónoma de México. Cuidad de México, [2]Facultad de Farmacia/ Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos. E-mail: alrep.ar@hotmail.com

An important activity in the health professional must be the rational use of medicines (RUM), where “patients receive the appropriate medication for their clinical needs, in the corresponding doses, during an adequate period of time and at the lowest possible cost”. The pharmacotherapeutic follow-up (PF) carried out by the hospital pharmacist helps to analyze, evaluate, inform, dispense and optimize the necessary and timely medication for the hospitalized patient. In order to do so, we follow the following methodology. 1.- Validation of the medical indication for hospitalized patients with the help of the pharmacotherapeutic profile. 2. Dispense validated medications for each patient for 24 hours (unit dose distribution system, UDDS). 3. The next day, return the medication not administered to the patient, due to suspension or change of indication. In the period January-March 2023, 444 records of hospitalized patients were reviewed, validating 2,982 medications. In 23.64% of the files reviewed, 314 near-misses were found. Being 247 drug interactions and 67 medication errors. Only 19.43% of the near misses were accepted and corrected. While the UDDS, together with the medication return process, helped to maximize the optimization of medication resources; since, IV paracetamol yielded 41% more and antibiotics such as ceftriaxone, ceftazidime, metronidazole yielded 17% altogether. In conclusion, the validation of the medical prescription helped prevent 61 near misses due to the use of medications.

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Resumen corto

Performance between traditional dispensing vs unit doses

Rivera-Bañuelos, J.H. [1], Patricia-Mancilla, M.P. [1], Abundes-Recilla, P. [2]*, Lira-Garnica, V.J. [3], Anaya-Miranda, S.Y. [1], Álvarez-Cortes, V.E. [2].

[1]Facultad de Medicina/ Universidad Nacional Autónoma de México. Ciudad de México, [2]Facultad de Farmacia/Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, [3]Instituto de Ciencias de la Salud/ Universidad Autónoma del Estado de Hidalgo. San Agustín Taxiaca, Hidalgo. E-mail: alrep.ar@hotmail.com

The use of antibiotics (cephalosporin) at the hospital level has become a priority in care, however, the use that these imply reflects a monetary expense from the perspective of traditional dispensing and unit dose dispensing within hospital services.It is a retrospective pharmacoeconomic study with a sample of 30,648 patients in a period that contemplates exactly the year 2022. The General Hospital of the Second Level of care has 60 census beds where performance is measured (Traditional Dispensation – Dispensation by Unit Dose). Results obtained:

JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
6.27%	7.54%	6.65%	8.57%	6.01%	6.65%	7.29%	6.27%	8.44%	6.01%	7.93%	22.38%

The graph shows the performance obtained throughout the year 2022 with respect to the use of cephalexin 500 mg orally through Unit Doses. In conclusion the use of antibiotic drugs for oral administration has benefited, both to make rational use of them as well as to reduce bacterial resistance factors in the community. In the same way, the rational use of antibiotics shows a performance that contrasts with the traditional dispensing in hospital services, which allows the re-administration of the resource and allocate it to different items.

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Resumen corto

Association of *VDR* polymorphisms with its mRNA expression, serum levels of calcidiol and calcitriol in rheumatoid arthritis patients

Rivera-Escoto, M. [1,2*]; Oregon-Romero, E. [3]; Meza-Meza, M.R., Campos-López, B. [1,2]; Mora-García, P.E. [1,2], Ruiz-Ballesteros, A.I. [1,2]; Pesqueda-Cendejas, K. [1,2]; Parra-Rojas, I. [1 4]; Montoya-Buelna, M. [1, 5], Luquin, S. [2], Cerpa-Cruz, S. [6]; De la Cruz-Mosso, U. [1, 2]

[1]Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [2]Instituto de Neurociencias Traslacionales, Departamento de Neurociencias, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [3]Instituto de Investigación en Ciencias Biomédicas, Departamento de Biología Molecular y Genómica, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [4]Laboratorio de Investigación en Obesidad y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, Chilpancingo de los Bravo 39087, Guerrero, Mexico. [5]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, Mexico. [6]Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara 44280, Jalisco, Mexico.
E-mail: ulises_cdm@hotmail.com ; ulises.mosso@academicos.udg.mx

Rheumatoid arthritis (RA) is an autoimmune disease. Genetics and enviromental factors such as hypovitaminosis D are risk factors for RA. Vitamin D deficiency is associated with higher clinical disease activity. Vitamin D receptor (VDR) is expressed in immune cells where acts a transcription factor dependent on its ligand calcitriol modulating the immune homeostasis gene expression. Polymorphisms in *VDR* such as *FokI, BsmI, ApaI* y *TaqI* could be associated with vitamin D deficiency. This study aimed to evaluate the association of *VDR* polymorphisms with its mRNA expression and with calcidiol and calcitriol serum levels in RA patients. A cross-sectional study was performed in 128 RA patients and 196 control subjects (CS). Calcidiol and calcitriol levels were measured by ELISA. Allelic discrimination with TaqMan® was used for *FokI, BsmI, ApaI* y *TaqI* genotyping. *VDR* mRNA expression were quantified by RT-qPCR and analyzed with $2^{-\Delta\Delta Ct}$ method. Calcitriol levels were higher in RA vs. CS (47.8 vs. 36.8 pg/mL, $p<0.05$). RA patients carriers of CT *TaqI VDR* has higher genetic risk for RA (OR: 1.8; IC 1.10 – 3.10; $p=0.01$). Regarding gene expression RA patients carrying the CT and TT genotypes in *FokI* expressed less *VDR* than SC carrying the same genotypes considering the CC genotype as reference (CT: RA= 7.06 vs. CS= 43.50; TT: RA= 21.25 vs.SC= 83.67). In conclusion, RA patients had higher calcitriol compared to CS. CT *TaqI VDR* genotype was associated with higher genetic risk for RA. CT and TT genotypes in *FokI* were associated with lower VDR expression.

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Resumen corto

Metabolite-induced metabolic reprogramming in the context of Neutrophil Extracellular Traps formation

Rivero-Silva, M.A. [1], Rojas-Espinosa, O. [1],
Sánchez-García, F.J. [1]

[1]Laboratorio de Inmunorregulación, Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México.
E-mail: miguel.rivero1995@gmail.com

Neutrophils are the first line of defense against a wide array of pathogens, as well as the most abundant leukocytes in the peripheral blood. One of the main neutrophil functions is the release of neutrophil extracellular traps (NETs), allowing different molecules to interact with the trapped microorganism. Recently, the effect that several metabolites present in the cell microenvironment has gained interest. We have previously observed that lactate, succinate, fumarate, acetate, and butyrate differentially modulate the mitochondrial activity of monocytes (mitochondrial reprogramming). Now, we suggest analyzing these metabolites impact on the release of NETs. Neutrophils were adhered to coverslips in 12 well assay plates, then the cells were exposed to the metabolites lactate, succinate, fumarate, acetate, and butyrate, separately, at 100 µM final concentration, after 30 minutes, PMA (0.1 ng/well) was added, and cells further incubated for 4 hours; cells with no PMA were used as a control. Cells were stained with Hoechst and analyzed by fluorescence microscopy. We found that lactate by itself induced low grade NETs formation, but no the other metabolites; when PMA was used to induce NETs, succinate increased the release of NETs, as assessed by the extracellular DNA area using ImageJ). On the contrary, fumarate significantly reduced the release of NETs, almost to the extent of completely eliminating their release. We conclude that changes in the metabolism that affect the concentration of metabolites such as lactate, succinate or fumarate in the cell microenvironment may have an impact on the neutrophils ability to release NETs. Rivero-Silva MA is the recipient of a Conacyt fellowship (965523). Project financed by Conacyt (CB-284602) and SIP-IPN (2023-0486)

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Resumen corto

Metabolic regulation of neonatal CD4⁺ T cell activation and function

Robles-Reyes, J.R. [1], Santana-Calderón, A. [1],
Rodríguez-Jorge, O. [1]

[1]Laboratorio de inmunología, Centro de Investigación en Dinámica Celular de la Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México.

One of the leading causes of neonatal death is their high susceptibility to infections by intracellular pathogens. CD4⁺ T cells are one of the main arms against this type of pathogen. These cells enter the circulation as naïve T cells, with a mainly catabolic metabolic program based on Glycolysis and OXPHOS for ATP synthesis. Naïve T cells are activated when they recognize their antigen through the TCR, along with costimulatory signals, such as those from CD28. CD28 cause the activation of signaling pathways, including PI3K/Akt, leading to enhanced TCR-mediated signaling and increased metabolic rate. Activation induces metabolic reprogramming, changing to a glycolytic and anabolic metabolism. In this new program, some metabolites have immunoregulatory activity, which can affect T cell activation under certain conditions. In this work, we used computational modeling to understand the effect of the neonatal metabolic state on the activation of these cells. We created a discrete logical model of CD4⁺ T cell activation and validated it by *in silico* analysis. Then, we computed the stable states and performed a probabilistic analysis with MaBoSS. We found that neonatal CD4⁺ T cells have a high metabolic rate with absent or decreased effector functions. Based on our analysis we proposed that the reduction of some immunoregulators like lactate and ROS can improve the response of neonatal CD4⁺ T cells.

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Resumen corto

Metformin promotes Mycobacterium tuberculosis killing and increases the production of human β-defensins in lung epithelial cells and macrophages

Rodriguez-Carlos, A. [1], Valdez-Miramontes, C. [1], Marin-Luevano, P. [1], González-Curiel, I. [2], Enciso-Moreno, J. A. [1], Rivas-Santiago, B. [1]

[1] Medical Research Unit-Zacatecas, Mexican Institute for Social Security-IMSS, Zacatecas, Mexico [2] Faculty of Chemistry, University Autonomous of Zacatecas, Mexico

Diabetes is associated with an increased risk of developing TB and increased risk of death or/and treatment failure in TB. The reasons involving the susceptibility of T2DM patients to develop TB have not been well understood, it has been attributed to several factors including several failures in diverse branches of the immune system. In the present study, we aimed to determine the role of metformin to regulate innate immune molecules such as host defense peptides and whether metformin might modulate the immune response in lung epithelia. Thus, we explore not only metformin but also other important antihyperglycemic drugs, such as glyburide and insulin. The expression of antimicrobial peptides (AMPs) was evaluated by qPCR and ELISA. Furthermore, the bacterial load was measured by CFUs/mL. Our results showed that metformin reduces bacillary loads in macrophages and lung epithelial cells and this correlates with higher production of b-defensin-2, -3 and 4. Given that b-defensins are clue molecules for controlling M. tuberculosis growth, these results suggest that the use of metformin would be the first choice in the treatment for T2DM2, in patients within tuberculosis-endemic areas.

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Resumen corto

Immediate, medium and late effects of vaccines against SARS-CoV-2 in older adults.

Rodríguez-Cortazar, L. [1,2]*, Cebreros-Santiago, D. [2], Camarillo-Nava, V.M. [2]

[1]Universidad Nacional Autónoma de México, División de estudios de Posgrado, Subdivisión de Medicina Familiar, UNAM Ciudad de México, CDMX, México. [2]Instituto Mexicano del Seguro Social OADD Norte, Ciudad de México, CDMX, México. E-mail: Lizandracel@outlook.com

The 12% of the Mexican population during 2020 were adults over 60 years of age, considered a vulnerable population; Therefore, they were the first age group that was considered a priority for the start of vaccination against SARS-CoV-2 with the various types of vaccines that are available. The objective is identify the immediate, mediate and late effects caused by the different vaccines against SARS-CoV-2 in older adults. This work is Observational, longitudinal, retroprolective, analytical study, Historical Cohort Type, information was obtained through questionnaires applied to patients with a complete vaccination scheme; taking as the main variable the effects caused after vaccination against SARS-CoV-2. Descriptive and differential statistics will be used, calculation of Odds Ratio to determine the most frequent effects and their incidence; establishing significance with $p < 0.05$. The 48.5% of the adverse effects found were local and are part of the Adverse Event Supposedly Attributable to Vaccination and Immunization (ESAVI) caused by any other vaccine. Vaccination presents an OR <1 and the incidence of patients who contracted COVID19 with a full vaccination schedule was 10.5%, with only 0.5% of those who fell ill with Severe COVID. According to the statistical analysis, we could infer that the Vaccines against SARS-CoV-2 from the Pfizer, AstraZeneca and Sputnik laboratories are safe for the Mexican population of older adults, since they did not cause any significant repercussions in any of the participants regardless of age, gender, occupation, previous SARS-CoV-2 disease or the type of vaccine they have received.

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Resumen corto

Logical modeling predicts an important role of metabolic modules in controlling T cell-mediated responses in newborns and along the lifespan.

Rodríguez-Jorge, O. [1]*, Robles-Reyes, J.R. [1], Yáñez-Romero, S. [2], Ventura-Martínez, C.J. [1], Kempis-Calanis, L.A. [1], Santana-Calderón, M.A. [1]

[1]Centro de Investigación en Dinámica Celular, Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México. [2]Escuela de Estudios Superiores de Jonacatepec, Universidad Autónoma del Estado de Morelos, Jonacatepec, Morelos, México. E-mail: orj@uaem.mx

Neonatal CD4+ and CD8+ T cells present a low response to TCR/CD28 stimulatory conditions, and CD8+ T cells present low cytotoxicity. Nutrition, metabolism, lifestyle, and disease, affect the development of the neonatal immune system and its response to pathogens and vaccines. At birth, neonatal T cells are predisposed to low, regulatory, and Th2 responses, which gradually progress to adult-like responses. In adults, the same factors continue to affect T cell-mediated responses. To decipher and predict their response to therapeutic interventions, we modeled T cell activation responses integrating signaling, genetic and metabolic pathways using a multivalued logical formalism and performed the computation of stable states and dynamic analyses under wild-type and mutant conditions. We proposed a molecular mechanism for the low response of neonatal CD4+ T cells and predicted that by targeting specific metabolic pathways of neonatal T cells, we could enhance their activation response. With the same strategy, we predicted that targeting the metabolic regulatory module could enhance the activation response of CD8+ T cells in diabetic patients, which was validated by published data. Our results show that logical modeling could be an important tool for predicting potential intervention points to modulate T cell responses.

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Resumen corto

Galectin 1 exerts an anti-inflammatory effect on the secretion of IL-6 and MMP-9 extravillous trophoblast HTR-8/SVneo cell line

Rodríguez-Flores, S. [1,2]*, Estrada-Hidalgo, N. [1,2], Flores-Mejía, R. [3], Godínez-Victoria, M. [4], Flores-Espinosa, P. [1], Olmos-Ortiz, A.[1], Mancilla-Herrera, I. [5], Velázquez-Sánchez, P. [6], Zamora-Escudero, R. [7], Islas-López, M. [7], Zaga-Clavellina. V, [1]

[1]Departamento de Inmunobioquímica, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, Ciudad de México 11000, México. [2]Maestría en Ciencias de la Salud, Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Plan de San Luis y Díaz Mirón s/n, Casco de Santo Tomas, Ciudad de México 11340, México. [3]Laboratorio de Inflamación y Obesidad, Inmunología Médica y Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Plan de San Luis y Díaz Mirón, Casco de Santo Tomas, Ciudad de México 11340, México. [4]Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional, Plan de San Luis y Díaz Mirón s/n, Ciudad de México 11340, México. [5]Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, Ciudad de México 11000, México, [6]Departamento de Ginecología y Obstetricia, Hospital Ángeles México, Ciudad de México 11800, México. [7]Ginecología y Obstetricia, Hospital Ángeles Lomas-UNAM, Huixquilucan 52763, México.
E-mail: sam.rofl185@gmail.com

Human pregnancy success requires multiple immuno-endocrine strategies to maintain the fetoplacental unit as an immunotolerant space to guarantee the fetus's protection; however, an infectious process can jeopardize this immune privilege. During the first trimester of pregnancy, galectin 1 (Gal-1), a molecule with immunomodulatory functions, is involved in the differentiation, migration, and invasion of trophoblasts; however, its functions in a placental inflammation milieu are still not fully understood. This study aimed to evaluate the effect of Gal-1 upon the secretion of cytokines, chemokines, and matrix metalloproteinases induced by 10 ng/mL LPS from E. coli in the cell line of extravillous trophoblast HTR-8/SVneo. Our results showed that the pre-incubation with 1.0 and 1.5 ng/ml of Gal-1 reduced in a significant way the secretion of IL-6 and MMP-9 induced by LPS. The secretion profile of TNF-α, IL-1β, IL-8, RANTES, MCP1, MIP-1α, IL-10, CXCL16, CXCL12, IL-4, IL-10 and TGF-β were not modified for the treatment with Gal-1. In conclusion, Gal-1 can decrease IL-6, a cytokine whose role in the subclinical infection process during pregnancy is essential to create adverse conditions for the fetus. Additionally, the capacity of Gal-1 to repress the synthesis and secretion of MMP-9 can be interpreted as a protective compensatory function to protect the maternal and fetal tissues, including the placenta, of weakness and degradation of extracellular which can represent a dangerous and harmful condition for the continuity of gestation.

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Resumen corto

High expression of Myosin 1g in pediatric Acute Lymphoblastic Leukemia detected by novel monoclonal antibodies

Rodríguez Téllez, R.I. [1], Ribas Aparicio, R.M. [2], Patiño López, G. [1]*

[1]Laboratorio de Investigación en Inmunología y Proteómica, Hospital Infantil de México, Fedrico Gómez, Ciudad de México, Mexico. [2]Laboratorio de Producción y Control de Biológicos, Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Cidad de México, Mexico. E-mail: gpatino@himfg.edu.mx

Previously we demonstrated that Myosin 1g (Myo1g) is highly expressed in pediatric patients with Acute Lymphoblastic Leukemia (ALL), especially those with High Risk, Myo1g is a mechanoenzyme associated with actin filaments, expressed exclusively in hematopoietic cells, and involved in various cellular functions, including cell migration, adhesion, and membrane trafficking. Despite the importance of Myo1g in distinct functions, there is currently no monoclonal antibody (mAb) against Myo1g. mAbs are helpful tools for the detection of specific antigens in tumor cells and other tissues. The development of mAbs against targeted dysregulated molecules in cancer cells remains a crucial tool for aiding in the diagnosis and the treatment of patients. Using hybridoma technology, we generated a panel of hybridomas specific for Myo1g. ELISA, immunofluorescence, and Western blot assay results revealed the recognition of Myo1g by these novel monoclonal antibodies in normal and transformed T and B cells. Here, we report the development and application of new monoclonal antibodies against Myo1g for their potential use to detect its overexpression in acute lymphoblastic leukemia (ALL) patients.

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Resumen corto

Identification of exhausted T and NK cell targets for immunostimulation in cervical cancer

Rojas-Díaz, J. M. [1]*, Haramati, J. [2], Ortiz-Lazareno, P. C. [3], Solórzano-Ibarra, F. [1], Urciaga-Gutiérrez, P. I. [1], García-Barrientos, N. T. [1], Domínguez-Hernández, A. P. [1,2], Güitrón-Aviña, M. S. [1,2], Del Toro-Arreola, S. [1,6]

[1]Instituto de Investigación en Enfermedades Crónico-Degenerativas, Departamento de Biología Molecular y Genómica, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Laboratorio de Inmunobiología, Departamento de Biología Celular y Molecular, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Zapopan, Jalisco, México. [3]División de Inmunología, Centro de Investigación Biomédica de Occidente, Instituto Mexicano del Seguro Social, Guadalajara, Jalisco, México. lqfb.manuel.rojas@gmail.com

Cervical cancer is a major public health problem in Mexico. The destruction of cancer cells is carried out mainly by cytotoxic T cells and Natural Killer (NK) cells. The inhibitory receptors PD-1, and TIGIT play a crucial role in T and NK cell exhaustion, characterized by hyporesponsiveness to tumors. Nevertheless, both cells may sometimes express inducible costimulatory receptors such as 4-1BB, OX-40, and ICOS that favor cell activation and may counteract exhaustion. In this work we evaluated the immunophenotype of inhibitory and costimulatory receptors in peripheral T and NK cell populations from women with cervical cancer through multiparametric flow cytometry with the aim of finding a target to reverse cytotoxic cell exhaustion.

We found PD1+ NK cells significantly increased in cervical cancer patients compared against age matched controls. These putatively exhausted NK cells also significantly overexpressed both 4-1BB and OX-40. This is a unique population of exhausted cells that will be potentially responsive to agonistic signaling through the 4-1BB and OX-40 receptors. We also found a population of TIGIT+ 41BB+ NK cells that were increased, as well as a population of PD1+ 41BB+ T cells that was also increased in cervical cancer patients. While TIGIT was not increased in total patient NK cells, nor PD1 in patient T cells, these later two subpopulations also are worthy of further investigation for the reversal of exhaustion.

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Resumen corto

Metaanalysis of gene expression in multiple sclerosis reveals type 1 interferon fingerprint as the main altered molecular pathway

Rojas-Gutiérrez, S. E. *[1], Elizondo-Solís, C. V. [1], Salinas-Carmona, M. C. [1], Montoya-Rosales, A. [2], Macias-Segura, N. [1]

[1] Laboratorio de Inmunología de Sistemas, Departamento y Servicio de Inmunología, Facultad de Medicina y Hospital Universitario, Universidad Autónoma de Nuevo León. [2]Laboratorio de Inmunomoduladores, Centro de Investigación y Desarrollo en Ciencias de la Salud, Universidad Autónoma de Nuevo León. santiago.rojasgu@uanl.edu.mx

Multiple sclerosis (MS) is a chronic inflammatory demyelinating disease of the central nervous system. Despite considerable progress in understanding the pathogenesis of MS, the precise molecular mechanisms remain elusive. This study presents a meta-analysis of gene expression profiles in MS patients, revealing the Interferon (IFN) type 1 signature and its possible role in disease progression. We performed a systematic search of public databases on the GEO (Gene expression Omnibus) platform to obtain gene expression datasets from MS patients and healthy controls. After rigorous quality control and preprocessing, we integrated the datasets and performed a meta-analysis using integrative bioinformatics tools to identify differentially expressed genes (DEGs) in the obtained databases. Subsequently, we performed functional enrichment analysis, co-expression analysis, and protein-protein interaction network analysis to explore the biological implications of the identified DEGs. Our meta-analysis revealed dysregulation of type 1 IFN-responsive genes in MS patients compared to healthy controls, supporting their crucial role in MS pathogenesis. The protein-protein interaction network further highlighted key regulatory factors and potential therapeutic targets within the type 1 IFN signature. In conclusion, this study provides a comprehensive analysis of the type 1 IFN signature in MS, emphasizing its importance in the molecular landscape of the disease. Our findings contribute to a deeper understanding of MS pathogenesis and may facilitate the development of new therapeutic strategies targeting the type 1 IFN pathway.

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Resumen corto

Molecular pathways associated with neutrophil degranulation in Type 1 Diabetes patients through integrative bioinformatic meta-analysis

Rojas-Gutiérrez, S. E. *[1], Gelinas-Martin del Campo, M. [1], Elizondo-Solis, C. V. [1], Salinas-Carmona, M. C. [1], Montoya-Rosales, A. [2], Macias-Segura, N.[1]

[1] Laboratorio de Inmunología de Sistemas, Departamento y Servicio de Inmunología, Facultad de Medicina y Hospital Universitario, Universidad Autónoma de Nuevo León. [2]Laboratorio de Inmunomoduladores, Centro de Investigación y Desarrollo en Ciencias de la Salud, Universidad Autónoma de Nuevo León. santiago.rojasgu@uanl.edu.mx

Type 1 diabetes (T1D) is an autoimmune disorder characterized by the destruction of insulin-producing pancreatic β-cells, resulting in a lifelong requirement for exogenous insulin. Despite significant advances in our understanding of T1D pathogenesis, the complex interplay of genetic, and environmental factors remains incompletely understood. This study aims to perform an integrative bioinformatic meta-analysis of gene expression data in PBMC of T1D patients to elucidate key molecular pathways, identify novel biomarkers, and suggest potential therapeutic targets. We systematically searched in the NCBI GEO database to compile a comprehensive dataset of transcriptomic studies in T1D patients and relevant control populations. Rigorous data preprocessing, normalization, and quality control measures were applied to ensure the comparability of datasets. We performed a meta-analysis using statistical methods to identify differentially expressed genes (DEGs) in T1D. Gene ontology, pathway analyses and co-expression analyses were conducted to gain insights into the molecular pathways implicated in T1D pathogenesis. Our meta-analysis identified a core set of DEGs consistently dysregulated in T1D across multiple studies, pathway analysis highlighted the involvement of neutrophil degranulation and other immune pathways. Additionally, several novel candidate genes were identified, warranting further investigation as potential biomarkers or therapeutic targets. In conclusion, this comprehensive meta-analysis of gene expression in T1D provides valuable insights into the molecular underpinnings of the disease. Our findings show the importance of integrating large-scale transcriptomic data to uncover the complex molecular landscape of T1D and other autoimmune diseases and pave the way for personalized medicine approaches in its management.

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Resumen corto

Efecto de la calreticulina recombinante de *Taenia solium* (rTsCRT) en macrofagos murinos.

Rojas Lara, J.I. [1]*, Chavez Vargas, M.D. [1],
Vázquez Rodríguez, S. [2], Flisser Steinbruch, A. [1],
Mendlovic Pasol, F. [1, 3], Cruz Rivera, M.Y. [1]

[1]Laboratorio de Inmunomodulación y Agentes Patógenos, Departamento de Microbiología y Parasitología, Facultad de Medicina, Universidad Nacional Autónoma de México, Av. Universidad 3000, Coyoacán, Ciudad de México, 04510, México. [2]Escuela Nacional de Ciencias Biológicas. Instituto Politécnico Nacional. Prolongación de Carpio y Calle Plan de Ayala s/n, Santo Tomás, Miguel Hidalgo, 11340 Ciudad de México. [3]Facultad de Ciencias de la Salud, Universidad Anáhuac, México Norte, Av. Universidad Anáhuac 46, Huixquilucan, 52786, Estado de México, México.
E-mail: jobisaacrl@ciencias.unam.mx

Los macrófagos participan en la respuesta innata del sistema inmune ante agentes infecciosos mediante procesos como la fagocitosis donde participan receptores como el scavenger receptor A (SR-A). La CRT es una proteína conservada localizada en el lumen del retículo endoplasmático, que interviene en la homeostasis de Ca2+ intracelular y funciona como señal "cómeme" en células apoptóticas. En nuestro laboratorio expresamos la calreticulina de *Taenia solium* como proteína recombinante (rTsCRT) y se ha observado que tiene efectos moduladores sobre macrófagos, además, interacciona con el SR-A. Para dilucidar la influencia de la rTsCRT sobre macrófagos murinos peritoneales y de la línea celular J774A.1 se analizó la interacción de la rTsCRT con el SR-A, así como en receptores como CD206, CD80, IA/IE y F4/80 mediante citometría de flujo. La rTsCRT se expresó en bacterias BL21 transformadas con el plásmido pET23a-TsCRT, se purificó mediante electroforesis y electroelución. Ratones hembras Balb/c se inmunizaron vía intraperitoneal con 10µg de rTsCRT una vez por semana en 3 ocasiones, los macrófagos peritoneales se aislaron y cultivaron, así como la línea J774A.1. Ambos cultivos se estimularon con la rTsCRT durante 24h. Hasta el momento no hemos observado diferencias en la actividad fagocítica en la línea celular; ni aumento en la expresión del SR-A. En macrófagos peritoneales de ratones inmunizados y estimulados con rTsCRT si aumenta la expresión del SR-A. Los datos sugieren que la inmunización con rTsCRT induce la expresión del SR-A, por ende, se analizará si esto influye en su capacidad de fagocitosis.

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Resumen corto

IL-2 effect in autophagy induction in cervical cancer cells treated with cisplatin

Romero-Hernández, C. B. [1*], Ortiz-Garrido, I. [1], Soto-Cruz, M. I. [1], Gutierrez-Hoya, A. [1,2]

[1] Molecular Oncology Laboratory, Cell Differentiation and Cancer Research Unit, FES Zaragoza, National University of Mexico, Batalla 5 de Mayo s/n Col. Ejército de Oriente, Mexico City 09230, Mexico. [2] Cátedra CONACYT, CONACYT, Avenida Insurgentes Sur 1582, Col. Crédito Constructor Del. Benito Juárez, Mexico City 03940, Mexico.

IL-2 is a growth factor for T lymphocyte. While in cervical cancer cell lines has a different effect, low doses promote cellular proliferation and high doses inhibit proliferation. Though, IL-2 high doses and cisplatin (IC50) treatment does not increase the apoptosis percentage, probably by autophagy activation, for this reason our aim is to define autophagy role in the IL-2 and cisplatin treatment in tumoral cells. We determined cisplatin IC50, apoptosis by flow cytometry and LC3B presence by confocal microscopy. We observed that previous IL-2 administration in cisplatin treated-cancer cells delay apoptotic process and this correlate with fluorescence intensity increment of LC3B. We conclude IL-2 and cisplatin treatment promotes autophagy induction and this could be correlated with chemoresistance and survival mechanisms.

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Resumen corto

Bioinformatic prediction of T cell epitopes from SARS-CoV-2 spike protein revealed a correlation of HLA-DRB1*01 with COVID-19 fatality in Mexico

Romero-López, J. P. [1,2]*, Carnalla-Cortés, M. [3], Pacheco-Olvera, D. L. [2,4], Ocampo-Godínez, J. M. [2,5], Oliva-Ramírez, J. [6], Moreno-Manjón, J. [7,8], Bernal-Alferes, B. [1,2], López-Olmedo, N. [3], García-Latorre, E. [2], Domínguez-López, M. L. [2], Reyes-Sandoval, A. [9], Jiménez-Zamudio, L. [10]

[1]Laboratorio de Patogénesis Molecular, Red MEDICI, Carrera de Médico Cirujano, Facultad de Estudios Superiores Iztacala, UNAM, Avenida de los Barrios 1, Tlalnepantla de Baz, Estado de México, Mexico. [2]Laboratorio de Inmunoquímica 1, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Carpio y Plan de Ayala SN, Mexico City, Mexico.[3]Centro de Investigación en Salud Poblacional, Instituto Nacional de Salud Pública, Cuernavaca, Mexico.[4]Unidad Médica de Investigación en Inmunoquímica, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, IMSS, Mexico City, Mexico. [5]Laboratorio de Ingeniería de Tejidos, Posgrado de la Facultad de Odontología, UNAM, Mexico City, Mexico. [6]Escuela de Ingeniería y Ciencias, Tecnológico de Monterrey, Mexico City, Mexico. [7]Laboratorio de Infectología, Microbiología e Inmunología Clínicas, Unidad de Investigación en Medicina Experimental, Facultad de Medicina, UNAM, Mexico City, Mexico. [8]Laboratorio de Bacteriología Médica, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Carpio y Plan de Ayala SN, Mexico City, Mexico. [9]Nuffield Department of Medicine, The Jenner Institute, The Henry Welcome Building for Molecular Physiology, University of Oxford, Oxford, UK. [10]Laboratorio de Inmunología Clínica 1, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico.
Contact: pabloromero@iztacala.unam.mx

SARS-CoV-2 infection caused a pandemic that resulted in health and economic problems worldwide. Human leukocyte antigen (HLA) mediates antigen presentation and T cell activation. Remarkably HLA polymorphisms can influence the susceptibility to diverse viral and bacterial infections, therefore, we aimed to predict which HLA antigens have a higher affinity for SARS-CoV-2 spike protein presentation, and to look for its epidemiological relevance.

A bioinformatic prediction of T cell epitopes and their restricted HLA Class I and II alleles was performed to obtain immunogenic epitopes and HLA alleles from the spike protein, also, a correlation with the predicted fatality rate of hospitalized patients in 28 states of Mexico was done.

We described a set of 10 highly immunogenic epitopes, together with different HLA alleles that can efficiently present these epitopes to T cells. Most of these epitopes are located within the S1 subunit of the spike protein, suggesting that this area is highly immunogenic. A statistical negative correlation was found between the frequency of HLA-DRB1*01 and the fatality rate in hospitalized patients in Mexico.

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Resumen corto

Frequency and phenotype of gut-homing positive T cells in patients with spondyloarthritis

Romero-López, J. P. [1,2]*, Gómez-Martínez, D. [1,2], Gómez-Mosqueira, R. [1,2], Burgos-Vargas, R. [3], Casasola-Vargas, J. C. [3], Meza-Olguín, G. [3], García-Latorre, E. [2], Domínguez-López, M. L. [2]

[1] Laboratorio de Patogénesis Molecular, Red MEDICI, Carrera de Médico Cirujano, Facultad de Estudios Superiores Iztacala, UNAM, Avenida de los Barrios 1, Tlalnepantla de Baz, Estado de México, Mexico. [2]Laboratorio de Inmunoquímica 1, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Carpio y Plan de Ayala SN, Ciudad de México, Mexico. [3]Departamento de Reumatología, Hospital General de México "Dr. Eduardo Liceaga", Ciudad de México, México.
Contact: pabloromero@iztacala.unam.mx

Spondyloarthritis (SpA) is a rheumatic disease characterized by oligoartritis, pathogenic osteoproliferation and subclinical intestinal inflammation. Although several genes have been related to its pathogenesis, the cause of inflammation is still unknown. The theory of aberrant cell migration proposes that lymphocytes can be activated in mucosal tissues and migrate to the joints where they can enhance the inflammatory response.

We aimed to determine the frequency of gut-activated (determined by the expression of the $\alpha4\beta7$ integrin) T and T$\gamma\delta$ lymphocytes and monocytes in the blood of patients with SpA and to determine the expression of TLR2, TLR4, IL-17 and IL-22. We correlated the expression of these markers with the level of intestinal inflammation measured by the concentration of faecal calprotectin, and with clinical parameters of disease activity.

We found high fecal calprotectin levels in patients with axSpA irrespectively of activity status. Also, a decreased expression of CD14 in monocytes was identified. Immunophenotyping experiments revealed high percentages of $\alpha4\beta7$-positive T ($p=0.026$) and T$\gamma\delta$ cells ($p=0.0118$) in the patients with axSpA; these cells showed differential expression of TLR2 and TLR4 when compared to $\alpha4\beta7$-negative cells and cells from healthy subjects.

IL-22 expression was shifted for the γδ T cell subset in both SpA patients and HD. γδ T cells of SpA patients and HD exhibited a population with higher expression of the TCR, defined as the γδ ^{hi} T cell subset; this was associated with an augmented expression of the α4β7 integrin and IL-22 compared with the γδ ^{int} T cell subset.

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Resumen corto

Detection of IgA antibodies against Mycobacterium tuberculosis antigens in colostrum samples from Mexican mothers

Romero-Ramírez, H. [1], Pedraza-Romero, M. R. [2], Barreto-Lesmes, A. N. [1], Baltierra-Uribe, S. B. [2], Sandoval-Montes, C. [3], Santos-Argumedo, L.[1].

[1]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, México. [2]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, México. hromero@cinvestav.mx.

Introduction: Colostrum is the first milk secretion with a high concentration of immunologically active molecules, which have neutralizing and antibacterial capacity, among them is IgA in an important concentration. *Mycobacterium tuberculosis* is a microorganism that infects, usually the lungs, but can also attack other non-pulmonary tissues. In Mexico there is a BCG vaccination coverage of more than 97%, but 28,000 cases of tuberculosis continue to be detected each year. Aim: Detect the presence of IgA antibodies against M. tuberculosis antigens in colostrum samples from Mexican mothers. Methodology: Indirect Elisas were performed using protein extracts of the H37Rv *M. tuberculosis* strain as antigens and secondary antibodies against total IgA and IgA2 immunoglobulins from 106 colostrum samples from healthy Mexican mothers between 17 and 43 years old. Results: 87.7% of the colostrum analyzed had total IgA antibodies and 77% IgA2 antibodies against *M. tuberculosis*, of these 22.6% and 17.9% had high titers, respectively. Conclusion: Most of the colostrum analyzed from Mexican women contain IgA antibodies against *M. tuberculosis* antigens, and most of these are of the IgA2 subclass, which could potentially protect nurslings from this infection.

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Resumen corto

Interleukin 35 serum levels in different stages of rheumatoid arthritis and its association with acute phase proteins and autoantibodies

Romero-Reynoso, K. S. [1,2] González-Curiel, I. E. [1],
Zapata-Zuñiga, M. [3], Ramos-Remus, C. [3], Rivas-Santiago, B. [1],
Enciso-Moreno, J. A. [1], Castañeda-Delgado, J. E. [4]

Maestría en Ciencias Biomédicas, Universidad Autónoma de Zacatecas.[1] Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México.[2] Hospital Rural No. 51 IMSS Bienestar, Villanueva, Zacatecas y Unidad Académica de Medicina Humana y Ciencias de la Salud, Universidad Autónoma de Zacatecas, México.[3] Instituto de Ciencias Biologicas, Universidad Autónoma de Guadalajara, Zapopan, México.[3] Cátedras CONACyT Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México.[4]

Rheumatoid arthritis is a systemic autoimmune disease that causes pain, inflammation and destruction of the joints. IL-35 is a recently described immunosuppressive and anti-inflammatory cytokine. Various roles of IL-35 in the immune and inflammatory regulation of autoimmune diseases have been described. In this work we determined the relationship among the serum concentrations of IL-35 expressed in different stages of RA pathology and its possible association with the presence of clinical variables and autoantibodies. Four groups of donor samples were collected (n=64): 1) Healthy, 2) CCP+, 3) Patients with early Arthritis, 4) Patients with chronic rheumatoid arthritis according to ACR-AULAR classification. Determinations of IL-35 were made by ELISA according to manufacturer´s instructions. Statistical analysis was carried out in Graph Pad Prism software. No significant differences were identified on the proportions of clinical variables and demographics among groups. A statistically significant difference ($P<0.05$) was identified when analyzing the concentrations of IL-35 in the CCP+ group compared to controls. This was more pronounced than those on early and established RA. Additionally, associations with autoantibodies were identified for both CCP and CarP autoantibodies and other clinically relevant variables. IL-35 has been described as negative regulator of immune response. The role of this cytokine has not been described in the context of autoimmune disease in the clinical setting. Our data suggest an important clinically relevant link among IL-35 and the presence of autoantibodies, particularly CCP. The clinical implications of such results await further experimentation.

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Resumen corto

Analysis of PDZ protein expression in human Macrophages and Dendritic Cells

Rosas-García, J. [1,3,*], Sevilla-Reyes, E. E. [2], Meraz-Ríos, M. A. [3], Santos-Mendoza, T. [1]

[1]Laboratorios de Transcriptómica e Inmunología Molecular y [2]Centro de Investigación en Enfermedades Infecciosas, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas. Tlalpan 4502, C.P. 14080, CDMX, México [3]Departamento de Biomedicina Molecular, Centro de Investigación y de Estudios Avanzados del IPN. Av. Instituto Politécnico Nacional 2508, C.P., 07360, CDMX, México.
*Email: jorg_rosgar@yahoo.com.mx

The PDZ (PSD95, Dlg and ZO-1) genes encode proteins that primarily function as scaffolds of diverse signaling pathways. PDZ proteins are prevalent in almost all biological species, these proteins mediate one of the most common protein-protein interaction found in animals and has been widely studied in epithelial and neural cells. However, their expression and function in immune cells have been poorly studied. Herein, we aimed to assess the transcriptional profiles of 83 PDZ genes in human macrophages (Mϕ) and dendritic cells (DCs) and changes in their relative expression during cell PRR stimulation by RT-qPCR in a microfluidic platform. Significantly distinct PDZ gene transcriptional profiles were identified under different stimulation conditions. Furthermore, a distinct PDZ gene transcriptional signature was found in Mϕ and DCs under the same phagocytic stimuli. Notably, more than 40 PDZ genes had significant changes in expression, with potentially relevant functions in antigen-presenting cells (APCs). We report different transcriptional and translational regulations by RT-qPCR and Western blot respectively in response to diverse PRRs of several PDZ proteins, as well as different localization between Mϕ and DC by immunofluorescence, our results suggest a distinct requirement for PDZ scaffolds in Mϕ and DC signaling pathways activation, which can confer different abilities to both APCs. This work provides the basis for more assessments of PDZ proteins functions in APCs and their role in APC activation mechanisms.

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Resumen corto

Co-Infection between Rhinovirus and Influenza Virus Leads to a Lower Inflammatory and Higher Antiviral Response in A549 Cells

Ruelas-Ruiz, L. C. *[1], Mejía-Torres, M. [1], Gonzalez-Chapa, J. A. [1], Diaz-Caldera, M. A. [1], Martinez-Castilla, A. M. [1], López-López, N. [1], Flores-Torres, A. S. [1], Salinas-Carmona, M. C. [1], Mata-Tijerina, V. L. [2], Rosas-Taraco, A. G.[1]

[1] Departamento de Inmunología, Facultad de Medicina, Universidad Autónoma de Nuevo León. Monterrey, N.L. México. [2] IMSS Centro de Investigación Biomédica del Noreste. Monterrey, N.L. México.
luis.ruelasr@uanl.edu.mx

Epithelial cells play an important role in innate immunity against respiratory viruses. Their response is modulated by environmental factors and past or concomitant infections. In this last scenario, there are reports of viral co-infections cursing with milder disease compared with either of the viral infections alone. However, the immune mechanisms of such phenomena are not fully understood. In this work, we analyzed the biological differences between single and simultaneous infection using human rhinovirus (RV) and influenza virus (IV) in epithelial A549 cells. The results showed that the co-infection both potentiates the protective (antiviral) state in epithelial cells and decreases the synthesis of inflammatory mediators. ICAM-1 (intercellular adhesion molecule-1 and receptor for RV) was increased during coinfection with RV and IV. Sialic acids used for IV to entry to epithelial cells showed lower levels ($P<0.05$). Additionally, the co-infection increased the synthesis of several micro-RNAs involved in the regulation of the inflammatory response (miR146a, miR155). In conclusion, our findings demonstrated that RV infection contributes an antiviral state against IV in the co-infection model with a controlled inflammatory response, important to avoid possible detrimental consequences.

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Resumen corto

Relationship of serum and dietary vitamin D with cardiometabolic risk status in Mexican systemic lupus erythematosus patients: A cross-sectional study

Ruiz-Ballesteros, A. I. [1,2*], Betancourt-Núñez, A. [1,3], Meza-Meza, M. R. [1,2] Rivera-Escoto, M. [1,2], Mora-García, P. E. [1,2], Pesqueda-Cendejas, K. [1,2], Vizmanos, B. [1,3], Parra-Rojas, I. [1, 4], Campos-López, B. [1,2], Montoya-Buelna, M. [1,5], Cerpa-Cruz, S. [6], De la Cruz-Mosso, U. [1,2,3]

[1] Red de Inmunonutrición y Genómica Nutricional en las Enfermedades Autoinmunes, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, México, [2] Instituto de Neurociencias Traslacionales, Departamento de Neurociencias, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, México, [3] Cuerpo Académico UDG-454, Alimentación y Nutrición en el proceso Salud Enfermedad, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara Jalisco, México, [4] Laboratorio de Investigación en Obesidad y Diabetes, Facultad de Ciencias Químico-Biológicas, Universidad Autónoma de Guerrero, Chilpancingo de los Bravo 39087, Guerrero, México, [5] Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara 44340, Jalisco, México, [6] Departamento de Reumatología, O.P.D. Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara 44280, Jalisco, México.
adolfo.ruba@gmail.com

Serum vitamin D as well as vitamin D intake could influence clinical disease activity and cardiometabolic outcomes in systemic lupus erythematosus (SLE). This study aimed to assess the relationship of serum calcidiol and vitamin D intake with cardiometabolic risk in SLE patients and healthy subjects (HS). 183 SLE patients and 175 HS were included in this cross-sectional study. Serum calcidiol was measured using a competitive ELISA assay. Vitamin D intake was assessed by collecting three 24h food records. Dietary patterns (DPs) were identified using principal component analysis (PCA). Cardiometabolic status was analyzed through biochemical measurements and cardiometabolic indexes. Calcidiol deficiency (<20 ng/mL) was associated with 1.7-fold higher risk of excess weight (BMI ≥25 kg/m2) (p=0.03), 2.92-fold higher risk to low HDL-C (HDL-C <40 mg/dL) (p<0.001), and 1.99-fold higher risk to high total cholesterol (TC ≥150 mg/dL) (p=0.02). Inadequate vitamin D intake was associated with 2.27-fold higher risk of presenting non-healthy waist circumference (WC) (>80 cm) (p<0.01), 1.99-fold higher risk of android waist to hip ratio (WHR ≥85) (p=0.02), and 1.83-fold higher risk to excess weight (p=0.02). Non-adherence to a DP rich in vitamin D food sources was associated to higher WC, WHR, triglycerides, and lower HDL-C; furthermore, in HS, non-adherence to the DP rich in vitamin D food sources provided 1.88-fold higher risk to calcidiol deficiency. Calcidiol deficiency, inadequate vitamin D intake as well as non-adherence to a DP rich in vitamin D food sources were related to high cardiometabolic risk in SLE patients and HS.

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Resumen corto

hsa-miR-361-5p regulates cell proliferation in a DLK1 and ARHGEF3 mediated mechanism: evidence from *in vitro* and RA patient samples

Ruiz-Carrillo, J. L. [1,2], Zapata-Zúñiga, M. [3,4], Bernal-Silva, S. [2], Enciso-Moreno J. A. [5], Comas-García, M. [2], López, J. A. [6], Lara-Ramírez, E. E. [1], Rivas-Santiago, B. T. [1], Castañeda-Delgado, J. E. [7]

[1]Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México [2] Centro de Investigación en Ciencias de la Salud y Biomedicina, Universidad Autónoma de San Luis Potosí, San Luis Potosí, México [3] Facultad de Medicina Humana y Ciencias de la Salud, Universidad Autónoma de Zacatecas [4] Hospital Rural 51 IMSS, Villanueva, Zacatecas, México [5] Postgrado en Química Diagnóstica, Facultad de Química, Universidad Autónoma de Querétaro Querétaro, México [6] Laboratorio de microRNAs y Cáncer, Unidad Académica de Ciencias Biológicas, Campus II, Universidad Autónoma de Zacatecas [7] Cátedras CONACYT. Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México.

Rheumatoid arthritis (RA) is a systemic autoimmune disease whose main symptoms include inflammation and destruction of the joints. Clinical symptoms arise from a delayed diagnosis and the inflammatory milieu in the joints. Recent work suggests that miRNA overexpression has an important role in the pathogenesis of RA. In our research group, miR-361-5p was found to be overexpressed in samples from patients with RA. Putative targets of miR-361-5p were identified by bioinformatics analysis, the mRNA levels of such targets were evaluated in a miRNA-transfected cell line and also in RA patient samples and we found an association with disease progression. Bioinformatic analyzes were carried out to determine the target genes with the greatest relationship with miR-361-5p, samples from patients with RA were evaluated by qPCR, the C33-A cell line was transfected with miR-361-5p, qPCR was performed to see the effect of miRNA on its possible targets, the proliferation was evaluated to define a possible role of miR-361-5p. SCAI, ARHGEF3 and DLK1 mRNA were found to be decreased in RA compared to subjects without the disease. In the transfection assays, a difference was found in the expression of DLK1 and ARHGEF3 mRNA in the presence of miR-361-5p in addition to that in the presence of miR-361-5p a greater cell proliferation was found. Our data suggests that miR-361-5p participates in a regulatory pathway associated with increased cell proliferation that is also observed in RA patient samples.

Approved by the ethics committee with registration numbers: CNCI-2015_785_128.

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Resumen corto

Development and immunological evaluation of a prototype multi-epitopic vaccine against SARS-CoV-2 deployed in VLP's of the VP2 protein of human parvovirus B19

Ruíz-Cruz, A. A. *[1], Bustos-Jaimes, I. [2], Jiménez-Chávez, Á. [1,2], Ilhuicatzi-Alvarado, D. [1], Moreno-Fierros, L. [1]

[1]Laboratorio de inmunidad de mucosas, UBIMED, Facultad de estudios superiores Iztacala, Universidad Nacional Autónoma de México, Estado de México, México. [2]Departamento de bioquímica, Facultad de medicina, Universidad Nacional Autónoma de México, Ciudad de México, México.

The severe acute respiratory syndrome caused by the SARS-CoV-2 virus, was and continues being a delicate health problem worldwide since its appearance in 2019, it is a disease that keeps on constant alert the entire population. Currently the number of cases and deaths has decreased significantly, due to vaccination campaigns; however, the potential development of mutations that increase the virulence of the virus is a latent risk.

The present study focuses on the development and immunological evaluation of a multi-epitope prototype vaccine against SARS-CoV-2 called meVP2Spike, which was designed to be expressed on a VLP (virus-like particle) platform. The VLP's used for this prototype are made of the VP2 protein of human parvovirus B19. This VP2 protein has a surface loop in 301-313 aminoacids site; at this region linear epitopes of the SARS-CoV-2 Spike protein were inserted in tandem. The epitopes were selected on basis of being reported as crucial sites for the induction of neutralizing antibodies. The results, show that the VLP's of the meVP2Spike prototype were successfully cloned and overexpressed in E. coli, and, most importantly, they form complete and stable VLP's. These VLP's are currently being tested to evaluate the immunogenicity mice of the C57BL/6 strain, by immunization via the intramuscular route to measure the production of IgG antibodies. While, the antigenicity of VLPs was confirmed by testing the recognition with human serum from Covid-19 convalescent patients. The results indicate this platform is a reliable platform to develop multiepitope SARS-CoV2 vaccine prototypes.

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Resumen corto

Dynamical changes in the expression of GABAergic and purinergic components determine THP-1 monocyte's polarization into proinflammatory macrophages

Ruiz-Rodríguez, V. M. *[1], Torres-González, C. A. [1,2], Salas-Canedo, K. M. [1,2], Pecina-Maza, N. Q. [1,2], Martínez-Leija, E. [2], Portales-Pérez, D. P. [2], Estrada-Sánchez, A. M. [1]

[1] División de Biología Molecular, Laboratorio de Neurobiología, Instituto Potosino de Investigación Científica y Tecnológica (IPICYT), San Luis Potosí, San Luis Potosí, México. [2] Translational and Molecular Medicine Laboratory, Research Center for Health Sciences and Biomedicine, Autonomous University of San Luis Potosí, San Luis Potosí, Mexico. victor.ruiz@ipicyt.edu.mx

Monocyte-derived macrophages, phagocytic cells with pro-inflammatory or anti-inflammatory phenotypes, are a key component of innate immunity. The mechanisms of differentiation and polarization of monocytes to macrophages are regulated by environmental signals, including gamma-aminobutyric acid (GABA) and adenosine triphosphate (ATP), two known neurotransmitters. Although monocytes and macrophages express GABAergic and purinergic receptors, it is unknown whether changes in their expression occur during activation, differentiation, and polarization. In the present study, we evaluated the expression levels of GABAergic and purinergic signaling components in the THP-1 monocyte cell line and the changes during activation, differentiation, and polarization induced by lipopolysaccharide (LPS), phorbol 12-myristate 13-acetate (PMA) or PMA + LPS combination, respectively. RNA was extracted from each condition and expression levels were determined by RT-qPCR. Our results showed that activated monocytes are characterized by the expression of GABA transporter 2 (GAT2), glutamic acid decarboxylase (GAD)-67, P2X4, and P2X7. After differentiation, the β2 subunit of the A-type GABA receptor (GABA-AR) expression increased, and P2X1 and P2X1del were reduced. On the contrary, macrophage M1 showed a marked reduction in the α4 subunit of GABA-AR and GAD67, while P2X4 was overexpressed. Our results indicate that changes in the expression of GABAergic and purinergic components occur during the transition from monocytes to macrophages. Since GABA and ATP are two neurotransmitters, our results suggest that monocytes and macrophages respond to neurotransmitter-induced stimulation. This may represent a path of interaction between the nervous and immune systems and contribute to the development of inflammation and neuroinflammation.

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Resumen corto

Expression of mBAFF, BR3, TACI, and BCMA on CXCR5+, CD11c- and CXCR5-, CD11c+ B cells subpopulations in SLE patients

Sagrero-Fabela, N. [1], Álvarez-Gómez, J. A. [2], Román-Fernández, I. V. [3], Ortíz-Lazareno, P. C. [4], Salazar-Camarena, D. C. [5], Muñoz-Valle, J. F. [3], Marín-Rosales, M. [5,6], Menchaca-Tapia, V. M. [2], Palafox-Sánchez, C. A.[3,5].

[1]Doctorado en Ciencias Biomédicas (DCB), Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Doctorado en Ciencias en Biología Molecular en Medicina (DCBMM), Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [3]Instituto de Investigación en Ciencias Biomédicas (IICB), Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [4]División de Inmunología, Centro de Investigación Biomédica de Occidente (CIBO), Instituto Mexicano del Seguro Social (IMSS), Guadalajara, Jalisco, México. [5]Grupo de Inmunología Molecular, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [6]Hospital General de Occidente, Secretaría de Salud Jalisco, Guadalajara, Jalisco, México.

Systemic lupus erythematosus (SLE) is an autoimmune disease characterized by the production of autoantibodies. Some B cells, such as double-negative 2 (DN2) and naïve activated (aNAV) B cells that are phenotypically recognized as CXCR5- and CD11c+, have been described as precursors to Antibody-Secreting cells (ASCs) that develop in extrafollicular pathways and have the potential to produce high amounts of autoantibodies. These cells are typically stimulated by IL-21 and IFNγ. Nevertheless, other cytokines, such as BAFF, could also play an important role in its stimulation, as therapy with Belimumab (an anti-BAFF drug) has been shown to deplete CD11c+ B cells. To determine the frequency of CXCR5+CD11c- and CXCR5-CD11c+ B cell subpopulations and their expression of mBAFF, BAFFR, TACI, and BCMA of SLE patients.

45 SLE patients and 15 healthy subjects (HS) were included. Peripheral blood mononuclear cells (PBMCs) were collected and stained by flow cytometry. The frequency of the different B cell subtypes stratified by CD27 and IgD (DN, Naïve, SWM, and USM) were compared between SLE patients and HS. These subpopulations were divided into CXCR5+CD11c- (DN1, rNAV, SWM+ and USM+) and CXCR5-CD11c+ (DN2, aNAV, SWM- and USM-). Some molecules of the BAFF system were increased in SLE patients compared with HS; mBAFF+ (DN, DN1, Naïve, rNAV, SWM, SWM+, USM and USM+), TACI+ (rNAV), and BCMA+ (rNAV, SWM+). In contrast, some molecules were decreased; BAFFR+ (DN, SWM) and TACI+ (DN, DN2). The molecules of the BAFF system have an important role in CD11c+ B cell subpopulations.

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Resumen corto

Association of circulating T follicular helper (cTfh) and T peripheral helper (Tph) cells with the B cell activating factor system in Systemic Lupus Erythematosus

Sagrero-Fabela, N.[1], Ortíz-Lazareno, P.C.[2], Salazar-Camarena, D.C.[3], Cruz, A.[4], Cerpa-Cruz, S.[5], Muñoz-Valle, J.F.[4], Marín-Rosales, M.[3,6], Alvarez-Gómez, J.A.[7], Palafox-Sánchez, C.A[3,4].

[1]Doctorado en Ciencias Biomédicas (DCB), Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]División de Inmunología, Centro de Investigación Biomédica de Occidente (CIBO), Instituto Mexicano del Seguro Social (IMSS), Guadalajara, Jalisco, México. [3]Grupo de Inmunología Molecular, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [4]Instituto de Investigación en Ciencias Biomédicas (IICB), Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [5]Departamento de Reumatología, Hospital Civil de Guadalajara Fray Antonio Alcalde, Guadalajara, Jalisco, México. [6]Hospital General de Occidente, Secretaría de Salud Jalisco, Guadalajara, Jalisco, México.

Circulating T follicular helper (cTfh) and T peripheral helper (Tph) cells are shown to be higher in systemic lupus erythematosus (SLE) patients and have been involved in promoting extrafollicular B cell responses. However, a possible association with the B cell activating factor (BAFF) system, has not been investigated. To evaluate the association of cTfh and Tph subpopulation with the BAFF system in SLE patients. 43 SLE patients and 12 healthy subjects (HS) were included. The identification of cTfh ($CD4^+CXCR5^+PD\text{-}1^+$), Tph ($CD4^+CXCR5^-PD\text{-}1^+$) cells and the expression of bound membrane BAFF (mBAFF), BAFFR, TACI, BCMA, as well as intracellular IL-21, was performed by flow cytometry. Data are shown as median and interquartile range (IQR). *p* values≤0.05 were considered significant. SLE patients showed a significantly increased percentage of cTfh and Tph cells compared with HS. cTfh as well as Tph cells from SLE patients had higher intracellular IL-21 expression than HS. We found a low expression of mBAFF and their receptors TACI and BCMA on cTfh and Tph cells of SLE and HS. SLE patients with clearly active disease showed decreased expression of BAFFR than patients with mildly active/ nonactive disease, on both cTfh and Tph subpopulations. This study demonstrates the expression of BAFFR on cTfh and Tph subpopulations and its association with disease activity in SLE patients. In addition to the key role that BAFF plays in B cell development, our results suggest an important but unexplored role of the BAFF/ BAFFR axis on T cell subpopulations in the autoimmunity context.

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Resumen corto

Immunomodulatory effect of cathelicidin LL-37 and its derived peptides in the prostate epithelium during the interaction with *Trichomonas vaginalis*

Salazar-Capistran, N.*[1], Reyes-Cortes, R.[2], Alva-Murillo, P.N.[1]

[1]Laboratorio de Inmunomicrobiología Molecular, Departamento de Biología, División de Ciencias Naturales y Exactas de la Universidad de Guanajuato, Ciudad de Guanajuato, Gto., México. [2]Laboratorio de Biología del parasitismo, Departamento de Biología, División de Ciencias Naturales y Exactas de la Universidad de Guanajuato, Ciudad de Guanajuato, Gto.
*E-mail: n.salazarcapistran@ugto.mx

Trichomonas vaginalis is the etiological agent of trichomoniasis, the most common non-viral sexually transmitted disease in the world that affects both men and women. More than 75% of men are asymptomatic and can transmit the disease. In addition, it has been shown that *T. vaginalis* induce an inflammatory response in pro, which increases the risk of acquiring HIV and prostate cancer. The 5-nitroimidazoles are the treatments for trichomoniasis; however, the number of drug-resistant strains have been increased. Thus, antimicrobial peptides (PAM) could be an alternative therapy against *T. vaginalis*. The human cathelicidin LL-37 and its derivative FK-13-NH_2 exert trichomonacidal activity, but whether they regulate the innate immune response of prostate epithelial cells infected with *T. vaginalis* is unknown, which was the aim of this work. In this study, the CDC-085 *T. vaginalis* strain (resistant to metronidazole) was used. The effect of the peptides on the viability of the prostate epithelial cell line (RWPE-1) was evaluated by the MTT assay. The results indicated that LL-37 reduces cell viability in a concentration-dependent manner, while FK-13-NH_2 does not affect it. The nitric oxide (NO) production was measured by the Griess reaction. *T. vaginalis* slightly increased NO production in RWPE-1 cells, and FK-13-NH_2 decreased the effect of the parasite. Our results suggest that the peptides can act as immunomodulators in the host-pathogen interaction, regarding NO production.

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Resumen corto

Plasmodium yoelii 17XL infection promotes high IL-4 and IL-10 and low IFN-γ levels by Mif $^{-/-}$ spleen cells and high levels of IL-12 and IL-10 and decreases in TNF-α by Mif $^{-/-}$ macrophages

Salazar-Castañón, V.H.*[1], Nolasco-Pérez, T.J.[1], Legorreta-Herrera, M.[1], Juárez-Avelar, I.[2], Rodríguez-Sosa, M.[2]

[1]Laboratorio de Inmunología Molecular. Unidad de Investigación Multidisciplinaria. Facultad de Estudios Superiores Zaragoza, UNAM. Batalla 5 de mayo, Esq. Fuerte de Loreto, Iztapalapa. Ciudad de México, México. [2]Laboratorio de Inmunidad Innata, Unidad de Investigación en Biomedicina, Facultad de Estudios Superiores Iztacala, UNAM, Tlalnepantla de Baz, Estado de México, México.
*E-mail: mestilom@hotmail.com

Malaria remains one of the most common lethal parasitic diseases globally, but the mechanism responsible for the high mortality remains unknown. Host proinflammatory cytokines have been shown to be important. Macrophage migration inhibitory factor (MIF) is a cytokine involved as an important regulator of immune and inflammatory responses and it participates in the protection or the pathogenesis of *Plasmodium* infection. This study aimed to understand the effect of MIF on the immune response and pathogenesis of *Plasmodium* infection. Wild-type (Wt) and MIF knockout (*Mif* $^{-/-}$) mice were infected with 1×10^3 *Plasmodium yoelii* (*Py*) 17XL-parasitized red blood cells. We evaluated parasitemia, survival rates, parameters related to the pathology, spleen-cell proliferation, and the cytokine production in splenocyte and macrophage cultures. *Py*17XL-infected Wt mice died 11 days postinfection, while *Mif* $^{-/-}$ mice increased survival at day 11th up to 58%. The increased survival rate in *Mif* $^{-/-}$ mice was associated with lower parasitemia, which delayed the development of anemia and prevented splenomegaly, as a result of a mixed Th1/Th2 cytokine profile, as evidenced by high levels IL-10 and IL-12 and reduced levels of TNF-α by macrophages from *Mif* $^{-/-}$ mice compared to *Py*17XL-infected Wt mice. And spleen cells showed a significant increase in proliferative response, high levels of IL-4 and IL-10, and reduced IFN-γ compared to *Py* 17XL-infected WT mice. Together, these data indicate that MIF has a key role as a mediator of cytokines involved in the immune response associated with pathogenesis and host lethality in *Plasmodium* infection. This work was parcially financed by PAPIIT IN228620.

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Resumen corto

Supplemented Database of Neutralizing Monoclonal Antibodies Against SARS-CoV-2 for Machine Learning Applications

Salazar-Hugalde, H.L.*[1,2], González-Sánchez, H.M.[1,3], Tellez-Sosa, J.M.[1], Martínez-Barnetche, J.[1], Godoy-Lozano, E.E.[1]

[1] Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México. [2] Licenciatura en Biología Molecular de la Universidad Autónoma Metropolitana (UAM), Ciudad de México, CDMX, México. [3] Cátedra CONACYT-Centro de Investigación sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, México. *E-mail: heidi.salazar@cua.uam.mx

A new virus, SARS-CoV-2, emerged and caused a pandemic that has resulted in 333,327 deaths in Mexico as of March 21, 2023. The etiological agent of coronavirus disease (COVID-19) has spread worldwide at an unprecedented speed, posing a global challenge due to the emergence of new viral variants. To combat the pandemic, researchers have found that neutralizing monoclonal antibodies (mAbs) against SARS-CoV-2 have the potential for both therapeutic and prophylactic applications, aiding in the design and development of vaccines. Additionally, researchers from the Protein Informatics Group at the University of Oxford created a database called “The Coronavirus Antibody Database (CovAbDab)” with information on antibodies and nanoantibodies that bind to different coronaviruses. We selected 3550 antibodies from the CovAbDab database that react against the S protein and the RBD domain. A systematic review of the original data source was performed to add neutralizing characteristics (IC50), antibody affinity (KD), and additional useful information for the supplemented database, which will serve as input for generating models for machine learning. The new database was systematically reviewed to add neutralizing characteristics, antibody affinity, and additional useful information. The IC50 neutralization values were found between 0.0001 and 10 mg/mL and affinity values between 0.001 and 15.8 nM for the most neutralizing and high-affinity antibodies. Machine learning will allow researchers to identify characteristic signatures of the antibody response to SARS-CoV-2 infection, guiding the *in silico* identification of potentially neutralizing monoclonal antibodies. This supplemented database will serve as input to generate machine learning models for combating the pandemic.

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Resumen corto

TGF-β receptor III (TβRIII) is preferentially upregulated on Th17 cells compared to Th1 effector cells.

Salgado-López, A.*[2], Ortega-Francisco, S.[2,3], Duesman, S.[1], Acevedo-Domínguez, N.[2], Montes de Oca-Lagunas, S.[2], Olguín-Alor, R.[3], Raman, C.[1], Soldevila, G.[2,3]

[1]Department of Dermatology, University of Alabama at Birmingham, United States; University of Alabama at Birmingham, Alabama, USA.[2] Department of Immunology and [3] National Laboratory of Flow Cytometry , Biomedical Research Institute, UNAM,Mexico City,Mexico.
*E-mail: Adriancitourive@ciencias.unam.mx

TβRIII is a co-receptor of TGFβ that is differentially expressed on naive/memory CD4+ T cells. We have recently shown that TβRIII is upregulated on activated T cells and downregulated on Foxp3+ Treg cells, suggesting that it may be involved in the regulation of T cell mediated immune responses. Here we evaluated the expression of TβRIII on CD4+ T cells by flow cytometry under Th1 and Th17 skewing conditions.To address this objective, we isolated CD4+ T cells from C57/BL6J mice splenocytes by magnetic sorting and cultured them under Th1 (IL-12), Th17 (IL-6, IL-23, TGF-β, anti-IFNγ) or non-skewing conditions after anti-CD3/CD28 stimulation. We observed that the level of TβRIII was highly increased on CD4+ T cells (RI 1.60+/-0.19) under Th17 conditions, while it was moderately increased (RI 1.19+/-0.28) under Th1 conditions, compared to non-skewing cultures. Interestingly, when we analyzed TβRIII expression on cytokine-producing T cells this coreceptor was only significantly increased in IL-17+ cells but not on IFNγ+ T cells compared to their non-skewed counterparts. In conclusion, the differential modulation of TβRIII on these effector subsets, suggests that TβRIII may play a more crucial role in Th17 mediated effector functions rather than in Th1 responses.

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Resumen corto

TIM-3 and PD-1 exhaustion markers on T lymphocytes in an experimental actinomycetoma model

Salinas-Carmona, M.C.[1], Vázquez-Marmolejo, A.V.[1], Mejía-Torres, M.G.[1], Duarte-Mata, D.I.[1], Reyes-Carrillo, J.[1], Zúñiga-González, M.A.*[1]

[1] Servicio de Inmunología, Facultad de Medicina y Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León. *E-mail: alezgzz@hotmail.com

In Mexico, *Nocardia brasiliensis* is responsible for 85% of the cases of actinomycetoma, an infectious disease of an inflammatory, destructive and disabling nature. The immunological events that occur during *N. brasiliensis* infection have not yet been elucidated in humans or experimental models. PD-1 and TIM-3 belong to the family of molecules that mediate the negative regulation of T cells; the increased and sustained co-expression of these markers has been widely related to the depleted T cell phenotype. In the present work, Balb/c mice infected in the foot pad with *N. brasiliensis* were used and the kinetics of expression of these markers in T lymphocytes was evaluated by flow cytometry. Lymphoid organs such as popliteal node and spleen and the infected tissue were studied during the acute and chronic phase of the infection. The results obtained show that the coexpression of PD-1 and TIM-3 increased in T lymphocytes in the chronic phase of the infection compared to the acute phase, occurring both in the studied lymphoid organs and in the infected tissue; therefore, it is suggested that the expression of both markers during the chronic phase could be associated with the depleted T cell phenotype, thus contributing to the persistence of the infection. The biological blockade of depletion markers has a therapeutic potential in patients.

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Resumen corto

Identification of immunodominant antigens of *Madurella mycetomatis* by antibodies from mice infected or immunized with this fungus

Salinas-Carmona, M.C.[1], Vázquez-Marmolejo, A.V.[1], Vera-Cabrera, L.[2], Solís-Marfil, P.A.[1], Espinoza-Martínez, P.E.*[1]

[1] Servicio de Inmunología, Facultad de Medicina y Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León. [2] Servicio de Dermatología, Facultad de Medicina y Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León.
*E-mail: espinoza.9919@outlook.com

Madurella mycetomatis is the most frequent etiological agent of eumycetoma, a chronic infectious disease that is acquired by traumatic inoculation, mainly in the lower limbs. It usually affects young people between the ages of 15 and 30 and its treatment is complicated, involving surgical approach, chronic use of antifungals and can often lead to amputation of the affected limb. Currently there is expensive and lack of accessible immunological test efective for the diagnosis of this disease. For all the above reasons, this work has the purpose of obtaining protein antigens from the cellular extract of *M. mycetomatis*, which can be used in the design of an immunodiagnostic test. The purpose of this work was to identify the immunodominant antigens of *M. mycetomatis* recognized by antibodies in infected or immunized mice. 27 8-12 week old female BALB/C mice were infected with a suspension of *M. mycetomatis* using 3 different inoculation routes: intraperitoneal, dorsal subcutaneous and foot pad. Crude cellular extract of *M. mycetomatis*, protein antigens were analyzed on an SDS-PAGE gel, which were recognized by serum of mice infected with *M. mycetomatis* or immunized with the crude cellular extract, using the Western blot technique. The immunodominant antigens of ≈ 95 kDa and 40 k-Da were identified, which are recognized by antibodies in mice infected with *M. mycetomatis* or immunized with the crude cell extract. The identification of these antigens by será from patients with eumycetoma has diagnostic potential.

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Resumen corto

Kinetics of specific immunoglobulins against *Anaplasma marginale* in susceptible cattle

Salinas-Estrella, E.*[1], Cobaxin-Cárdenas, M.E. [1], Amaro-Estrada, I. [1], Preciado-de la Torre, J.F. [1], Rodríguez-Camarillo, S.D. [1]

[1]Centro Nacional de Investigación Disciplinaria en Salud Animal e Inocuidad (CENID-SAI), Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP), Jiutepec, Morelos.

*E-mail: salinas.elizabeth@inifap.gob.mx

The immune response to bovine anaplasmosis is a determining factor in the evolution of this pathogenesis. Detection of immunoprotected animals will contribute to guarantee mobilization of improved cattle to enzootic zones of bovine anaplasmosis, without economic losses caused by the disease. The objective of this work was to evaluate the evolution of the bovine immune response to infection with different strains of *A. marginale* through the detection of specific immunoglobulins. Monitoring of susceptible cattle inoculated with different strains of *A. marginale* with calculation of the percentage of infected erythrocytes (PIE), rectal temperature (RT) and agglomerated cell volume (ACV). Infection was confirmed by PCR for the *msp5* gene and index of positivity (IP) by means of the indirect enzyme-linked immunosorbent assay PAdianaVET. Oxytetracyclines administration at a dose of 20 mg/kg IM when clinical status indicated. Inoculation with some *A. marginale* strains and isolates induced high antibody production represented by the IP values, which did not ensure control of the bacterium by the immune system due to the subsequent presentation of several additional rickettsemia cycles. Maximum IP for one isolate was never higher than 1, but did not presented clinical signs of disease. However, it is not possible to ensure that the antibody titer corresponds to protection against the disease with these data, since it is necessary to determine differences in the titers and isotype ratios of specific antibodies and correlate it with the presentation or absence of clinical signs when challenged in field conditions.

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Resumen corto

Shock waves for transfection of human monocyte cell line THP-1

San Román Bernardette, Fernández, F., Loske Achim, M., López-Marín, L. M.

Centro de Física Aplicada y Tecnología Avanzada, Universidad Nacional Autónoma de México, Boulevard Juriquilla No. 3001, Querétaro, México, C.P. 76230. E-mail: sanromanb@comunidad.unam.mx

Cells of the innate immune system, such as monocytes and macrophages, recently gained interest to develop cell therapies. As immune effector cells, macrophages play key roles in maintaining homeostasis and responding to pathological conditions. Their use after genetic modification could present great potential; however, these cells are hard to transfect, and only viral approaches have been approved for clinical settings. The application of shock waves (SW), as used in medicine to pulverize urinary calculi, recently has been reported as a physical transfection method, that induces transient cell membrane permeability by cavitation effects. Their utility to transform recalcitrant fungal or plant cells has been already demonstrated. This project aims to transfect THP-1 monocytes using SW, to record reporter transgene expression in monocyte-derived macrophages. Treatments varying the number of SW were performed using a Piezoson 100 Plus equipment (Richard Wolf ™) and the naked plasmid *pCX::GFP-GPI2*. Cells were analyzed for viability and GFP expression by flow cytometry and confocal microscopy. Results showed that 32, 64, and 128 SW, having a positive peak pressure of 18.1 MPa, were associated with cell mortalities from 1 to 18% in a dose-dependent manner. Moreover, our method proved to induce the expression of GFP, in contrast to a commercially available chemical method, which resulted in no transfection. Other scenarios, such as the use of gene carriers, must be explored to improve transfection efficiencies; however, our data reveals SW as a promising method for the genetic modification of monocytes.

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Resumen corto

In vivo analisis of DEC-205^{+} DC in Peyer's patches and mesenteric lymph nodes of BALB/c mice orally infected with *Brucella abortus* 2308

Sánchez-Argáez, A.B.*[1], Moreno-Lafont, M.C.[1],
Flores-Romo, L.[†2], López-Santiago, R.[1]

[1]Departamento de Inmunología. Escuela Nacional de Ciencias Biológicas. Instituto Politécnico Nacional. Prol. de Carpio y Plan de Ayala s/n. Del. Miguel Hidalgo. CP 11340. Ciudad de México. México. [2]Departamento de Biología Celular. Centro de Investigación y de Estudios Avanzados (CINVESTAV). Instituto Politécnico Nacional. Av. IPN No. 2508. Del. Gustavo A. Madero. CP 07360. Ciudad de México. México
*E-mail: sanchezargaezana@gmail.com

Brucellosis is mainly acquired as a food-borne zoonosis. Due to the natural route of entry, Peyer's patches (PP) and mesenteric lymph nodes (MLN), are expected to be involved. In these tissues reside different subpopulations of dendritic cells (DC), responsible for capturing, processing, and presenting antigens. Intestinal DCs express DEC-205, which enables them to present exogenous antigens to CD8^{+} T lymphocytes and thus triggering the cytotoxic responses required to eliminate intracellular microorganisms, such as Brucella. In the present work, mice were inoculated orally with 5x10^{6} CFU of *Brucella abortus* 2308. Then, mice were sacrificed at different times to recover the bacteria from PP and MLN in selective broth. The phenotype analysis showed a significant increase of CD103^{+}CD8α^{-}DEC-205^{+} DCs in the MLN at 4 weeks (P<0.001), and a tendency to increase at 48 h and 14 days. CD103^{+}CD11b^{-}DEC-205^{+} DCs increased significantly at 48 h (P<0.01), 14 days (P<0.01) and 4 weeks (P<0.01). However, DCs did not present changes in the expression of co-stimulation molecules compared to the control group. On the contrary, CD103^{+}CD8α^{+}DEC-205^{+} DCs decrease significantly (P<0.01) at 4 weeks. CD103^{-}CD8α^{+}DEC-205^{+} DCs decreased at 48 h (P<0.001) and 14 days (P<0.05); CD103^{-}CD8α^{-}DEC-205^{+} DCs decrease significantly during the first 48 h (P<0.01) and at 14 days. In the PP only two populations were significantly decreased during the infection, the DC CD103^{+}CD8α^{-}DEC-205^{+} DCs and CD103^{+}CD11b^{-}DEC-205^{+} DCs. This non-activation phenotype could be associated to brucella´s evasive mechanisms and infection.

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Resumen corto

MIF increase the development of the skin lesion in a *Leismania mexicana* infection in a murine model

Sánchez-Arteaga, D.A.[1]*, Mendoza-Sánchez, D.B. [1], Andrade-Meza, U. [1], Ortiz-Sánchez, B.J. [1], Juárez-Avelar, I. [1], Rodríguez-Sosa, M. [1]

[1]Unidad de Biomedicina Laboratorio de Inmunología Innata, Facultad de Estudios Superiores Iztacala-UNAM, Tlalnepantla, México.

Leishmaniasis in Mexico is mainly caused by the protozoan parasite Leishmania mexicana (L. mexicana), which affects the skin and mucous membranes causing ulcerative lesions. Several proinflammatory molecules are involved in the immune response against intracellular parasites, including macrophage migration inhibitory factor (MIF). However, recent evidence suggests that MIF could be responsible for the lesion prevalence in L. Mexicana infection. To clarify the role of MIF during infection with *L. mexicana*, MIF-deficient (*Mif-/-*) and wild-type (*Mif+/+*) ♂ and ♀ BALB/c mice were infected with $2x10^6$ *L. mexicana* promastigotes. Parasitemia was determined by limiting dilution assay and histology at different times. Cytokines and nitric oxide (NO-) were quantified in serum and supernatant from culture of lymph node cells. Although, the *Mif-/-*♂ mice developed parasite load, these showed significantly less lesion and lower concentration of NO- in serum and lymph node cells compared to *Mif-/-*♀, *Mif+/+*♂ and *Mif-/-* ♀ mice. Importantly, *Mif+/+*♂ and *Mif-/-*♀ groups developed larger lesions associated with high inflammatory cytokines in serum and supernatant from lymph node cells. In conclu|sion, these results suggest that MIF does not increase the parasite load, but it does positively influence the production of proinflammatory cytokines and NO, which favors the growth of the lesion caused by the infection.

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Resumen corto

Host immunoglobulins in excreted/secreted helminth products recognize colorectal cancer-associated proteins

Sánchez-Barrera, C.A.[*1], Mendoza-Rodríguez, M.G.[1], Fernández-Muñoz, K.V.[1,2], Terrazas-Valdés, L.I.[1,3]

[1]Unidad de Biomedicina, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla de Baz, Estado de México, México. [2]Departamento de Biomedicina Molecular, Centro de investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, México. [3]Laboratorio Nacional en Salud, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla de Baz, Estado de México.
*E-mail: angel.casb@hotmail.com

Helminth parasites evade host´s immune response and survive for a long time without killing the host. Modulation of the immune response by helminths is mediated by excreted/secreted products (ES). Although helminth infections are a public health problem, ES helminth products are currently analyzed as possible therapeutic alternatives in several inflammatory diseases including colitis-associated colon cancer (CAC). In a mouse model of CAC, *Taenia crassiceps* excreted/secreted products (TcES) reduced tumor formation trough inhibition of NF-kB and STAT3 phosphorylation. In addition, TcES also inhibited NF-kB phosphorylation in RKO human colon cancer cells. However, the interaction between TcES or other helminth products and human colon cancer cells is poorly understood. This work analyzes TcES composition and its interaction with RKO and HCT116 human colon cancer cell lines. TcES composition was first analyzed by SDS-PAGE; here we found protein bands corresponding to host immunoglobulin molecular weight (50 kDa); western blot confirmed the presence of host IgG in TcES. Then we demonstrated inhibition of proliferation and migration in both cell lines after exposure to TcES. Fluorescence microscopy showed TcES biding to HCT116 and RKO cell membrane. Finally, we demonstrated that immunoglobulins in TcES recognize tumoral proteins of RKO and HCT116 cell lines, as well as non-cancer molecules in CCD-18-CO cell line. All together these data suggest that host immunoglobulins in TcES could bind to colorectal cancer cells and inhibit cell proliferation and migration.

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Resumen corto

IL-17RA promotes tumorigenesis in a murine model of ovarian cancer

Sánchez-Bello, M.E.*[1], Martínez-Vargas, I.U.[1],
Osorio-Trujillo, C.[1], Flores-García, Y.[2], Talamás-Rohana, P.[1]

[1]Departamento de Infectómica y Patogénesis Molecular, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, México. [2] Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Malaria Research Institute, Johns Hopkins University, Baltimore, Maryland, United States of America.
*E-mail: maria.sanchezb@cinvestav.mx

IL-17A is a pleiotropic cytokine involved in inflammation, autoimmunity and cancer. This cytokine is produced by several immune populations in various types of cancers and has been associated with both anti-tumor and pro-tumor functions. This cytokine signals via IL-17RA and RC receptors, which are expressed in various cell lineages, including ovarian tumor cells. Although several works have demonstrated the role of IL-17A *in vitro* and *in vivo* cancer models, the function of the IL-17RA receptor remains poorly studied. In this work, we found that IL-17A/F homodimers or heterodimers did not produce a significant effect on proliferation, but showed effects in chemoresistance and migration of ID8 cells, acting as anti-tumoral *in vitro*. However, *in vivo*, the absence of the IL-17RA receptor reduced tumor development and the production of ascites, due to a reduction in ERK1/2 activation, leading to an increase in overall survival. These results suggest that IL-17RA is necessary for tumor development. Overall, we demonstrate that IL-17RA promotes tumor development in the ID8 murine model of ovarian cancer *in vivo*.

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Resumen corto

Optimization of extracellular vesicles (EV) isolation from human plasma as potential source of exosomes for nanoscale immunodetection by flow cytometry

Sánchez-González, M.[1,2,3], Lopez-Pacheco, C.[2,3], Herrera-Noreña, S.[2], Vergara, I.[2], Soldevila, G.[2,3], Ortega-Soto, E.[2]

[1]Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad de México, México. [2]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Ciudad de México, México. [3]Laboratorio Nacional de Citometría de Flujo, Instituto de Investigaciones Biomédicas, Ciudad de México.

Extracellular vesicles (EVs) play an important role in physiological and pathological processes. They carry specific molecules that provide biogenesis information and the cellular state, making them useful tools as biomarkers. Nano flow cytometry (nanoFC) offers advantages over other conventional methodologies for EVs analysis; this technique requires a highly purified sample. Hence, it is imperative to optimize a methodology to purify EVs for functional analysis of immune cells and its characterization by nanoFC. Here used a combination of ultrafiltration (UF) and size exclusion chromatography (SEC) as an alternative for the enrichment of EVs from human plasma. EVs obtained from SEC fractions of the plasma from 7 individuals were analyzed by western blot for the expression of exosomal markers, including tetraspanins CD63 and CD9, the intracellular proteins TSG101 and proteins characteristic of microvesicles, such as Calnexin. In addition, we analyzed albumin and lipoproteins APO-A1 and APO-E1, as potential contaminating proteins that are abundant in plasma. Concentration and EVs size in each fractions were evaluated by Nanosight. We were able to identify specific fractions enriched with exosomal markers, but with lower potential contamination, that may be considered optimal for further nanoFC characterization. Furthermore, the enrichment of exosome-like EVs was confirmed by nanoFC, showing a significant increase in the expression levels of CD9 in comparison with the rest of the fractions. In conclusion, our results suggest that nanoFC will be an important tool for exosomes analysis for the first step in a better understanding of exosomes subpopulations and their relationship functional activities in cells.

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Resumen corto

Expression analysis of SLAM-Family Receptors: 2B4, NTB-A and CRACC in Nk cells from pediatric patients with acute lymphoblastic leukemia.

Sánchez-Herrera, J. [1,2*], Nuñez-Enriquez, J.C. [3], Valenzuela-Vázquez, L. [1,2], Mancilla-Herrera, I. [4], Mejía-Aranguré, J.M. [5,6,7], Cruz-Munoz, M.E. [1]

[1]Facultad de Medicina, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México. [2]Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México. [3]Unidad de Investigación Médica en Epidemiología Clínica, Unidad Médica de Alta Especialidad (UMAE) Hospital de Pediatría, Centro Médico Nacional (CMN) "Siglo XXI", Instituto Mexicano del Seguro Social (IMSS), Ciudad de México, México. [4]Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología, Ciudad de México, México. [5]Unidad de Investigación Médica en Genética Humana, Unidad Médica de Alta Especialidad (UMAE) Hospital de Pediatría, Centro Médico Nacional (CMN) "Siglo XXI", Instituto Mexicano del Seguro Social (IMSS), Ciudad de México, México. [6]Laboratorio de Genómica del Cáncer, Instituto Nacional de Medicina Genómica, Ciudad de México, México. [7]Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, México.
*E-mail: jacqueline.sanchezhr@uaem.edu.mx

NK cells play a critical role in the immune response against viral infections and cancer cells. The effector functions of NK cells are regulated by a balance between signals from activation or inhibition receptors. The SLAM family receptors, including 2B4, NTB-A, and CRACC, have recently been identified as important regulators of NK cell function. Hematological cancer patients often exhibit impaired NK cell function due to abnormal expression of these receptors, resulting in a deficiency in NK cell cytotoxic capacity. Acute lymphoblastic leukemia (ALL) is the most common pediatric cancer worldwide, and NK cells have emerged as an important target for developing immunotherapies for this disease. Despite the progress made in the study of NK cells and ALL, there is still a significant amount of information yet to be discovered regarding the behavior of NK cells at the beginning stages of ALL. This study investigates the phenotype and function of NK cells in pediatric patients diagnosed with ALL, focusing on members of the SLAM family receptors (2B4, NTB-A, CRACC). The results indicate that NK cells in ALL patients exhibit an altered phenotype of 2B4, NTB-A, CRACC with a considerable decrease in overall expression compared to age-matched controls. The dominant phenotype among patients was NK cells with concurrent reduced expression. Furthermore, the NK cells from patients demonstrated a significant reduction in their ability to sustain antibody-dependent cellular cytotoxicity (ADCC). These findings show an association between an abnormal expression of SLAM family receptors in NK cells and the phenomenon of leukemia during childhood.

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Resumen corto

Effect of epicatechin encapsulated in a MIL-100 (Fe) matrix on stem cells derived from the AGS gastric adenocarcinoma cell line

Sánchez-Herrera, D.O.*[1,2], Ortiz-Sánchez, E.[2], Flores-Moreno, J.L.[3], García Pérez, B.E.[1]

[1]Laboratorio de Microbiología General, Escuela Nacional de Ciencias Biológicas del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Laboratorio de células troncales cancerosas de tumores sólidos, Instituto Nacional de Cancerología, Ciudad de México, CDMX,México. [3]Departamento de Ciencias Básicas, Universidad Autónoma de México Unidad Azcapotzalco, Ciudad de México, CDMX, México. *E-mail: davids.herrera@gmail.com

Gastric cancer (GC) is the fifth leading cause of cancer mortality worldwide and one of the most aggressive known cancer stem cells (CTCs) are currently known to contribute to the aggressiveness, invasiveness and chemo resistance of this type of cancer. Epicatechin (EC) is a flavanol with anticancer properties whose use is largely limited by its low bioavailability. Today, the use of MIL-100 (Fe) nanoparticles has attracted attention due to its great versatility, high degree of biocompatibility and low toxicity, which makes them ideal as pharmacological carriers. The present work aims to establish the effects of EC encapsulated in MIL-100 (Fe) nanoparticles on a culture of gastric adenocarcinoma cells (AGS) in 2D models and on cancer stem cells (CSC) enriched from the formation of tumor spheres in 3D cultures for 72 h under ultra-low adherence conditions, as well as the determination of CD44, CD24, CD326, CD54 and PD-L1 expression in the CSC population. Encapsulated EC reduces cell capacity and induces a higher percentage of apoptosis than free EC in 2D models. On the other hand, when treating the AGS cells with free EC and encapsulated EC under conditions of last adherence, the percentage of CSC [CD44+ CD24+] as well as invasive CSC [CD54+ CD326+] was reduced. Also, the formation and growth of the tumor sphere showed a significant decrease in the expression of CD44, CD326 and PD-L1. In conclusion, encapsulated EC induces a greater apoptotic effect than free EC on 2D cultures of gastric cancer cells, decreasing the expression of CSC-enriched functional markers and preventing tumor formation as well as their number.

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Resumen corto

Serum levels of CXCL13 as potential biomarkers for lupus nephritis and kidney transplant

Sánchez-Muñoz, F. [1*], Juárez-Villa, D. [2], Paredes-González, I.S. [1], Hernández-Solano, L. [1], Zenteno-Pérez, H. [1], Guzmán-Martín, C. [1], Zepeda-Quiroz, I. [2], Martínez-Martínez, L.A. [3], Flores-Gama, C. [2], Rodríguez-Castellanos, F.E. [2], Juárez-Vicuña, Y. [1]

[1]Departamento de Inmunología, Instituto Nacional de Cardiología – Ignacio Chávez, México.
[2]Departamento de Nefrología, Instituto Nacional de Cardiología – Ignacio Chávez, México.
[3]Departamento de Reumatología, Instituto Nacional de Cardiología – Ignacio Chávez, México.

Chemokines are implicated in inflammatory and immune responses to immune complexes. Several chemokines with the C-X-C motif (CXCL) concentrations in serum or plasma have been assessed in these scenarios. CXCL13 is one of the most potent B-cell and T follicular helper-cell chemoattractants. However, there are few studies on the potential use of CXCL13 for diagnostic of Systemic Lupus Erythematosus nephritis patients and kidney transplant patients in a clinical scenario. Thus, the AIM of this study was to analyze the CXCL13 levels in Lupus Nephritis and transplant patients. In this study, CXCL13 was analyzed by ELISA (Quantikine R&D) in Healthy subjects (n=20, 61.84 pg/mL, 44.51 to 88.46 IQR), Lupus patients with (n=20, 88.46 pg/mL, 88.46 to 88.46 IQR) and without kidney involvement (n=15, 88.46 pg/mL, 88.46 to 88.46 IQR) and kidney transplant (n= 28, 88.46 pg/mL, 88.46 to 88.46 IQR) patients from the Rheumatology and Nephrology department. The serum levels of CXCL13 were upregulated in Lupus Patients with ($p=0.004$) or without ($p=0.0087$), while only a trend was observed for kidney transplant ($p=0.0695$) as compared to healthy subjects. Also, CXCL13 positively correlated with SLEDAI ($p<0.05$). Finally, ROC area under curve has the capacity to discriminate between subjects with lupus and healthy controls (0.7969, with IC 0.6846 to 0.9091) and $p=0.0002$.

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Resumen corto

Tandem Human Antibodies Constructions, Strategies to Improve their Neutralizing Capabilities against SARS-CoV-2

Sansanwal, D.*, Rosas-Ramirez, E., Muñoz-Herrera, J.C., Vázquez-Leiva, S., Pelcastre-Gómez, A.Y., Salinas-Trujillo, J.R., Pérez-Tapia, S.M., Pedraza-Escalona, M. [1]

Unidad de Desarrollo e Investigación en Bioterapéuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México

Due to the existence of SARS-CoV-2 variants of concern and their consequences, the development of strategies to improve the inhibitory capacity of neutralizing antibodies (NAbs) that recognize conserved RBD epitopes is mandatory. In this work, we selected human B cells, producers of antibodies that recognize SARS-CoV-2 RBD, from seven convalescent COVID-19 patients. Overall, 800 lymphoblastic cell lines were obtained after Epstein-Barr virus immortalization. 29 clones secreted antibodies with IgA isotype and 58 with IgG isotype that recognize RBD and S1-protein of SARS-CoV-2 by ELISA. We selected five antibodies with the highest recognition capacity, and their variable regions of the heavy and light chains were amplified, sequenced, and analyzed. These sequences were compared with the germ-line sequence, and somatic hypermutation regions, especially in the FRW3 were found. The HCDR3 sequences of these antibodies have an identity percentage from 50 to 100%, when are compared with the CoV-AbDab database (Raybould *et al*., 2021). Therefore, it is confirmed that there is a broad diversity of antibodies for anti-SARS-CoV-2. Eventually, we selected the variable regions of the antibody S56G9, due to its high binding affinity and neutralizing capacity, and the antibody G6E8, due to its ability to recognize the Omicron RBD variant to construct heterodimers and evaluate their binding and neutralization capacities against different variants of SARS-CoV-2. The construction of the dimer VHS56G9-$(G_4S)_4$linker-VLS56G9-K6/K9linker-VHG6E8-$(G_4S)_4$linker-VLG6E8 was cloned in the pFUSEss-CHIg-hG1 and expressed in eukaryotic system. This heterodimer and the monomers used as controls are yet to be evaluated for binding affinity and neutralization capacity.

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Resumen corto

Immunogenicity and protective capacity study of porins from three different Salmonella enterica serovar Typhimurium isolates

Santana-Segovia, S. [1*], Vázquez-González, A. [1], Lozano-Cisneros, D. [1*], Gordillo-López, S. [1], García- Valeriano, M. [1], Calva-Mercado, E. [2], López-Macías, C. [1], Rivera-Hernández, T. [1,3]

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE, Hospital de Especialidades, Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, México. [2]Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, México. [3]Consejo Nacional de Ciencia y Tecnología, México.

Non-typhoidal Salmonella (NTS) infections represent a significant cause of morbidity and mortality around the world affecting particularly immunocompromised individuals, infants and young children. This pathology is caused by a wide number of *Salmonella enterica* serovars, with serovar Typhimurium being one of the main causative agents. An emergent concern within the NTS field is the world-wide spread of more virulent antibiotic resistant strains. Introduction of an effective vaccine that can be safely used in infants and young children would contribute to reducing disease burden, prevent the use of antibiotics to treat the disease, and contribute to the fight against multi-drug resistant (MDR) infections. Our laboratory is studying the outer membrane proteins (OMP), also known as porins, to develop a multivalent vaccine against this pathology. The objective of this study is to determine the antibody response and the protective capacity of porins obtained from two different *Salmonella* Typhimurium clinical isolates in a mouse model. To do this, the total IgG and IgM titles obtained post immunization were determined by ELISA. The protective capacity was determined through an *in vivo* infection model with a MDR strain and subsequent quantification of the bacterial burden in the spleen and liver. The data generated in this project will allow us to push forward porins purified from one of these clinical isolates as a promising vaccine candidate to be used in the following phases of vaccine development.

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Resumen corto

CD38 favors the differentiation of effector memory T lymphocytes and regulates the senescent phenotype of central memory T lymphocytes in inflammaging

Santiago Cruz, W. [1]*, Espinosa Arciniega, H.E. [2], Flores Muñoz, M. [3], García García, F. [4], Maravillas Montero, J.L. [5], Romero Ramírez, H. [6], Rodríguez Alba, J.C. [7]

[1]Departamento de Biomedicina, Programa de Doctorado en Ciencias de la Salud, Unidad de Citometría de Flujo, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, México. [2]Laboratorio de Inmunología Integrativa, Instituto Nacional de Enfermedades Respiratorias (INER), CDMX, México. [3]Departamento de Investigación Clínica, Programa de Doctorado en Ciencias de la Salud, Laboratorio de Medicina Traslacional, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, México. [4]Departamento de Biomedicina, Programa de Doctorado en Ciencias de la Salud, Laboratorio de Biología del sueño, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, México. [5]Red de apoyo a la investigación, Laboratorio de Inmunobiología de Células B, Universidad Nacional Autónoma de México e Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, CDMX, México.[6]Departamento de Biomedicina Molecular, Centro de Investigación y Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV-IPN), CDMX, México. [7]Departamento de Biomedicina, Programa de Doctorado en Ciencias de la Salud, Unidad de Citometría de Flujo, Instituto de Ciencias de la Salud, Universidad Veracruzana, Xalapa, México.
*E-mail: wendii.santiago@gmail.com

Inflammaging describes the low-grade inflammation associated with aging. This scenario is favored by the presence of senescent cells and an increase in proinflammatory mediators. CD38, a glycoprotein with enzymatic and receptor functions, is considered one of the main NAD+ consuming enzymes. The study of CD38 and inflammaging has been focused on its enzymatic function, mainly in innate immune cells. Nevertheless, the function of CD38 as a receptor in inflammaging on adaptative immune cells has been not described. The objective of this work was to analyze the function of CD38 in the activation and proliferation of memory T-lymphocytes in the inflammatory response of an aged murine model. 18 months old C57BL/6. Cd38+/+ (WT) and C57BL/6.Cd38-/- (KO) mice were injected intraperitoneally with LPS for 5 days to induce acute inflammation. Then, we analyzed central (Tcm) and effector memory T lymphocytes (Tem) by flow cytometry, as well as pro- and anti-inflammatory serum cytokines. Our data suggest that, in aging, CD38 promotes the differentiation to pre-effector T lymphocytes and Tem and negatively regulates the differentiation towards Tcm. Under acute inflammation, the Tcm cells from aged KO mice possess lower proliferation and activation capacity, which is characteristic of a senescent phenotype. Finally, serum cytokine levels were higher in WT compared to aged KO mice. These results establish CD38 as a regulator of T-lymphocyte response in aging and as a possible regulator of senescence of Tcm. It is necessary to continue this research to clarify the role of CD38 in T lymphocytes in the face of inflammaging.

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Resumen corto

Effect of LPS on the expression of sialic acid in MCF-7 cells

Santiago-Olivera, B.L.*, Caballero-Sanchez, M.D., Gallegos-Velasco, I.B., López-Castellanos, M.S., Hernández-Cruz, P.A.

Laboratory of Cancer Genomics, Proteomics and Glycobiology of the UABJO-UNAM Faculty of Medicine Research Center. Oaxaca de Juarez, Mexico.
*E-mail: brenda.santiago1530@gmail.com

Alterations in the expression of sialic acid cause the expression of new sialylated antigens.Activation of TLR4 occurs through the binding of its ligand lipopolysaccharide (LPS), leading to protein expression related to cancer cell proliferation, survival, invasion, and metastasis. In order to determine the expression of sialic acidα2,3 and α2,6 in stimulated MCF-7 cellswith LPS itevaluated the expression of sialic acid through cytochemistry, flow cytometry, and real-time RT-qPCR. In cytochemistry as cytometry, α2, 3 and α2, 6 sialic acid is expressed, recognized by the Maackia amurensis (MAA) and Sambucus nigra (SNA) lectins, respectively, there is sialic acid expression in MCF-7 cells under basal conditions and with LPS stimulation. , α-2.6 sialic acid increases its expression after 2 hours, while α-2.3 sialic acid increases its expression up to 6 hours. In the amplification by RT-qPCR analyzed by the delta Ct method, it is observed that at 4 hours there is greater expression of ST3GAL1 and at 6 hours the expression level of ST6GAL1 is higher. The results of this work indicate that sialic acid in position α-2,3 and α-2, favoring the truncated expression of oligosaccharides or the expression of new sialylated antigens that may be related to the progression of breast cancer.

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Resumen corto

HDACi as a potential inducers of Host Defense Peptides for their therapeutic use in diabetic foot ulcers

Santos-Mena, A. [1,4*], Guerrero-Rivas, A. [2], Rodríguez-Mendieta, C. [3], Rivas-Santiago, B. [4]

[1]Facultad de Ciencias Químicas, Posgrado en Ciencias Farmacobiológicas, Universidad Autónoma de San Luis Potosí, San Luis Potosí, México. [2]Unidad Académica de Ciencias de la Salud, Univiversidad Autónoma de Zacatecas Francisco García Salinas, Zacatecas, México. [3]Medicina Interna, Hospital General de Zona No. 1 "Dr. Emilio Varela Lujan" Instituto Mexicano del Seguro Social, Zacatecas, México. [4]Unidad de Investigación Biomédica de Zacatecas, Instituto Mexicano del Seguro Social, Zacatecas, México.
*E-mail: rondo_vm@hotmail.com

Diabetic foot ulcers (DFU) are a chronic wound considered the most problematic complication in patients with diabetes mellitus (DM) being the first amputation cause in low-income countries, there are several mechanisms involved in this wound healing that are downregulated like HIF-1α and STAT3 pathway and the persistent bacterial infection. Although several potential therapeutic drugs have been developed for the treatment of DFUs, most of them are unaffordable and don't take all the therapeutic points, furthermore, the development of multidrug resistance by bacteria has worsened the landscape. Has been reported that the activation of the HIF-1α-STAT3 axis by the histone deacetylase inhibitor (HDACi) Entinostat, increases the induction of the Host Defense Peptide (HDP) LL-37, a potent and promising treatment against infections. In this work, we evaluated the induction of the HDPs mRNA of LL-37 and HBD-3 on HaCaT cells and primary human epidermal keratinocytes (HEK) cell cultures from 6 healthy individuals and 6 patients with type II diabetes mellitus by 3 possible HDACi molecules found by bioinformatics tools. On HaCaT cells only 1 from 3 molecules induce the expression of LL-37 and HBD-3, the same result has been seen on HEK by the same molecule named 1,3-diphenylurea, using a Western Blot we found significantly expressed the nuclear factor HIF-1α being possibly the activation pathway.

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Resumen corto

Immune system and gut microbiota profile from birth to 12 months in preterm infants exposed to neonatal antibiotic treatment

Silva-Aguilera, F. [1], Vazquez-Angel, G. [1], Reyes-Garcia, D. [2], Olivera-Vergara, I. [1], Canul-Euan, A. [3], Mendoza-Ortega, J. [4], Mancilla-Herrera, I. [5], Diaz-Valencia, J.D. [1], Estrada-Gutierrez, G. [6], Gonzalez-Perez, G.[1]*

[1]Physiology and Cellular Development Department, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City. [2]Neonatal Intensive Care Unit, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City. Developmental Neurobiology, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City. [6]Research Division, National Institute of Perinatology Isidro Espinosa de los Reyes, Mexico City,

Preterm infants have an immature immune system and are at high risk of infectious and inflammatory diseases that should be treated with antibiotics. Antibiotics influence neonatal immune system and gut microbiome development. We analyzed the effect of neonatal antibiotic treatment on the stool pattern and enteral tolerance, immune system, and gut microbiota in 88 preterm infants <33 weeks gestational age from birth to 12 months. Neonates were classified in 3 groups according to neonatal antibiotic (ABT) treatment days: no antibiotics, 3-7d ABT, and ≥8d ABT. Preterm infants from the ≥8d ABT group took longer to pass the meconium and to start green and yellow stools and reached reduced volumes in enteral feeds at day 14 and 28 than infants from no ABT and 3-7d ABT groups. At 12 months, preterm infants from the ≥8d ABT group had higher frequencies of eosinophils and IgM than infants from no ABT and 3-7d ABT groups. Finally, the gut microbiota profile of preterm infants from the 3-7d ABT and ≥8d ABT groups was different with respect to the no ABT group.

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Resumen corto

Effect of urban particulate matter on the pulmonary immune response against *Pseudomonas aeruginosa* in a murine model

Solís-Torres, N.G. [1]*, Escudero-Lourdes, C. [2], González-Curiel, I.E. [3], Rivas-Santiago, B. [4], Osornio-Vargas, A. [5], Quintana-Belmares, R.O. [6], Rivas-Santiago, C.E. [7]

[1]Posgrado en Ciencias Farmacobiológicas, Universidad Autónoma de San Luis Potosí, San Luis Potosí, México. [2]Departamento de Inmunotoxicología, Universidad Autónoma de San Luis Potosí, San Luis Potosí, México. [3]Laboratorio de Inmunotoxicología y Terapéutica Experimental, Universidad Autónoma de Zacatecas, Zacatecas, México. [4]Unidad de Investigación Biomédica del Instituto Mexicano del Seguro Social, Zacatecas, México. [5]Departamento de Pediatría, Universidad de Alberta, Canadá. [6]Instituto Nacional de Cáncer, Ciudad de México, México. [7]Cátedra CONACYT-Unidad Académica de Ciencias Químicas, Universidad Autónoma de Zacatecas, Zacatecas, México. *E-mail: nnancy_618@hotmail.com

Outdoor air pollution is an important public health problem associated with more than 4 million deaths worldwide. One of the most concerning pollutants with the worst health effects on human health is particulate matter (PM). Its exposure has been related to developing or exacerbating infectious and non-infectious diseases. Exposure to this pollutant alters the immune response. Recently, our investigation work group demonstrated that PM exposure negatively affects different innate immune response mechanisms. To evaluate if these alterations enhance the development of infectious diseases, we decided to assess in BALB/c mice the effect of long-term exposure to $PM_{2.5}$ during opportunistic bacteria infection such as *Pseudomonas aeruginosa.* Eighty BALB/c mice will be divided into mock (No infection/ no PM exposure), infection control (Infection/ no PM exposure), PM control (No infection/ PM exposure), and experimental (Infection/ PM exposure), then every other day will be exposed intratracheally to urban $PM_{2.5}$ or injectable solution respectively. After thirty days of exposure, mice will be infected with *P. aeruginosa.* Afterward, at 3, 7, and 14 days post-infection, mice will be euthanized by exsanguination. The whole blood and lungs will be collected to assess CFU loads, lung damage, and gene and protein expression of critical immune factors (pro- and anti-inflammatory). We suppose that long-term exposure to urban PM will alter host immunity and enhance the development of *P. aeruginosa* infection.

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Resumen corto

TOX, a novel T cell exhaustion regulator in cervical cancer: could this molecular marker be a promising immunotherapeutic target?

Solórzano-Ibarra, F. [1,2], García-Barrientos, N.T. [1], Güitrón-Aviña, M.S. [1], Rojas-Díaz, J.M. [1], Haramati, J. [3], Ortiz-Lazareno, P.C. [4], Ceja-Flores, F.J. [1], Alejandre-González, A.G. [1],Téllez-Bañuelos, M.C. [3], Cruz-Ramos, J.A. [5], Ayala-Rojas, I.J. [5], Urciaga Gutiérrez, P.I. [1], Bustos-Rodríguez, F.J. [6], Vázquez-Limón, J.C. [7], Gálvez-Toro, L. [7], del Toro-Arreola, S. [1,8*]

[1]Instituto de Investigación en Enfermedades Crónico-Degenerativas, Departamento de Biología Molecular y Genómica, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. [2]Estancias posdoctorales por México. [3]Laboratorio de Inmunobiología, Departamento de Biología Celular y Molecular, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Guadalajara, Jalisco, Mexico. [4]División de Inmunología, Centro de Investigación Biomédica de Occidente, Instituto Mexicano del Seguro Social, Guadalajara, Jalisco, México. [5]Instituto Jalisciense de Cancerología, Guadalajara, Jalisco, México. [6]Nuevo Hospital Civil de Guadalajara “Dr. Juan I. Menchaca”, Guadalajara, Jalisco, México. [7]Antiguo Hospital Civil de Guadalajara “Fray Antonio Alcalde”, Guadalajara, Jalisco, México. [8]Laboratorio de Inmunología, Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México.

*E-mail: susana.darreola@academicos.udg.mx

In recent years, immune checkpoint inhibitors have become one of the most promising therapeutic treatments for patients with cancer, including cervical cancer. The use of monoclonal antibodies to block inhibitory receptors (for example, PD-1 and its ligand PDL-1) helps to reinvigorate exhausted cytotoxic T cells, which are a common feature of chronic viral infections and cancer. Exhausted cells are characterized by a progressive reduction of effector functions, accompanied by an increased expression of inhibitory receptors and an altered transcriptional program. An important transcription factor in this process is TOX, which has recently been associated as a master regulator of exhaustion. Therefore, we have here evaluated the expression of TOX and associated it with other exhaustion markers in circulating and tumor-infiltrating T cells from patients with cervical cancer throughout conventional treatment. By designing a multiparameter flow cytometry analysis, we observed a significant increase in the percentage of TOX+PD-1+CD69+CD8+ T cells in patients with cervical cancer. We also classified the cells as progenitor, intermediate exhausted, and terminally exhausted T cells, accordingly to the level of PD-1 expression and we observed an increased number of terminally exhausted CD8+ T cells (PD-1^{hi}+CD69+cells) expressing TOX. A similar pattern was also observed in the region of the helper T cells, in which, exhaustion might have an important impact in orchestrating immune responses. Therefore, TOX could represent a new promising immunotherapeutic approach for the treatment of cervical cancer.

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Resumen corto

Identification of cytokine-producing type 1 and 2 conventional dendritic cells in a mouse model of lupus

Sotelo-Rodríguez, A.*, Barrera-Aveleida, G.B., Galarce-Sosa, E.I., Isidro-Magallán, J.E., Reséndiz-Mora, C.A., Baeza-Ramírez, M.I., Wong-Baeza, C.

Laboratorios de Biomembranas y de Enzimología, Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, Ciudad de México, México.
*E-mail: anasotelor@gmail.com

Type 1 and 2 conventional dendritic cells (cDC1/cDC2) can develop immune responses by polarizing and maintaining T-cell responses. Besides, as they are highly efficient in maintaining self-tolerance, these cells have been associated with various autoimmune diseases such as Systemic Lupus Erythematosus (SLE). SLE is an autoimmune pathology with loss of self-tolerance and generation of autoantibodies including the anti-lipid antibodies. In our research group we developed a mouse model of lupus, through the administration of liposomes bearing non-bilayer phospholipid arrangements (NPA), that produce anti-NPA antibodies which trigger the lupus like disease. Therefore, in this work we determine the participation of cDCs in the development of this lupus mouse model. cDC1 and cDC2 cells from spleen and inguinal lymph nodes were analyzed by flow cytometry to evaluate their cytokine production after 5, 10 and 15 days of the administration of stable lipidic particles. We found a significant statistical increase of cDC1 ($P \leq 0.001$) and cDC2 ($P \leq 0.05$) from spleen of mice administered with liposomes bearing lipidic particles compared to those that receive saline solution. We also found that cDC1 from mice administered with liposomes bearing lipidic particles mainly produce TGF-β at all evaluated times in spleen and IL-12 in the inguinal node at 10 days after the administration. While cDC2 from mice administered with liposomes bearing lipidic particles mainly produce TGF-β at days 5 and 15 and IL-6 at day 5 in spleen and IL-4, IL-6, IL-12 and TGF-β in the inguinal node at 10 days after the administration.

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Resumen corto

Role of CD43 in cellular transformation

Sotomayor-Vivas, C.I. [1,2]*, Melchy-Pérez, E. [1], Chipres-Naranjo, L.E. [1], Rosenstein, Y. [1]

[1]Departamento de Medicina Molecular y Bioprocesos, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México, [2]Licenciatura en Ciencias Genómicas, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México.
*E-mail: cristina@lcg.unam.mx

CD43 is a sialoglycoprotein expressed in lymphoid cells and tumors of diverse origins, where its aberrant expression correlates with poor prognosis. By signaling through its intracellular domain, CD43 regulates several cellular processes, including adhesion, activation, differentiation, proliferation, and apoptosis. We have previously shown that, when combined with oncogenic signals, CD43 promotes cell transformation by abrogating the contact inhibition of growth through a molecular mechanism that involves AKT-dependent Merlin phosphorylation and degradation. In this work, we generated HeLa and NIH-3T3 cells with stable expression of an inducible system, where we can express human CD43 with or without its intracellular signaling domain (IC domain) by the addition of tetracycline. We evaluated the inducible expression of CD43 by flow cytometry. The results of wound healing and proliferation assays indicate that the intracellular domain of CD43 generates intracellular signaling that favors cellular transformation. Particularly, AKT, an essential kinase involved in proliferation and wound healing, was more phosphorylated in sub-confluent cells expressing wildtype CD43 than cells lacking the IC domain. Altogether, these data suggest that CD43-dependent signals enhance the tumorigenic capacity of non-hematopoietic tumor cells.

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Resumen corto

White spot syndrome virus (WSSV) in *Penaeus vannamei* shrimp induces the exacerbated production of proteins with allergenic potential

Soto-Muñoz, A. [1]*, Rodriguez-Canul, R. [1]

[1]Departamento de Recursos del Mar, Laboratorio de Inmunología y Biología Molecular; Centro de Investigación y de Estudios Avanzados del I.P.N. Unidad Mérida, Yucatán, México.
*E-mail: axel.soto@cinvestav.mx

Pacific white shrimp (*Penaeus vannamei)* aquaculture supports a large industry worldwide. This species has been threatened primarily by the white spot syndrome virus (WSSV). Shrimp allergens are generally resistant to denaturation by heat or acid and can remain intact even after storage, cooking, and digestion. In this work, we hypothesized that the presence of WSSV may exacerbate the production of proteins with allergenic potential in humans. Of the identified proteins, tropomyosin (TM), arginine kinase (AK), myosin light chain (MLC) and sarcoplasmic calcium binding protein (SCP) stand out. Through bioinformatics analysis, data for the prediction of B and T cell epitopes (human) derived from allergens reported for *P.vannamei* and WSSV structural proteins (VP28, VP24, VP26 and VP19) were analyzed for their possible cross-reactivity. The identity percentage was ≤ 80%. In the same way, the prognosis of the infection (1, 3, 6, 12, 24, 48 and 72 hours post-infection) was characterized in static bioassays in *P. vannamei* shrimp infected with WSSV, evaluating through gene expression (RT- qPCR) of the allergenic proteins associated with this viral infection. A greater number of transcripts of the genes of the allergenic proteins (TM, AK, and MLC) were found due to the infection with WSSV in the last hours of the bioassay. The increased number of transcripts during WSSV infection could be a health risk in commensals.

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Resumen corto

Effect of *Mycobacterium tuberculosis*-derived extracellular vesicles on dendritic cell maturation and CD4 T cell activation

Sta.Maria-Peregrino, E. [1*], Castañeda-Casimiro, J. [1,2], Vázquez-Flores, L. [3], Wong-Baeza, C. [3], Estrada-Parra, S. [1], Estrada-García, I. [1], Serafín-López, J. [1], Wong-Baeza, I. [1]

[1]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN), Ciudad de México, México. _[2]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN), Ciudad de México, México.[3]Departamento de Bioquímica, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN), Ciudad de México, México. *E-mail: astamaria@ipn.mx

During tuberculosis (TB), the activation of IFNɣ-producing CD4 T cells by dendritic cells (DCs) is an essential response against the infection. Extracellular vesicles derived from *Mycobacterium tuberculosis* (Mtb-EV) could contain molecules that induce DC maturation, and they also could transfer mycobacterial antigens to DCs for T cell activation. In this study, with the aim of understanding the immunogenicity of Mtb-EV, we stimulated monocyte-derived immature DCs with purified Mtb-EV, and after 24 h we observed an increased expression of HLA-DR, CD80 and CD86, which are associated with mature DCs. We then co-cultured Mtb-EV-maturated DCs with Mtb-specific autologous CD4 T cells, and after 24 h we detected the production of IFNɣ by CD4 T cells, especially by the effector memory subset. A previous proteomic characterization of Mtb-EV documented the presence of 208 Mtb proteins. We selected the 20 most abundant proteins and evaluated their immunogenicity with the Immune Epitope Database bioinformatics platform. We found that Rv1435, SodB, Rv3722c and Rv0831c contained the most immunogenic epitopes, which can be recognized by MHC-II alleles found in at least 12.1% of the Mexican population. Our results confirm that Mtb-EV contain molecules that induce DC maturation, and that Mtb-EV-treated DC are able to induce IFNɣ production by Mtb-specific memory CD4 T cells. These DCs were never in contact with live Mtb, indicating that Mtb-EV carry proteins with immunogenic epitopes that can be presented by DCs to T cells. Our research contributes to understand the potential of Mtb-EV molecules for the development of protective strategies against TB.

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Resumen corto

Aggressive breast cancer spheroids promote the formation of M1-like macrophages with migratory activity

Suárez-Arriaga, M.C. [1]*, Mendoza-Coronel, E. [1], Taba-Escoto, D. [1], Martínez-Valderrama, J.R. [1], Méndez-Tenorio, A. [2], Fuentes-Pananá, E.M. [1]

[1]Unidad de Investigación en Virología y Cáncer del Hospital Infantil de México "Federico Gómez", Ciudad de México, CDMX,México. [2]Laboratorio de Biotecnología y Bioinformática Genómica de la Escuela Nacional de Ciencias Biológicas, IPN, Ciudad de México, CDMX, México.
*E-mail: mostancmayra@hotmail.com

An in-depth characterization of the tumor microenvironment has been carried out, paying special attention to lymphoid cells resulting from using therapies based on the use of immune checkpoint inhibitors. However, a good response has not been observed in patients with breast cancer. Therefore, the study of infiltrated myeloid populations such as macrophages is essential. In this study, we evaluated the differences in the phenotype of macrophages that were cocultured with spheroids generated from primary and commercial cultures of aggressive (A-BrC) and non-aggressive breast cancer cells (NA-BrC). Through a characterization by flow cytometry, the evaluation of RNASeq, and secreted proteins Th1, Th2, and Th17, we found that macrophages cocultured with A-BrC cells preferentially express cytokines associated with proinflammatory responses such as CXCL8, IL1b, IL6 and CD86, and processes linked to cell migration are enriched. We also observed that only with the spheroids of the A-BrC cells there is a detachment event of the macrophages, an increase in the expression of the CD14 marker, and high maintenance of the expression of CD68. We performed a migration assay to corroborate the enrichment processes found by RNASeq, we used SFB, CXCL12, and MCP1 as chemoattractant factors. We observed a greater migratory capacity in macrophages that were in contact with A-BrC spheroids, and using SFB, and CXCL12 as chemoattractant factors. This study supports that M1-like macrophages could also contribute to tumor progression and not only to antitumor responses as has been classically established. CONACyT Ciencia de Frontera (Project no. 40757), and Fondo de Apoyo a la Investigación, Hospital Infantil de México Federico Gómez (Projects no. HIM-2014-053 and HIM 2018-076).

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Resumen corto

IL-2 abundance regulates Helios expression in CD8 T cells

Suárez-Rojas, G. [1,2]*, Rubio, R.M. [1], Esperante, D. [1,3], Aguilar-Fuentes, R.E. [1,4], García-Garza, M.F. [1,4], Ruiz-Gómez, M.F. [1,4], Albarrán-Godínez, A. [1,2], Madera-Salcedo, I.K. [1], Rosetti, F. [1], Crispín, J.C. [1,4].

[1]Departamento de Inmunología y Reumatología, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, México. [2]Programa de Doctorado en Ciencias Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, México. [3]Plan de Estudios Combinados en Medicina, Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, México. [4]Escuela de Medicina y Ciencias de la Salud, Instituto Tecnológico de Estudios Superiores de Monterrey Campus CDMX, Ciudad de México, México.

*E-mail: gerardo.suarez.699@gmail.com

Helios is a transcription factor expressed in nTregs and exhausted CD8 T cells. Preliminary data suggests that Helios expression regulates CD8 T cell effector function. Here, we analyzed the role of factors relevant during CD8 T cell priming, to understand their contribution to Helios expression in CD8 T cells.

First, we analyzed the role of TCR affinity. To this end, we compared Helios expression in OT-I cells primed in the presence of a high affinity (SIINFEKL) versus a low affinity ligand (SIIGFEKL). Whereas activation with a high affinity antigen caused a modest induction of Helios, priming with a low affinity antigen led to robust Helios expression. We observed that increased co-stimulation blunted expression of Helios, suggesting that this inhibitory transcription factor is induced in CD8 T cells activated in suboptimal conditions. We hypothesized that this effect could be mediated by IL-2 abundance. In support of this, we observed that IL-2 neutralization increased Helios expression, whereas IL-2 addition inhibited Helios in a dose-dependent manner. To identify the signaling pathway responsible for this effect, we tested the effect of different inhibitors and found that only the JAK inhibitor tofacitinib increased Helios expression. Finally, we demonstrated in a luciferase reporter system that constitutively activated STAT5 inhibited the promoter activity of Helios. Collectively, these results indicate that the strength of the CD8 T cell activation, through its effect on the abundance of IL-2, regulate the expression of Helios in a STAT5-dependent manner. This mechanism could limit the activation and effector differentiation of CD8 T cells activated by lower affinity ligands.

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Resumen corto

Non-neuronal leukocyte cholinergic system as a target of the regulation of immunological processes induced by organophosphate pesticide

Toledo-Ibarra, G.A. [1]*, Covantes-Rosales, C.E. [1], Ramírez-Ibarra, K.M. [2], Diaz-Resendiz, K.J.G. [1], Ventura-Ramón, G.H. [1], Pavón, L. [3], Girón-Pérez, M.I. [1]

[1]Laboratorio Nacional para la Investigación en Inocuidad Alimentaria (LANIIA) Unidad Nayarit. Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [2]Maestria en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Tepic, Nayarit, México. [3]Laboratorio de Psicoinmunologia, Dirección de Investigaciones en Neurociencias, Instituto Nacional de Psiquiatría "Ramón de la Fuente Muñiz", Ciudad de México, CDMX, México.
*E-mail: Gladys.toledo@uan.edu.mx ; itzel.navarro@cinvestav.mx

In the environment, some compounds can disrupt neuroimmune communication, such as organophosphate pesticides (diazinon), whose neurotoxicity mechanism is based on enzymatic inhibition of acetylcholinesterase (AChE), which increases acetylcholine levels and overstimulates cholinergic receptors. Diazinon and its metabolite diazoxon have toxic effects on the immune system in several organisms. However, the mechanism of immunotoxicity remains unclear. Therefore, this study was designed to evaluate the effect of diazoxon exposure on the cholinergic system and pro- and anti-inflammatory cytokines in Nile tilapia (*Oreochromis niloticus*) spleen mononuclear cells *in vitro* and to suggest a possible mechanism by which organophosphate pesticides induce immunotoxicity in vertebrates. The results show the effect of diazoxon on the non-neuronal cholinergic system in mononuclear cells through AChE inhibition and upregulation of mAChR M2 and M4. Furthermore, the induction of inflammatory response was demonstrated, with an increased IL-6 and TNF-α expression when cells were exposed to diazoxon *in vitro*. The mechanisms underlying the diazoxon-induced increase in cytokine expression include not only the canonical mechanisms of organophosphate toxicity involving AChE inhibition but also the modulation of cholinergic receptors. Thus, cholinergic agonists and antagonists have demonstrated the ability to modulate pro- and anti-inflammatory cytokines through nicotinic and muscarinic pathways. The inflammatory phenomenon must be a physiological mechanism perfectly controlled by neuro-immunological interactions, but data show that diazoxon induces changes in key components of the non-neuronal leukocyte cholinergic system, as well as the regulation of immunological processes.

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Resumen corto

Cellular infiltrate and high viral load in bronchoalveolar lavage are associated with hospital outcome in critically patients with COVID-19

Torres-Flores, A. [1]*, Madera-Sandoval, R. [1], Zamudio-Meza, H. [1], Sánchez-Hurtado, L. [2], Romero-Gutiérrez, L. [2], Calleja-Alarcón, S. [2], Mena-López, J. [2], Wong-Baeza, M. [3], Arriaga-Pizano, L. [1], Cérbulo-Vázquez, A. [4], Ferat-Osorio, E. [5], López-Macías, C. [1].

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI. IMSS. Ciudad de México, México. [2]Instituto Mexicano del Seguro Social, Centro Médico Nacional Siglo XXI, Hospital de Especialidades "Dr. Bernardo Sepúlveda Gutiérrez", Unidad de Cuidados Intensivos. Ciudad de México, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN). Ciudad de México, México. [4]Departamento de Medicina Genómica, Dirección General. Hospital General de México "Dr. Eduardo Liceaga". Ciudad de México, México. [5]Dirección de Educación e Investigación en Salud, Hospital de Especialidades del Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social, Ciudad de México, México.
*E-mail: t.alejandro78@yahoo.com.mx

To date, remained undetermined about the immune responses correlates of protection in patients affected by the infection with SARS-CoV-2 and how the immune responses characteristics are related to severity. One of the important effector pathways for the generation of long-term immunity against pathogens and especially against viruses is the antibody response; however, not all antibodies that are generated in response to a viral infection are capable of inducing protection. The presence of IgG and IgA has been reported extensively in patients with COVID-19; these antibodies significantly regulate the immune response in mucosa, neutralizing viral particles and regulating the inflammatory response by binding to FcαR receptors on monocytes and macrophages in the respiratory and digestive systems. Therefore, the objective of this project was to describe the presence and neutralizing capacity of IgA and the presence of infiltrating leukocytes in the mucous membrane of the respiratory tract of the bronchoalveolar lavage of critical patients with COVID-19. We also performed correlation analysis with acute phase proteins, with the severity and favorable or fatal outcome of the pathology; which led us to propose the use of the SOFA scale and acute phase proteins such as Ferritin and C-reactive protein together with the presence of IgA antibodies and their neutralizing capacity to help in the handling and decision making of patients with COVID-19 in the intensive care unit. Correlates of protection have not been defined yet; it is therefore of extreme importance to continue with the study of the protective immune responses in these patients.

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Resumen corto

Newcastle Disease virus vector-based SARS-CoV-2 vaccine candidate AVX/COVID-12 "PATRIA" activate T cells and is recognized by antibodies from COVID-19 patients and vaccinated people

Torres-Flores, A. [1]*, Ontiveros-Padilla, L. [1], Madera-Sandoval, R. [1], Tepale-Segura, A. [1], Gajón-Martínez, J. [1], Rivera-Hernández. T. [1], Ferat-Osorio, E. [2], Cérbulo-Vázquez, A. [3], Arriaga-Pizano, L. [1], Bonifaz-Alfonzo, L. [4], Ramírez-Martínez, L. [6] , Suárez-Martínez, A. [6], Castro-Peralta, F. [6], Chagoya-Cortés, H.E. [5], Lozano-Dubernard, B. [6], López-Macías, C. [1].

[1]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI (IMSS). Ciudad de México (CDMX), México. [2]División de Investigación en Salud, UMAE Hospital de Especialidades, Centro Médico Nacional Siglo XXI (IMSS). CDMX, México. [3]Departamento de Medicina Genómica, Dirección General. Hospital General de México "Dr. Eduardo Liceaga". CDMX, México. [4]Coordinación de Investigación en Salud, Centro Médico Nacional Siglo XXI (IMSS) CDMX, México. [5]Consultora Mextrategy, S.A.S. de C. V. (Mextrategy), CDMX. [6]Laboratorio Avi-Mex, S. A. de C. V. (Avimex), CDMX, México.

Several effective vaccines for SARS-CoV-2 have been developed and used in the population. However, current production capacity cannot meet global demand, thus novel vaccine platforms that can fill in the distribution gap are needed to be further developed. AVX/COVID-12 is a vectored-based vaccine that uses New Castle Disease virions to present the SARS-CoV-2 S protein to the immune system. This work describes the analysis of the antigenicity of this vaccine candidate by means of the binding of antibodies and activation of T cells from patients infected with SARS-CoV-2 and its variants of concern (VOCs) or healthy volunteers vaccinated against COVID-19. We found that the "Patria" vaccine binds antibodies and activate T cells from both infected or vaccinated (2 or 3 doses of BNT162b2 or ChAdOx1 vaccines) people. In addition, stimulation of T cells from patients and vaccinees with AVX/COVID-12 induced its proliferation and secretion of interferon gamma (IFN-γ) in both $CD4^+$ and $CD8^+$ T cells. In conclusion, the AVX/COVID-12 vectored vaccine candidate can stimulate cellular responses and is recognized by antibodies that were primed by the native S protein present in SARS-CoV-2 viruses that infected patients and in the BNT162b2 and ChAdOx1 vaccines. These results support the use of AVX/COVID-12 vaccine as a booster in vaccination programs to tackle COVID-19 caused by SARS-CoV-2 and its VOCs.

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Resumen corto

Microglia agglomeration and TSPO over-expression in a murine model of Alzheimer Disease and CAA

Torres-Paniagua, A.M. [1*], Rodríguez-López, G.A. [1], Gevorgyan, G. [1]

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.
*E.mail: alicia_97@comunidad.unam.mx

Cerebral amyloid angiopathy (CAA) is a condition where amyloid protein deposits accumulate in the walls of small blood vessels in the brain, resulting in inflammation and damage. In response to these amyloid deposits, microglia and astrocytes are activated. The role of TSPO (translocator protein 18kDa) in neurodegenerative and psychiatric diseases has been widely studied, as it is known to be up-regulated in activated microglia and astrocytes. We conducted a study to evaluate the expression of TSPO in astrocytes and microglia of Tg-SwDI mice, a model of CAA, and compared the results with those obtained in wild-type (WT) control C57/BL6 mice. Our findings showed that microglia agglomerated in the thalamus of 6-month-old Tg-SwDI mice, regardless of gender. We also found an over-expression of TSPO in the Tg-SwDI mice, which increased with the severity of the amyloid pathology. Remarkably, even the old WT mice did not express TSPO. The expression of TSPO was observed only in microglia and not in astrocytes.

Our results suggest that microglia play a critical role in the progression of CAA and that TSPO may be involved in this process. The up-regulation of TSPO in microglia indicates that these cells are actively responding to the amyloid deposits in the brain. Moreover, the over-expression of TSPO in Tg-SwDI mice may represent a potential therapeutic target for CAA. These findings could provide a better understanding of the pathology of CAA, and lead to the development of novel treatments for this debilitating condition.

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Resumen corto

Administration of Transferon Oral® ameliorates allergic rhinitis in an ovalbumin-induced mouse model.

Trejo-Martínez, I. [1,2,3], Fragozo, A. [1,2,3], Lucas-González, A. [1,2], Dominguez-Bernal, K. [1,2] Mendoza-Salazar, I. [1,2,3], Pavón, L. [4], Pérez-Torres, A. [5], Vallejo-Castillo, L. [1,2], Pérez-Tapia, S.M. [1,2,3].

[1]Unidad de Desarrollo e Investigación en Bioterapeuticos (UDIBI), Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [2]Laboratorio Nacional para Servicios Especializados de Investigación, Desarrollo e Innovación (I + D + i) para Farmoquímicos y Biotecnológicos (LANSEIDI-FarBiotec-CONACyT), México City, México. [3]Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México City, México. [4]Laboratorio de Psicoinmunología, Dirección de Investigaciones en Neurociencias, Instituto Nacional de Psiquiatría Ramón de la Fuente Muñiz, México City, México. [5]Laboratorio de filogenia del sistema inmune de piel y mucosas, Departamento de Biología Celular y Tisular, Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, México.
*E-mail: itrejom1400@alumno.ipn.mx; ismael.trejo@udibi.com.mx.

Allergic Rhinitis (AR) is a type-I hypersensitivity mediated by IgE and characterized by itching, sneezing, runny nose, nasal congestion, hypertrophy of the turbinates, fatigue, and irritability. Transferon-Oral® is a complex mixture of peptides whose main component is extracellular monomeric Ubiquitin (EmUb). In this study, We evaluate the immunomodulatory effects of Transferon-Oral® in a murine pilot model of OVA-induced AR in 8-week-old female BALB/c mice. Once the AR condition was established, the following conditions were evaluated: Intranasal Challenge with OVA (RIN), RIN+0.750µg of Transferon Oral®, and a self-recovery group (without RIN). On days 0, 14, and 21, NALT and serum were obtained for histological evaluation and IgE levels, respectively. The clinical status of mice was determined by measuring nasal irritation and peeling. The results showed that in the RIN group, there were changes in skin tone in the secondary vibrissae area due to irritation from scratching, sneezing in bursts, an increment in specific IgE serum levels, and abundant infiltration of mast cells and eosinophils in NALT. The administration of Transferon-Oral® significantly decreased Anti-OVA IgE levels ($F=10.13$ df (2,62) $P< 0.002$) compared to T0 and mast cell infiltration in NALT. The self-recovery group also improved when the allergen was removed but to a minor extent compared to the Transferon Oral® group. These preclinical results suggest that Transferon-Oral® is a useful immunomodulator in AR. The effects might be mediated by EmUb, which modulates cell migration through CXCR4/CXCL12 axis. This study was funded by Frontier Science 2023 (CONACYT), Project number CF-2023-G-836. F A and M-S I thank CONACYT for the postgraduate scholarship (787378 and 789864, respectively).

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Resumen corto

Effect of *Cucumis sativus* on the activation of RAW 264.7 macrophages induced by LPS

Trejo-Moreno, C. [1] Corona-Alarcón, M.A. [1], Zamilpa-Álvarez, A. [2], González-Christen, J. [3], Fragoso-González, G. [4], Rosas-Salgado, G. [1*]

[1]Laboratorio de inflamación y enfermedades crónico-degenerativas. Facultad de Medicina, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México, 62350. [2]Laboratorio de Fitoquímica. Centro de Investigación Biomédica del Sur, Instituto Mexicano del Seguro Social, Xochitepec, Morelos, México. 62790. [3]Laboratorio de Inmunidad Innata. Facultad de Farmacia, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México, 62350, [4]Laboratorio A116. Inmunología. Instituto de investigaciones biomédicas, Universidad Nacional Autónoma de México, 04510, CDMX, México.
*E-mail: gabriela.rosas@uaem.mx

Noncommunicable chronic-degenerative diseases are a global health problem. Inflammation underlies the development of these pathologies, in which macrophages play an important role. Natural products have been proposed as a good option to control this kind of diseases. The aim of this work is to evaluate the immunomodulatory effect of the aerial parts of *Cucumis sativus* (cucumber) on the activation of RAW 264.7 macrophages induced by LPS.

The hydroalcoholic extract of the aerial parts of *C. sativus* was obtained, thereafter the organic fraction was isolated and fractionated by column chromatography.

The *C. sativus* fractions did not alter cell viability under the concentrations used, except the concentration 100 µg/mL. Production of IL6, TNFα, and IL10 cytokines, activation of the respiratory burst, and phagocytosis were measured. The extract and fractions of *C. sativus* prevented the production of proinflammatory cytokines (IL-6 and TNFα), increased the production of IL-10, and decreased the respiratory burst and phagocytosis, which are characteristic of M1 profile macrophages. In conclusion, *C. sativus* could be a candidate for the development of a phytomedicine for the treatment of non-communicable chronic-inflammatory degenerative diseases.

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Resumen corto

Expression of purinergic receptors and their possible association in COVID-19

Urbina-Rodríguez, R.O. [1,2]*, Briones-Rodríguez, L. [2], Juárez-Barrón, D.L. [2], Rodríguez-Aquino, E.J. [2], Euan-Ayala, D.B. [3], Turiján-Espinoza, E. [4], Vargas-Morales, J.M. [4], García-Hernández, M.H. [3], Portales-Pérez, D.P. [2, 4]

[1]Posgrado en Ciencias Farmacobiológicas de la Facultad de Ciencias Químicas de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, S. L. P., México. [2]Laboratorio de Medicina Molecular y Traslacional, Centro de Investigación en Ciencias de la Salud y Biomedicina de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, S. L. P., México. [3]Unidad de Investigación Biomédica de Zacatecas del Instituto Mexicano del Seguro Social, Zacatecas, Zac., México. [4]Laboratorio de Inmunobiología Celular y Molecular de la Facultad de Ciencias Químicas de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, S. L. P., México.
*E-mail: omar.urbina.rdz@gmail.com

During COVID-19 disease, patients present elevation in extracellular concentrations of adenosine triphosphate (ATP). Extracellular ATP is split into adenosine by the ectoenzymes CD39 and CD73. ATP and its hydrolysis products are ligands for purinergic receptors (PR). The activation of PR P2X and P2Y by ATP is related to proinflammatory processes, while the activation of P1 receptors by adenosine is related to anti-inflammatory processes. Independent studies have shown that there is an increased relative expression of P2X and P2Y and increased CD39 levels on peripheral blood mononuclear cells (PBMCs) in COVID-19. However, there is currently no information on other members of the P2X family, such as $P2X_1$ and $P2X_4$, the $P2X_7$ isoforms ($P2X_{7A}$ and $P2X_{7B}$) or receptors with anti-inflammatory activity, such as $A2_A$. In this study, the expression of $P2X_1$, $P2X_4$, $P2X_7$ and $A2_A$ PR, and CD39, was evaluated by flow cytometry and qPCR in PBMC from patients with COVID-19 (n=22) and control subjects (n=10). We found a high percentage of T lymphocytes and monocytes $P2X_7^+$/$CD39^+$ as a well a decrease in $A2_A^+$, which showing a correlation with body mass index and c-LDL in COVID-19. We also found elevated percentages of $P2X_7^+/A2_A^+$, $P2X_7^+$/$CD39^+$ and $P2X_1^+/CD39^+$ T lymphocytes, $CD3^-$ lymphocytes and monocytes. An increase in mean fluorescence intensity of CD39, $P2X_1$ and $P2X_7$ was evidenced in COVID-19. $P2X_{7B}$, $A2_A$ and $P2X_4$ showed an increase in relative expression, while $P2X_{7A}$ and $P2X_1$ a decrease in COVID-19. These results could provide information of the relationship of purinergic signaling during COVID-19.

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Resumen corto

Expression of purinergic receptors and their possible association in COVID-19

Urbina-Rodríguez, R.O. [1,2]*, Briones-Rodríguez, L. [2], Juárez-Barrón, D.L. [2], Rodríguez-Aquino, E.J. [2], Euan-Ayala, D.B. [3], Turiján-Espinoza, E. [4], Vargas-Morales, J.M. [4], García-Hernández, M.H. [3], Portales-Pérez, D.P. [2, 4]

[1]Posgrado en Ciencias Farmacobiológicas de la Facultad de Ciencias Químicas de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, S. L. P., México. [2]Laboratorio de Medicina Molecular y Traslacional, Centro de Investigación en Ciencias de la Salud y Biomedicina de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, S. L. P., México. [3]Unidad de Investigación Biomédica de Zacatecas del Instituto Mexicano del Seguro Social, Zacatecas, Zac., México. [4]Laboratorio de Inmunobiología Celular y Molecular de la Facultad de Ciencias Químicas de la Universidad Autónoma de San Luis Potosí, San Luis Potosí, S. L. P., México.
*E-mail: omar.urbina.rdz@gmail.com

During COVID-19 disease, patients present elevation in extracellular concentrations of adenosine triphosphate (ATP). Extracellular ATP is split into adenosine by the ectoenzymes CD39 and CD73. ATP and its hydrolysis products are ligands for purinergic receptors (PR). The activation of PR P2X and P2Y by ATP is related to proinflammatory processes, while the activation of P1 receptors by adenosine is related to anti-inflammatory processes. Independent studies have shown that there is an increased relative expression of P2X and P2Y and increased CD39 levels on peripheral blood mononuclear cells (PBMCs) in COVID-19. However, there is currently no information on other members of the P2X family, such as $P2X_1$ and $P2X_4$, the $P2X_7$ isoforms ($P2X_{7A}$ and $P2X_{7B}$) or receptors with anti-inflammatory activity, such as $A2_A$. In this study, the expression of $P2X_1$, $P2X_4$, $P2X_7$ and $A2_A$ PR, and CD39, was evaluated by flow cytometry and qPCR in PBMC from patients with COVID-19 (n=22) and control subjects (n=10). We found a high percentage of T lymphocytes and monocytes $P2X_7^+$/$CD39^+$ as a well a decrease in $A2_A^+$, which showing a correlation with body mass index and c-LDL in COVID-19. We also found elevated percentages of $P2X_7^+/A2_A^+$, $P2X_7^+$/$CD39^+$ and $P2X_1^+/CD39^+$ T lymphocytes, $CD3^-$ lymphocytes and monocytes. An increase in mean fluorescence intensity of CD39, $P2X_1$ and $P2X_7$ was evidenced in COVID-19. $P2X_{7B}$, $A2_A$ and $P2X_4$ showed an increase in relative expression, while $P2X_{7A}$ and $P2X_1$ a decrease in COVID-19. These results could provide information of the relationship of purinergic signaling during COVID-19.

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Resumen corto

Tumor-associated neutrophils with an antitumoral phenotype are predominantly present at the invasive margin of early-stage human colon cancer.

Vadillo, E. [1*§], Mantill, A. [2], Aguilar-Flores, C. [3], De Leon-Rodríguez, S. [4], Vela-Patiño, S. [5], Badillo, J. [1], Taniguchi-Ponciano, K. [5], Marrero-Rodríguez, D. [5], Ramírez-Lourdes, [6], Fuentes-Castañeda, C. [1], Piña-Sánchez, P. [1], Prieto-Chávez, J.L. [7], Pérez-Kondelkova, V. [8], Montesinos, J.J. [1], Bonifaz, L. [4,9], Pelayo, R. [10,11], Mayani, H. [1], Schnoor, M. [12].

[1]Unidad de Investigación Médica en Enfermedades Oncológicas, UMAE Hospital de Oncología. Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social (CMN S.XXI IMSS), Mexico City 06720, Mexico. [2]Servicio de Patología, Hospital de Oncología CMN S.XXI IMSS, Mexico City 06720, Mexico. [3]UMAE Hospital de Pediatría, CMN S.XXI IMSS, Mexico City 06720, Mexico. [4]Unidad de Investigación Médica en Inmunoquímica, UMAE Hospital de Especialidades, CMN S.XXI IMSS, Mexico City 06720, Mexico. [5]Unidad de Investigación Médica en Enfermedades Endocrinas. UMAE Hospital de Especialidades, CMN S.XXI IMSS, Mexico City 06720, Mexico. [6]Servicio de Colon y Recto, Hospital de Oncología CMN S.XXI IMSS, Mexico City 06720, Mexico. [7]Laboratorio de Citometría - Centro de Instrumentos, División de Desarrollo de la Investigación en Salud. CMN S.XXI IMSS, Mexico City 06720, Mexico. [8]Laboratorio Nacional de Microscopía Avanzada. División de Desarrollo de la Investigación, CMN S.XXI IMSS, Mexico City 06720, Mexico. [9]Coordinación de Investigación en Salud, CMN S.XXI IMSS, Mexico City 06720, Mexico. [10]Unidad de Educación e Investigación, IMSS. Mexico City 06720, Mexico. [11]Centro de Investigación Biomédica de Oriente, IMSS. Atlixco-Metepec, 74360, Puebla, Mexico. [12]Departmento de Biomedicina Molecular, CINVESTAV-IPN, 07360 Mexico City, Mexico.§ First and corresponding author.

Neutrophils are a component of the immune infiltrate in several types of cancer; however, whether their presence and characteristics can be associated with the evolution of the disease remains controversial. Here, we show that neutrophils are more represented at the invasive margin (IM) and the central part (CT) of colon cancer samples when compared to healthy adjacent tissues (HAT). Confocal microscopy revealed tumor-associated neutrophils (TAN) expressing TNFα were more represented at the IM than the CT of colon cancer samples. Flow cytometry revealed that TAN within the IM displayed an activated phenotype marked by higher expression of ICAM-1 and Fas than neutrophils from HAT. In vitro co-culture of colon cancer cell lines and primary neutrophils confirmed our in situ findings. The patient´s peripheral blood Neutrophil Lymphocyte Ratio (NLR) of ≤3.5 thresholds distinguished the early from late stages of colon cancer. Surprisingly, this stratification revealed that samples of the early stages of colon cancer had more neutrophils at the IM and the CT compared to the late stages. Moreover, TAN at the IM had a higher expression of ICAM-1 and Fas in earlier stages of the disease when compared to their later counterparts. Thus, our data suggest TAN are more represented at the early stages of the disease at the IM; these cells possess a more activated phenotype revealed by higher ICAM-1 and Fas expression.

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Resumen corto

Implementation of a serological method for detection of antibodies against SARS-CoV2 in animals

Valdovinos-Torres, H. [1]*, Tellez-Sosa, J.M. [1], Palomares, L.A. [2], Ramírez, O.T. [2], Palma-Irizarry, M. [3], Martinez-Barnetche, J.[1]

[1]Centro de Investigación Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública. Cuernavaca, Morelos, México. [2]Instituto de Biotecnología. UNAM. Cuernavaca, Morelos. México. [3] Asociación de Zoológicos, Criaderos y Acuarios de México (AZCARM). CDMX, México.
E-mail: htorres@insp.mx

The SARS-CoV2 coronavirus gave rise to the COVID-19 pandemic. According to studies, the disease was initially transmitted from wild animals to humans. During these years of pandemic, the transmission of the virus from humans to different domestic and wild animals has been reported. This represents a latent risk because, given evolutionary pressure in non-human hosts, new viral variants could emerge that are potentially more virulent and/or that evade the human immune system. Therefore, exposure monitoring in domestic and wild animals is of importance for the epidemiological surveillance of SARS-CoV2. The objective of this work is to develop a universal serological method that allows the identification of anti-SARS-CoV2 antibodies in animals, regardless of the species. For this, we developed an immunoenzymatic inhibition test (IEI) directed against the receptor-binding domain (RBD) of the Spike protein of SARS-CoV2 with two human anti-RBD monoclonal antibodies. The enzymatic activity of this reaction will be inhibited by anti-RBD antibodies in the test serum, while in a negative sample the activity will be positive. The test was validated with pre-immune sera from BALB/c mice, Wistar rats, gerbils, and with sera from these animals immunized with SARS-CoV2 RBD. Our preliminary results showed that with a cut-off of ≥20% inhibition, this test has a sensitivity and specificity of 96%. We conclude that IEI method is potentially useful for screening the seroprevalence of SARS-CoV2 in these animals. The performance of this method in free-living and/or captive animals will be studied.

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Resumen corto

Analysis of the effect of Ge/HA hydrogels coupled with MAGE-A5 and CpGs over T lymphocytes from C57BL/6 inoculated with melanoma

Valencia-Escamilla, E.A. [1]*, Castell-Rodríguez, A.E. [1], Jarquín-Yáñez, K. [1], Hernández-Téllez, B. [1], Herrera-Enríquez, M. [1], Fuerte-Pérez, A.E. [1], Piñón-Zarate, G. [1]

[1]Laboratorio de Inmunoterapia e ingeniería de tejidos, departamento de biología celular y tisular, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.
E-mail: avael@ciencias.unam.mx

Gelatin (Ge)/Hyaluronic Acid (HA) biomaterials favor cell migration and the development of pro-inflammatory environment that promotes an immune response. Ge/HA scaffolds have been studied for the treatment of melanoma where the recruitment of leukocytes was found, including T lymphocytes, relevant cells in the development of successful antitumor response. The activation of T lymphocytes depends on APC, which first recognize PAMPs such as CpGs and tumor associated antigens (MAGE). In this work we analyzed the effect of an injectable Ge/HA hydrogel coupled to CpGs and MAGE on T lymphocytes of C57BL/6 mice. First, hydrogels were inoculated subcutaneously and after one and three weeks, splenocytes and lymph node cells were obtained and treated with MAGE-A5. Subsequently, all cells were stained with anti- CD3, anti-CD4, anti- CD8 and anti- CD137, and then analyzed by flow cytometry. Additionally, mice were treated with the hydrogels and then inoculated with B16-F10 melanoma cells to evaluate the effect of the hydrogels in the tumor growth and the stroma. We obtained an increase of 20% and 40% for week 3 in the activation of T CD4+ lymphocytes from spleen and lymph nodes, while T CD8+ lymphocytes showed an increase of 15% and 10%. Besides, reduced tumor growth and increased necrosis area could be observed in groups treated with CpGs or MAGE-A5 hydrogels. In conclusion, Ge/HA hydrogels coupled to CpGs or MAGE showed the best effects on C57BL/6 mice. Funding: PAPIIT: IN221419.

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Resumen corto

The Gal-9 expression regulates the microglia activation in a neuroinflammation model induced by the peptide Amyloid-β_{25-35}

Valencia-Gil, M.L. [1]*, Ramírez-Hernández, E. [1], Sánchez-Salgado, J.L. [1], Segura-Pérez, E. [1], Nava-Catorce, M. [3], Hernández-Zimbrón, L.F. [2] Zenteno-Galindo, E. [1]

[1]Departamento de Bioquímica, Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México. [2]Escuela Nacional de Estudios Superiores, Universidad Nacional Autónoma de México, León, Guanajuato, México. [3] Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad de México, CDMX, México.
E-mail: lucero98valencia15@gmail.com

A common factor in the AD is the neuroinflammation response, caused by Aβ aggregation. This kind of response involves the microglia activation in the CNS and a participation of galectins has been found as pro or anti-inflammatory elements. Specifically, it has been found in NS and it promotes a modulation of this response through the Tim-3 receptor in microglia. The objective of this project was to study the microglia activation and the changes in the expression of Gal-9 and Tim-3 in a neuroinflammation model induced by the administration of the $A\beta_{25-35}$ peptide. The number of microglial cells was quantified by immunohistochemistry and immunofluorescence. In addition, the expression of Gal-9 and Tim-3 was quantified by Western Blott in the hippocampus. The model has shown microglia activation, which increased the neuroinflammatory response induced by $A\beta_{25-35}$. Likewise, it increased the expression of Gal-9 and Tim-3 in microglia as modulators of the immune response. The neuroinflammatory response in microglia caused by the accumulation of Aβ implies a progression of AD, so the expression of Gal-9 and its receptor Tim-3 imply a regulation of the response, which may lead to future treatments in AD.

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Resumen corto

NK cells with decreased expression of multiple activating receptors is a dominant phenotype in pediatric patients with acute lymphoblastic leukemia

Valenzuela-Vázquez, L. [1,2]*, Nuñez-Enriquez, J.C. [3], Sánchez-Herrera, J. [1,2], Mancilla-Herrera, I. [4], Mejía-Aranguré, J.M. [5,6,7], Cruz-Munoz, M.E. [1]

[1]Facultad de Medicina, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México, [2]Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México. [3]Unidad de Investigación Médica en Epidemiología Clínica, Unidad Médica de Alta Especialidad (UMAE) Hospital de Pediatría, Centro Médico Nacional (CMN) "Siglo XXI", Instituto Mexicano del Seguro Social (IMSS), Ciudad de México, México. [4]Departamento de Infectología e Inmunología, Instituto Nacional de Perinatología, Ciudad de México, México. [5]Unidad de Investigación Médica en Genética Humana, Unidad Médica de Alta Especialidad (UMAE) Hospital de Pediatría, Centro Médico Nacional (CMN) "Siglo XXI", Instituto Mexicano del Seguro Social (IMSS), Ciudad de México, México, [6]Laboratorio de Genómica del Cáncer, Instituto Nacional de Medicina Genómica, Ciudad de México, México, [7]Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, México.
E-mail: lucero.valenzuelavz@uaem.edu.mx

Acute lymphoblastic leukemia (ALL) is the most common pediatric cancer worldwide. Natural Killer (NK) cells play an important role in immunosurveillance against cancer. The effector capacity of NK cells is regulated by the balance of signals emitted by their activation and inhibition receptors. The objective of this project was to determine the phenotype and effector capacity of NK cells in pediatric patients with ALL. In this study, the receptor expression and cytotoxic function of NK cells from pediatric patients with ALL at diagnosis were analyzed using flow cytometry. Our results showed that the dominant NK cell phenotype among patients was concurrent reduced expression at various activation receptors. An alteration in the relative frequencies of NK cells expressing NKG2A and CD57 within the mature NK cell population was also observed. In addition, NK cells from the patients showed a significant reduction in antibody-dependent cellular cytotoxicity (ADCC). Finally, linear regression analysis demonstrated that an aberrant expression of activating receptors is associated with the phenomenon of ALL in pediatric patients. In conclusion, the significant reduction in the expression of activating receptors was not limited to a single type of activating receptor family, instead we observe a concurrent downregulation of multiple receptor types belonging to different families. Furthermore, our data suggest that a reduction in the percentages of NK cells expressing a specific type of activating receptor is associated with the ALL phenomenon during childhood. Therefore, a normal expression of activating receptors on NK cells may be important to show efficient cytotoxicity towards ALL.

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Resumen corto

Maternal IL-33 signaling is essential for uterine tissue remodeling and pregnancy progression in mice.

Valero-Pacheco, N. [1,2*], Tang, E.K. [1,2], Massri, N. [3], Loia, R. [1,4], Chemerinski, A. [1,4], Wu, T. [1,4], Begum, S. [1,4], El-Naccache, D.W. [1,5], Gause, W.C. [1,5], Arora, R. [3], Douglas, N.C.[1,4,6], Beaulieu, A.M. [1,2,6]

1Center for Immunity & Inflammation, New Jersey Medical School, Rutgers Biomedical and Health Sciences, Rutgers - The State University of New Jersey, Newark, NJ, USA. 2Department of Microbiology, Biochemistry, and Molecular Genetics, New Jersey Medical School, Rutgers Biomedical and Health Sciences, Rutgers - The State University of New Jersey, Newark, NJ, USA. 3Department of Obstetrics, Gynecology and Reproductive Biology, Michigan State University, East Lansing, MI, USA. 4Department of Obstetrics, Gynecology and Reproductive Health, New Jersey Medical School, Rutgers Biomedical and Health Sciences, Rutgers - The State University of New Jersey, Newark, NJ, USA. 5Department of Medicine, New Jersey Medical School, Rutgers Biomedical and Health Sciences, Rutgers - The State University of New Jersey, Newark, NJ, USA.
E-mail:. nuribanv@gmail.com

IL-33 is a pleiotropic cytokine with central roles in tissue remodeling and homeostasis. During pregnancy, the uterus undergoes rapid and dramatic changes fundamental for pregnancy progression. The maternal immune system is a critical player in regulating uterine tissue remodeling. Clinical studies have linked many pregnancy complications with an abnormal expression of IL-33 and its receptor, ST2. However, it remains unclear what are the cellular and molecular mechanisms by which IL-33 may support pregnancy progression. Here, we demonstrate that, in mice, maternal IL-33 signaling is essential for proper uterine tissue remodeling and immune cell function in early gestation. IL-33 deficient dams show defective decidualization and uterine vascular tissue remodeling. Further, embryos from IL-33 deficient dams exhibit developmental defects, including delayed embryogenesis, increased resorptions, and intrauterine growth restriction in late gestation. We identify that in the early pregnant uterus, the primary IL-33 cellular sources are decidual endothelial and stromal cells and myometrial fibroblasts, whereas ST2 is expressed by many immune cells involved in Type 2 immunity. Critically, we find that uterine lymphocytes and M2 macrophages from IL-33 deficient dams show impaired Type 2 cytokine responses that coincide with the tissue remodeling defects in early pregnancy. Our results reveal a regulatory pathway involving IL-33 signaling that is crucial for pregnancy progression in mice and provides potential mechanisms of how maternal IL-33 signaling may support human pregnancy.

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Resumen corto

Effect of Bisphenol A (BPA) exposure on development, immune response, and vector competence to dengue virus in *Aedes aegypti* mosquito

Vargas, V. [1,2]*, Lanz-Mendoza, H. [2], Morales-Montor, J.[1]

[1]Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Cuidad de México, CDMX, México. [2]Centro de Investigaciones Sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México. E-mail:

Bisphenol A (BPA), is an industrial monomer, considered an endocrine disruptor, which has been associated with degenerative diseases such as breast, colon, prostate and lung cancer; as well, has been implicated in parasitic and viral infectious diseases. Exposure to BPA in food and beverage containers and in the environment, due to the decomposition of the matrix of various plastics, has led to the increase and risk of contracting these chronic degenerative and infectious diseases. Due to the life cycle of the *Aedes aegypti* mosquito, which includes the development of its larvae and pupae in aquatic environments. It is proposed that in the artificial niches of this vector, which are mostly plastic containers generated by human waste, there could be an interaction between BPA and mosquito larvae, such as bottles, polyethylene trays, drums of drinking water, promoting effects on the development, fitness and immune response of these insects. For these reasons, we evaluated the dose-response effects of BPA exposure on egg-laying preference, development, fertility, fecundity and repercussions on the antiviral immune response by qPCR, as well as its relationship with the ability to transmit pathogens such as the dengue virus. It should be noted that the background on the effects of BPA in insect communities, including vectors of medical importance. This work will contribute to the knowledge of these components on the dynamics of mosquito populations of medical importance.

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Resumen corto

Anti-inflammatory effect of insulin and metformin in an *in vitro* hyperglycemic human placental model

Vargas-Alcantar, D. [1,2*], Martínez-Garfias, K. [1,3], Jiménez Escutia, R. [1,4], Flores-Espinosa, P. [1], Velázquez-Sánchez, M.P. [5], Zaga Clavellina, V. [1], Olmos-Ortiz, A.[1]

[1]Departamento de Inmuno-bioquímica, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, Mexico City, Mexico. [2]Posgrado en Ciencias de la Salud, Escuela Superior de Medicina, Instituto Politécnico Nacional, Mexico City, Mexico. [3]Bioquímica Diagnóstica, Facultad de Estudios Superiores Cuautitlán, Universidad Nacional Autónoma de México, Mexico City, Mexico. [4]Posgrado en Ciencias Biológicas, Unidad de Posgrado, Universidad Nacional Autónoma de México, Mexico City, Mexico. [5]Departamento de Ginecología y Obstetricia, Hospital Ángeles México, Mexico City, Mexico 54740. E-mail: donoepoxico@gmail.com.

Gestational diabetes mellitus (GDM) is one of the most common complications during pregnancy. Hyperglycemia associated to GDM led to an state of low grade inflammation, named meta-inflammation. This chronic metabolic inflammation during pregnancy is linked to negative short-and long-term adverse outcomes. Particularly, placental cell lines are sensitive to high glucose environments, increasing production of pro-inflammatory cytokines. Insulin and metformin represent the first- and second-line pharmacotherapy in GDM patients. Both drugs can attenuate the inflammatory response in multiple cells and animal models, however, there were no studies in the human placenta, particularly in an state of meta-inflammation caused by hyperglycemia. Our experimental model is the culture of human term placental explants obtained from normoevolutive pregnancies, incubated with glucose (10 and 50 mM), insulin (50, 100, 500 nM), and metformin (125, 250 and 500 µM). We measure pro-inflammatory cytokines release by ELISA. Also, we probed cell signaling inhibitors of MAPK and PI3K to dilucidate the mechanism involved in the anti-inflammatory effect of insulin. We observed that high glucose levels increased placental TNF-a, IL-1b and IL-6 secretion. The co-incubation with insulin and metformin reduced the inflammatory response associated to hyperglycemia. Finally, we preliminarily observed that PI3K pathway is involved in the anti-inflammatory effect of insulin by reducing NFκB phosphorylation. Our results demonstrated hyperglycemia exacerbates the inflammatory profile of placenta, and that insulin and metformin are effective anti-inflammatories which may help to controlled meta-inflammation in GDM patients. Funding: INPer (2018-1-152), CONACyT (CB-A1-S 27832). D. Vargas received bachelor (No. 30823) and master fellowships (No. 824474) from CONACyT.

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Resumen corto

Arpin depletion increases migration of acute myeloid leukemia cells

Vargas-Robles, H. [1]*, Montoya Garcia, A. [1], Picon Villamizar, J. [1], León-Vega, I.I. [1], Schnoor, M. [1]

[1]Departamento de Biomedicina Molecular, CINVESTAV-Zacatenco, Ciudad de México.
E-mail: hvargas@cinvestav.mx

The actin cytoskeleton is involved in different cellular processes, which require the controlled Arp2/3 complex-mediated polymerization of new actin filaments. The Arp2/3 complex is activated by nucleation promoting factors (NPFs), and inhibited by other proteins such as arpin. Low arpin expression in different solid tumors correlates with a poor prognosis of the disease, but the impact of the loss of arpin on myeloid leukemia (ML) is still unknown. To fill this knowledge gap, we first anlyzed arpin expression in different ML cells, and found that K562, U937 and HL60 cells did not produce arpin protein. By contrast, THP1 cells produced arpin protein, but at levels corresponding to less than 50% of the levels found in control mononuclear cells. In order to determine the role of arpin in the migration and proliferation of myeloid leukemia cells, we knocked-down arpin in THP1 cells and obtained an arpin depletion efficiency of 80%. Arpin depletion increased the migratory capacity by 50 % in chemotaxis assay, compared to control THP1 cells. Additionally, we were able to generate K562 cells that stably overexpress arpin. We are currently analyzing the role of arpin in the migratory abilities of these cells. Also, arpin-depleted THP1 and arpin-expressing K562 cells will be used in mouse xenotransplantation assays to determine the role of arpin in organ infiltration, a well-known complication of all types of leukemia. These studies will improve our knowledge about the role of arpin in the onset and progression of myeloid leukemia.

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Resumen corto

Effect of the combination of Fenofibrate and Linezolid, on actinomycetoma by *Nocardia brasiliensis* in BALB/c mice

Vázquez Marmolejo, A.V. [1], Salinas Carmona, M.C. [1], López López, N. [1]
Castro Corona, M.A. [1], González Mireles, A.F. [1],
Figueroa Constantino, A.K. [1], Suárez Vázquez, T.A. [1],
Duran Garces, J.M. [1*]

[1]Servicio de Inmunología, Facultad de Medicina y Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León.
E-mail: juanm.duran24@gmail.com

Actinomycetoma is an infectious, chronic, inflammatory disease, mainly caused by *N. brasiliensis*. Treatment with Amikacin and Trimetroprim is the most widely used and needs to be administered for years. Angiogenesis could contribute to the persistence and spread of the infection, while inflammation prevents the elimination of the infectious agent. Fenofibrate is a widely used drug to reduce triglyceride levels as a PPAR agonist, it has great anti-inflammatory and anti-angiogenic effect; therefore, its use, combined with an antibiotic such as Linezolid could be an alternative treatment for actinomycetoma. The purpose of this study is to evaluate the effect of the combination of fenofibrate and linezolid as a treatment of actinomycetoma by *N. brasiliensis* in an experimental model. The effect of the drugs alone or in combination was evaluated in BALB/C. mice with *N. brasiliensis* actinomycetoma, and the clinical and histopathological evolution of the lesions, angiogenesis, IL-1β and IL-6 production, VEGF and expression of pro- and anti-angiogenic factors (VEGF, COX-2 and TSP-1) were analyzed. Improvement was observed in all treatments. The combination of Linezolid/ Fenofibrate decreased the percentage of IL-1β, as well as the PMN infiltrate, the presence of VEGF in the tissue and the expression of the mRNA thereof; these effects were greater compared to Linezolid and Fenofibrate alone. The treatment with Linezolid decreased the percentage of foam cells in the tissue more effectively, compared to the combination and Fenofibrate alone, although the latter induced greater expression of TSP-1 in the tissue at day 7 of the treatment. All treatments significantly decreased COX-2 levels. The combination of Fenofibrate/ Linezolid, has a synergistic effect by more effectively decreasing inflammation, lesions and the angiogenic process, in the actinomycetoma and offers a therapeutic potential.

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Resumen corto

Evaluation of proinflammatory cytokines in metabolic dysfunction-associated fatty liver disease (MAFLD)

Vázquez-Ballescano, A. [1,2]*, Hernández-Flores, K.G. [2], Domínguez-Alemán, C.A. [2], Priego-Parra, B.A. [2] Vivanco-Cid, H.[2]

[1]Facultad de Bioanálisis, Universidad Veracruzana, Región Veracruz 91700, México [2]Instituto de Investigaciones Médico-Biológicas, Universidad Veracruzana, Región Veracruz 91700, México.
E-mail: karinhernandez@uv.mx ; alemán_815@gmail.com ; hvivanco@uv.mx

The fatty liver disease associated with metabolic dysfunction (MAFLD) is caused by an imbalance in the lipid metabolism which leads to fat accumulation in the liver. It has been demonstrated that some inflammatory mechanisms are responsible for the evolution of the clinical stages of MAFLD. Therefore, it is essential to know the immune status of the patient at all stages. The prevalence of hepatic steatosis in the Mexican population is high, reaching 41.3%. Thus, it is of vital importance evaluate the proinflammatory status during the pathology. The following project focuses on the evaluation of proinflammatory cytokines such as IL-6, IL-17A, and TNF-a, which behaviors in the establishment of the disease in comparation with healthy subjects. Samples from patients diagnosed with MAFLD were quantified by ELISA. Frozen serum from patients diagnosed with MAFLD (n=268) and hepatic fibrosis (n=39) and healthy subjects (n=49) were used. No differences were reported between the groups for TNF-a and IL-6, in the other hand, for IL-17A we observed low levels for MAFLD and fibrosis groups than healthy subjects. Our results describe for first time the serum levels of proinflammatory cytokines in a mexican population with MAFLD and fibrosis.

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Resumen corto

miRNAs as biomarkers of acute antibody-mediated rejection in kidney transplant patients

Vázquez-Toledo, M.A. [1]*, Zepeda-Quiroz, I. [2], Flores-Gama, C. [2], Juárez-Villa, D. [2], Peña-Peña, M. [1,3], Guzmán-Martín, C. [1], Sánchez-Muñoz, F. [1]

[1]Departamento de inmunología, Instituto Nacional de Cardiología – Ignacio Chávez, Cuidad de México, CDMX, México. [2]Departamento de Nefrología, Instituto Nacional de Cardiología – Ignacio Chávez, Cuidad de México, CDMX, México. [3]Maestría en Ciencias de la Salud. Posgrado Escuela Superior de Medicina, Cuidad de México, CDMX, México.
E-mail: miguelpradyu1401@gmail.com

The kidney allograft biopsy is considered the gold standard for rejection diagnosis but is invasive and could be indeterminate. Several publications point to the role of miRNA expression in suggesting its involvement in the acceptance or rejection of organ transplantation. This study aimed to evaluate the concentrations (expression) of the miRNAs 1, 21, 126, 150 and 155 in the plasma of renal transplant recipients with and without antibody-mediated rejection. A total of 28 KT patients with and without acute rejection (AR/NAR) were analyzed and quantified by miRNA PCR-RT. The functions and biological pathways were analyzed to predict the potential targets of differential expressed miRNAs. miRNA 150 expression was increased in the RA group and miRNA 1, 21, 126 and 155 expressions did not show significant difference. In silico studies showed a total of 2603 target genes for the increased miRNAs in AR, while for the decrease miRNA, a total of 1107 target-potential genes were found. Our results show that KT with AR shows an increase in miR-150-5p expression compared to NAR, suggesting that the increase in miR-150.

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Resumen corto

Tolerogenic Dendritic Cells in Parkinson's disease: an *in vitro* model.

Vega-Angeles, V.T. [1]*, Delgadillo, U. [1], Guevara, A. [1],
Alvarez-Luquin, D. [1], Romero-Rodriguez, D. [2], Adalid-Peralta, L. [1]

[1]Laboratorio de Neuroinflamación, Unidad Periférica para el estudio de la Neuroinflamación, Instituto de Investigaciones Biomédicas en el Instituto Nacional de Neurología y Neurocirugía, Manuel Velasco Suárez, Ciudad de México, México. [2]Unidad de Citometría de flujo, Subdirección de Investigación Biomédica, Instituto Nacional de Enfermedades Respiratorias, Ciudad de México, México.
E-mail: draveravega42@gmail.com

Dendritic cells (DCs) constitute a heterogeneous and plastic population whose main functions are antigen presentation and T-cell priming. DCs can be either proinflammatory or anti-inflammatory, depending on the microenvironment. In fact, they are responsible for inducing and maintaining tolerance to certain antigens, regulating the immune response. Under physiological conditions, DCs are not found in the brain parenchyma, but they are recruited when an inflammatory process occurs. In a model of MPTP-induced PD, induction of tolerogenic dendritic cells (tol DC) by GM-CSF enhanced the regulatory response, resulting in neuroprotection. In this work, we developed an *in vitro* model of tol DC from healthy donor PBMC using GM-CSF and IL-4. The presence of surface markers like CD11c and ILT-3 was detected by flow cytometry, and the desired tol DC population was purified by cell sorting. Purified tol DC were then cultured either with or without pramipexole. RNA extraction from the stimulated tol DCs was also standardized to obtain nucleic acids that were included on a Fluidigm chip. This will allow us to genotype tol DC obtained by this method and pramipexole-stimulated tol DC, yielding important information on the relationship between the presence of some DC phenotypes and their response to PD treatment. Funding: CONACyT Frontera 64382

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Resumen corto

Combined Immunization With Epitope-Based Antigens To Prrsv-2 Induced Integral (Mucosal And Systemic) Binding And Neutralizing Antibody Response

Vega-López, M.A. [1]*, Fragoso-Saavedra, M. [1], Ramírez-Estudillo, C. [1], Alonso-Morales, R. [2]

[1]Centro de Investigación y de Estudios Avanzados del IPN, Depto. Infectómica y Patogénesis Molecular, Laboratorio de Inmunobiología de las Mucosas, Ciudad de México, México. [2]Laboratorio de Genética Molecular, Departamento de Genética y Bioestadística, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad de México, México.
E-mail: mavega@cinvestav.mx.

Porcine respiratory and reproductive syndrome virus (PRRSV) is an emerging and re-emerging virus causing important losses to the pig industry all over the world. Available intramuscular vaccines are ineffective to prevent infection and disease. Therefore, developing effective mucosal vaccines is needed. Here, we investigated a combined (parenteral/mucosal) immunization protocol to induce local and serum antibody responses, employing a soluble version of the epitope-based antigen 3BT, which contains conserved epitopes from the GP5 envelope protein of PRRSV-2. Vietnamese mini pigs were immunized employing different inoculation routes: subcutaneous (SC), intranasal (IN), or a combination of both (SC/IN). Soluble 3BT was a potent immunogen to elicit binding and neutralizing antibodies in serum, nasal mucus, and vaginal swabs, with varying patterns of concentration and activity, depending on the immunization schedule. Our results showed that intranasal immunization, alone or combined with subcutaneous delivery of epitope-based antigens, generated local and systemic binding and neutralizing antibodies. Further investigation is needed to evaluate the capability of the induced responses to prevent infection and reduce transmission. This work received funding from CONACyT-México (grant 2015-01-235 and scholarship 449596 MFS) and Asociación IPVS Mexico 2014 A.C.

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Resumen corto

Characterization of the inflammatory response of prostate epithelial cells modulated by *Trichomonas vaginalis*

Vega-Muñoz, F. [1]*, Ramírez-Ledesma, M.G. [1], Alva-Murillo, P.N. [1]

[1]Laboratorio de Inmunomicrobiología Molecular, Departamento de Biología, División de Ciencias Naturales y Exactas de la Universidad de Guanajuato, Ciudad de Guanajuato, Gto, México.
E-mail: f.vegamunoz@ugto.mx

Trichomoniasis is the world's most common non-viral sexually transmitted infection, caused by the flagellate protozoan parasite *Trichomonas vaginalis* (TV). Women and men are affected by this disease; however, little is known about the host-pathogen interaction in men. In this sense, prostate epithelial cells play an important role in the male genitourinary tract immune response by the recognition of invading pathogens. The innate immune response of prostate epithelial cells is dependent on TV strain. Thus, it is important to characterize the inflammatory response of prostate epithelial cells against a drug-resistant TV strain (CDC-085), which was the aim of this study. We evaluated i) the cytotoxic effect of TV on prostate epithelial cell line (RWPE-1) by MTT assay, ii) nitric oxide (NO) production, and iii) relative cytokines gene expression (IL-1β, TNF-α, IL-8, IL-10, and TGF-β) on TV-stimulated RWPE-1 (0-48 h) by Griess reaction and ΔΔCT method, respectively. The results showed that the multiplicity of infection (MOI) of 1:4 (epithelial cell:parasite) reduced RWPE-1 cell viability after 6 h of interaction. TV (MOI 1:0.4) induced NO production reaching the higher concentration at 6 h of interaction. In addition, TV increased the mRNA expression of IL-8 at 3 h; while IL-1β and TNF- α mRNA levels were augmented by 3- and 10-fold induction, respectively, at 6 h. After 24 h, TV increased IL-10 mRNA level. Our results suggest that TV regulates the inflammatory response in prostate epithelial cells, with implications for understanding trichomoniasis pathogenesis in men.

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Resumen corto

Evaluation of the cellular and humoral immune response of a vaccine candidate against COVID-19 with different alum adjuvant formulations

Vega-Rojas, L.J. [1]*, Velasco-Elizondo, M.A. [1], Ruiz-Manzano, R.A. [1], Hernández-Silva, D.J. [1], Carbajo-Mata, M.A. [2], Rocha-Solache, M. [1], Castro-Acosta, R.M. [3], Zarate, E. [3], Pérez Serrano, R. [4], Zaldívar-Lelo, G. [4], Ocampo-Gutiérrez, D.A. [3], García Gasca, T. [5], Mosqueda, J. [1]

[1]Immunology and Vaccines Laboratory, Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Qro, México. [2]Instituto de Neurobiología UNAM, Laboratorio Universitario del Bioterio, Universidad Nacional Autónoma de México, Querétaro, Qro, México. [3]Laboratorios Alpharma, Ciudad de México, CDMX, México, [4]Advanced Biomedical Research Center, School of Medicine, Universidad Autónoma de Querétaro, Querétaro, México, [5]Laboratorio de Biología Celular y Molecular, Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Qro, México.
E-mail: l.julianavega@gmail.com.

Vaccine development is a major contribution of immunology and medicine in the history of humanity against illness and epidemies. Different platforms are currently being used for the development and delivery of vaccines. Recombinant proteins are the antigens of choice for the generation of modern vaccines, however, the formulation of these vaccines with adjuvants is necessary. In Mexico, alum adjuvants are the only ones approved for use in human vaccines. The disease known by the WHO as COVID-19, is caused by the SARS-CoV-2 Coronavirus, in March 1rst, 2021, it was officially declared a pandemic. In this work we evaluated the humoral and cellular immune response of a recombinant protein with two alum adjuvants in different formulations in mice inoculated subcutaneously, with an immunization schedule of two doses for 31 days. Antibody titers were determined by indirect ELISA, lymphoproliferation assays and determination of cytokine production were performed by flow cytometry, and neutralizing antibodies were assessed by simulated neutralization assays. Higher titers of IgG, IgG_{2a} and IgG_1 antibodies were observed in the formulation with 60 µg protein and Adju-Phos with PHAD®, and specific $CD4^+$ and $CD8^+$ T cells were also observed. The highest levels of TNF-α and IFN-γ were also observed with this formulation. The presence of neutralizing antibodies against the Delta and Omicron variants of SARS-CoV-2 was detected. The formulation with 60 µg protein and Adju-Phos plus PHAD® was shown to be antigenic and immunogenic in mice vaccinated with a full two-dose schedule and with a Th_1 rather than Th_2 cell response.
Funding: the collection of economic funds that finance the research of the QUIVAX 17.4 vaccine (VACUNATON-UAQ), CONACyT postdoctoral fellowship.

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Resumen corto

Carbon nanotubes bioconjugated with *Entamoeba histolytica* 220 kDa lectin-derived peptides protect against amoebiasis through Th17 immune response

Velarde-Calderón, A. [1]*, Guzmán-Mendoza, J.J. [1], Talamás-Rohana, P. [1], González-Horta, M.C. [2], Sánchez-Ramírez, B. [2]

[1]Departamento de Infectómica y Patogénesis Molecular. Centro de investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Facultad de Ciencias Químicas, Universidad Autónoma de Chihuahua, Chihuahua, Chih, México.
E-mail: alejandro.velarde@cinvestav.mx

Amoebiasis is an infection that continues to be a health problem in Mexico; to date, there are no effective vaccines. The main problem lies in the evasion of immune response by this parasite. Looking for an effective immune response against this parasite, we bioconjugated carbon nanotubes with peptides derived from the 220 kDa lectin of *E. histolytica* (PL220-CNTs) and tested their immune response in an amoebiasis model. For this, hamsters were immunized with PL220-CNTs, and the antibodies response and cytokines pattern were analyzed. Additionally, we tested their efficacy to protect against amoebic liver abscess (ALA) formation in a hamster model. PL220-CNTs plus adjuvant elicited a high humoral response (antibody titers 1:1000); on the contrary, hamsters immunized only with PL220-CNT showed low antibodies titers (1:50). Cellular immune response was determined by Th1/Th2/Th17 cytokine analyses in serum and supernatants of splenocyte cultures by flow cytometry. Results suggest a strong Th17 response triggered by immunization with PL220-CNTs. Additionally, PL220-CNTs showed 100% protection in an ALA model, demonstrating a high protection efficacy. In conclusion, these results suggest that PL220-CNTs evoke a Th17 response against amoebiasis, which protects against ALA formation in a hamster model.

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Resumen corto

Evaluation of a chimeric protein as a multi-epitope vaccine designed against SARS-CoV2 variants of concern

Velasco-Elizondo, M.A. [1]*, Hernández-Silva, D.J. [1], Ruiz-Manzano, R.A. [1], Vega-Rojo, L.J. [1], Rodríguez-Torres, A. [2], Pérez-Serrano, R.M. [3], Zaldívar-Lelo, G. [3], García-Gasca, T. [5], Gómez-Soto, J. [6], Mosqueda, J. [1]

[1]Laboratorio de Inmunología y Vacunas, Universidad Autónoma de Querétaro, Facultad de Ciencias Naturales, Querétaro, México.[2]Laboratorio de Neurobiología Molecular, Universidad Autónoma de Querétaro, Facultad de Ciencias Naturales, Querétaro, México. [3]Laboratorio de Genética y Biología Molecular, Centro de Investigación Biomédica Avanzada, Facultad de Medicina, Universidad Autónoma de Querétaro, Querétaro, México. [5]Laboratorio de Biología Celular y Molecular, Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Qro, México. Laboratorio de nutrición animal Universidad Autónoma de Querétaro, Facultad de Ciencias Naturales, Querétaro, México.
E-mail: miguel.velasco@uaq.mx

Variants of Concern (VOC) of SARS-CoV2 are an ongoing worldwide problem with the main characteristic of evading the immune response in vaccinated people. Vaccines based on a single VOC cannot keep up with the mutation rate of the virus. Several peptides of the spike (S) protein have been observed to be conserved in all VOC. Epitope prediction software and bioinformatics tools for protein analysis allow the in-silico design of a protein constructed with multiple epitopes on a single polypeptide chain, called a chimeric protein. The aim of this work was the evaluation of C56BL/6 mice immune response vaccinated with different concentrations of the chimeric protein formulated with alum hydroxide. Three groups of five mice each were evaluated using two doses of 10, 20 and 30 µg of protein inoculated subcutaneously at days 0 and 21 and formulated with adjuvant. A fourth control group received only the adjuvant. T and B cell populations from the spleen and peripheral blood were analyzed by flow cytometry. Antibody production and antigen binding specificity were determined by ELISA and Western blot, respectively. Specific CD4+ and CD8+ T cells, as well as a higher titer of specific IgG antibodies, were observed in the sera of mice inoculated with the 30µg dose. The chimeric protein can polarize the immune response based on T cell populations as occurs in natural infection. The rational design of chimeric proteins as vaccines is a promising strategy for the control of SARS-CoV2 and the prevention of other emerging diseases.

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Resumen corto

Bariatric surgery reduces circulating mitochondrial DNA damage related to high levels of proinflammatory cytokines

Velásquez-Esparza, M. M. [1], González-Elena C.[1], Cuellar-Tamez, R. [1], Elizondo-Montemayor, L.[1], García-Rivas, G. [1,2], García, N. * [1,2]

[1]Tecnológico de Monterrey, Escuela de Medicina y Ciencias de la Salud. [2]The Institute for Obesity Research, Hospital Zambrano-Hellion, San Pedro Garza García, Nuevo León, México. Av. Batallon de San Patricio 112, Real San Agustín, 66278 San Pedro Garza García, N.L. garcianr@tec.mx Tel: (81) 8888 0466.

Bariatric surgery has shown reduce systemic inflammation. However, the mechanisms involved are still unclear. Mitochondrial DNA (mtDNA) has recently been proposed as a possible DAMP that binds to proinflammatory receptors which promotes the synthesis of cytokines, leading to a chronic inflammatory response. In a previous study, we identified higth relation between the loss of mtDNA integrity and markers oxidation with cytokines such as IL-6, IL-8, IL-18, and IL-17 in the plasma of patientsm with obesity. However, it has not yet been determined whether bariatric surgery could modify these parameters. In this work we identify the presence of mtDNA in plasma and relationship it with pro-inflammatory cytokines levels in a cohort of patients with obesity pre and post bariatric surgery. Methods: DNA oxidized (8-OH-dG) was measured by ELISA. A large mtDNA fragment was amplified by Long-PCR and normalized with small mtDNA fragments (MTND3, MTCO1) to evaluate its integrity. Cytokines were measured with flow cytometry. Results: A significant decrease in 8-OH-dG levels was observed after 3 and 6 months ($p = <0.001$) of surgery compared to pre-surgery. The presence of less damage was observed in the 3 and 6 months after surgery ($p = <0.0001$). A positive correlation was identified for 8-OH-dG with IL-18 ($r=0.458$, $p= 0.0094$) pre-surgery. After 3 months, 8-OH-dG had a negative and significant correlation with IL-8 ($r =-0.6708$, $p= 0.007$). Thus, bariatric surgery may reduce the damage and fragmentation of mtDNA, which may have directly related to the immune system response.

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Resumen corto

Phenotypic and genotypic study of patients with Hyper IgM syndrome

Velásquez-Ortíz, M. G. *[1], Nuñez-Nuñez, M. E. [2]. Zarate-Hernández, M. C. [3], Staines-Boone, T. [4], Yamazaki-Nakashimada, M. A. [5], Campos-Téllez, H. [6], Bustamante-Ogando, J. C. [7], Maravillas-Montero, J. L. [8a], Berrón-Ruiz, L. [7a].

[1] Posgrado en Ciencias Biológicas UNAM, Ciudad Universitaria, México, [2] Servicio de Alergia e Inmunología Clinica Pediatría, Hospital Civil de Guadalajara "Dr. Juan I Menchaca", [3]Departamento de Alergias, Hospital Universitario Monterrey, NL, [4] Servicio de Alta Especialidad, Centro Médico Noreste IMSS, Monterrey, NL, [5] Servicio de Inmunología y Alergia, Instituto Nacional de Pediatría SSA, Ciudad de México, [6]Servicio de Alergia e Inmunología del Hospital de Pediatría del CMNO IMSS, Guadalajara, Jalisco, [7]Laboratorio en Inmunodeficiencias, Instituto Nacional de Pediatría SSA, Ciudad de México, México, [8] Red de Apoyo a la Investigación, Universidad Nacional Autónoma de México e Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, México. [a] Co-corresponding authors.

Among the Inborn Errors of Immunity is the Hyper IgM syndrome (HIGM), which is clinically characterized by the presence of recurrent infections, phenotypically patients have high levels of IgM in serum and low levels of the rest of the immunoglobulins; this is because these patients have a defect in the germinal center reaction, that is to say, the B lymphocytes of these patients do not perform the isotype change so the only antibody they can produce is IgM. This work aims to identify phenotypic characteristics and mutations in the CD40 ligand (CD40L) gene. Phenotyping of cell populations and subpopulations was performed from the peripheral blood of patients by flow cytometry, as well as PBMCs from patients and healthy controls, which were activated with ionomycin and PMA for 24 hours to subsequently evaluate the expression of CD40L, as well as from gDNA, the mutations were determined by Sanger sequencing. The results of 19 patients with HIGM show low percentages of memory B cells with isotype change. CD40L expression after in vitro activation was decreased ($p<0.0001$), and 12 of the 19 mutations in the CD40LG gene were identified. From the identification of the pathogenic variant, it has been possible to confirm the clinical diagnosis, and it is expected to place it in all the patients; likewise, the pertinent functional studies will be carried out to prove that the genotype corresponds with the phenotype to contribute to the knowledge of the disease.

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Resumen corto

The pharmacological modulation of the hypoxia inducible factor 1 (HIF-1) modified the expression of IL-33, IL-17 and their receptors in a murine allergic inflammatory airway model

Ventura-Maqueda, D. [1]*, Rodríguez-Hernández, A. P. [1], Rodriguez-Jimenez, M. [1], Cocoletzi-Bautista, J. E. [1], Anaya-Estrada, D. [1], Hernández-Cueto, D. [1], Luria-Pérez, R. [1], Baay-Guzmán, G. J. [1]

[1]Unidad de Investigación en Enfermedades Oncológicas, Hospital Infantil de México Federico Gómez, Ciudad de México, CDMX, México.
E-mail: guillebaay@hotmail.com

The hypoxia inducible factor 1 (HIF-1) have a role in asthma regulating chemokines, proinflammatory cytokines and growth factors, associating with disease severity. Recently, it was reported that regulates transcriptionally the Interleukine-33 (IL-33), this alarmin is highly expressed in bronchial epithelium and regulates the production of Th2 cytokines, activates mast cells and type 2 innate lymphoid cells (ILC2). Besides, also regulates the IL-17 responsible of the neutrophilia associated with severe asthma. However, the link-up HIF-1/IL-33/IL-17 in asthma is a little understand. In this work we evaluate the effect of the pharmacologic modulation of HIF-1 in the IL-33 and IL-17 expression in a murine allergic inflammatory airway model with different severity grades. To achieve this, 5 mice per group receive ovalbumin (OVA) challenges 1 (mild), 2 (moderate) or 3 (severe) via intratracheal, with previous sensibilization with the allergen, besides the groups with induction or inhibition of HIF-1, receive intraperitoneal EDHB (OVA+EDHB) or intratracheal 2ME (OVA + 2ME) respectively. The control groups were treated in the same way, but with saline solution instead (SS). There were performed H&E (inflammatory infiltrate), PAS (mucous production) and immunohistochemistry (of HIF-1, IL-33, IL-17) stains, and were quantitatively analyzed with digital pathology. As results, we get different severity grades in the mice with more challenges, increasing the expression of HIF-1, correlated con the expression of IL-33/ST-2 and IL-17/IL-17R, increasing or decreasing, respectively for the pharmacologic modulation. These suggest that the high expression of HIF-1 favors the production of IL-33 and IL-17 contributing to pulmonary tissue damage and disease severity, and that this can be regulated via HIF-1 modulation.

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Resumen corto

Impact of the form of birth on the activation of neonatal CD4⁺ and CD8⁺ T cells

Ventura-Martínez, C. J.* [1], Kempis-Calanis, L. A. [1], Santana-Calderón, M. A. [1], Rodríguez-Jorge, O. [1]

[1]Centro de Investigación en Dinámica Celular, Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México.
*E-mail: carlos.ventura@uaem.edu.mx

Neonates are a highly vulnerable population, accounting for over 40 % of deaths in children under 5 years of age, with infection being a major cause of death. Neonatal T cells respond to antigens with a low activation and in CD8⁺ T cells, low cytotoxicity. Several factors impact neonatal health, such as maternal nutrition, smoking, and the form of birth. Several studies have highlighted the predisposition of neonates born by cesarean section to the development of childhood asthma and, later in life, metabolic and immunological chronic inflammatory diseases. We studied the response of neonatal CD4⁺ and CD8⁺ T cells from the cord blood of babies born by cesarean section or vaginal delivery. We used two stimulatory conditions: 1) anti-CD3+anti-CD28 and 2) anti-CD3+Flagellin, as we have previously published that TLR5 signals may provide co-stimulatory signals. We evaluated proliferation (homeostatic and in response to stimulation) and the activation of NFAT, NF-κB, and AP-1 transcription factors' activation. Our preliminary results show that differences in transcription factors' stimulation and cell proliferation are observed between T cells from neonates born by cesarean section and vaginal delivery. Overall, a higher proliferation induced by T cell stimulation were observed in the cells from cesarean section delivered babies. These results suggest that the form of birth has an impact on T cell activation. In addition, stimulation with CD3+flagellin leads to a higher proliferation rate of cells from the two forms of birth, suggesting that neonatal cells are sensitive to these stimulatory conditions.

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Resumen corto

The miRNA-TLR8-ROS axis, a new route to inflammation in childhood acute lymphoblastic leukemia

Vilchis-Ordoñez, A. [*1,2,6], Ramírez-Ramírez, D. [1], Romo-Rodríguez, R. [1], Rios de los Rios, J. [1], Maycotte, P. [1], Fabbri, M. [3], Ortíz-Navarrete, V. [4], Parra-Ortega, I. [2], Pelayo, R. [1,5].

[1]Laboratory of Oncoimmunology and Cytomics of Childhood Cancer, CIBIOR-IMSS, Puebla, México. [2]Children Hospital of Mexico, Federico Gómez, CDMX Mexico. [3]Center for Cancer and Immunology Research. Children's National Hospital. Washington DC, USA. [4]Molecular Biomedicine CINVESTAV, Mexico, Mexico.[5] Education and Research Unit, Mexican Institute of Social Security, CDMX, Mexico. [5]Clinical Biochemistry PhD program, School of Medicine, UNAM, Mexico. * vilchisarmando82@hotmail.com

Recent findings in our laboratory point towards the abnormally high production of microenvironmental pro-inflammatory elements within the bone marrow (BM) from Acute Lymphoblastic Leukemia (ALL) patients. miRNAs as hTLR8 ligands open the possibility of co-participating in the induction of pro-inflammatory microenvironments. We have identified three tumor-derived miRNAs contributing leukemia progression by switching on inflammation pathways that further induce the activation of stem/progenitor cells and innate immune cell populations. To investigate the TLR8 functional expression within the BM ALL niche, including normal and leukemic hematopoietic cell precursors, innate and adaptive immune cell populations and mesenchymal stromal cells (MSCs) as a potential mechanism of pro-inflammatory microenvironmental induction of leukemia progression. TLR8 expression levels were identified by multiparametric flow cytometry in early hematopoietic and immune BM cells from pediatric ALL patients. Mitochondrial/cytosolic and exclusive mitochondrial ROS production were investigated by dihydroethidium and Mitosox™ respectively, and analyzed by multiparametric flow cytometry. Treatment using pro-oxidant agents (H_2O_2 and antimycin) for ROS induction NF-kB and ASC (NLRP3 adapter) activation were studied. Cell sorting for TLR8 positive CD11c and CD34 population from mobilized peripheral blood was performed for R848 (resiquimod) stimulation. While $CD45^{int/low}CD34^{+}CD19^{+}$ BM leukemic precursors from pediatric patients showed mild expression of TLR8, residual hematopoietic stem cells and early lymphoid/myeloid progenitors displayed higher levels such PRR. Strikingly, innate immune cells, especially CD11c+ conventional dendritic cells and CD13+ myeloid cells were endowed with the highest expression and potential ability of proinflammatory responses upon miRNA activation. Moreover, ALL BM-derived MSCs cooperate to create a pro-inflammatory feedback loop. Unlike their normal counterparts, leukemic precursors produced high amounts of mitochondrial/cytosolic ROS and could not be induced to display more ROS by chemical methods with H_2O_2 or antimycin exposure, whereas low ROS production was observed in MSCs. There is moderate induction of NF-kB by induction of mtROS or tROS, particularly in lymphoid progenitors and NK cells. ASC expression is significantly higher in CD11c+ cells than in the rest of the BM hematopoietic populations in ALL patients. TLR8 expression in leukemic and normal hematopoietic BM cells from pediatric ALL may confer the niche the capacity of triggering pro-inflammatory responses due to activation of the TLR8-miRNAs-ROS axis. The use of innate immunomodulators as therapeutical strategy is suggested.

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Resumen corto

Role of Insulin and metformin in the modulation of inflammatory profile against *Escherichia coli* infection in a model hyperglycemia in human placenta

Villafuerte-Pérez, A. A. [1,2*], Jiménez-Escutia, R. [1,3], Vargas-Alcantar, D. [1,4], Flores-Espinosa, P. [1], Zaga-Clavellina, V. [1], Velázquez-Sánchez, M. P.[5], Olmos-Ortiz, A. [1]

[1]Departamento de Inmunobioquímica, Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, Ciudad de México 11000, México. [2]Facultad de Estudios Superiores Zaragoza, Universidad Nacional Autónoma de México, Ciudad de México 09230, México. [3]Posgrado en Ciencias Biológicas, Unidad de Posgrado, Universidad Nacional Autónoma de México, Ciudad de México 04510, México. [4]Posgrado en Ciencias de la Salud, Escuela Superior de Medicina, Instituto Politécnico Nacional, Ciudad de México 11340, México. [5]Departamento de Ginecología y Obstetricia, Hospital Ángeles México, Ciudad de México 11800, México. alineearumi@comunidad.unam.mx

Gestational Diabetes Mellitus (GDM) is a common metabolic disorder during the pregnancy, particularly in Mexico the reported prevalence of GDM was 23.7% in 2018. GDM is associated with the increase of serum inflammatory markers and increased risk for genitourinary infections during pregnancy. In addition, hyperglycemia is positively associated with vaginal dysbiosis and adverse maternal-fetal outcomes. On the other hand, insulin and metformin are prescribed as treatments for the glycemic control during GDM, however, its modulatory role in the inflammatory profile of placenta as well as its antimicrobial activity is not yet known. Therefore, in the present work we developed an *in vitro* model of hyperglycemia that resembles the conditions of GDM using third trimester placental explants to evaluate the modulatory effect of insulin and metformin on the inflammatory profile of the human placenta against *Escherichia coli* bacterial infection. Placental explants were cultured with glucose (10 and 50mM), insulin (500mM) or metformin (500 µM) for 48h, then infected with *Escherichia coli* ($1x10^5$ CFU/mL) and finally we evaluated the inflammatory cytokine secretion (TNF-α, IL-1β and IL-6) by ELISA and bacterial tissue invasiveness after 4 and 8 h of infection. We found that under hyperglycemia conditions the two hypoglycemic agents decreased the inflammatory effects and reinforced the inmune placental response by decreasing the number of CFU/mL and cytokine release. Altogether, these results suggest that the use of insulin and metformin could improve adverse maternal and fetal outcomes during GDM.

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Resumen corto

Microglia activation in hypoxic-ischemic encephalopathy: The two faces of Janus

Villanueva-Valle, J. S. [1], Hernández-Hernández, M. E. [2], Barrientos, Z. E. [2]

Academia de Bioquímica. Facultad de Medicina. BUAP. Puebla, Puebla, México.
julietavillvall2203@gmail.com

Hypoxic-ischemic encephalopathy (HIE) is a syndrome resulting from oxygen depletion that generates ATP depletion triggering a set of events that produce inflammation, blood-brain barrier (BBB) disruption and edema, causing cellular damage. In inflammation, as a result of cell damage, immune cells are activated as "watchdogs" of the neuronal environment, naturally immunoprivileged, including microglial cells that perform "macrophage-like" functions such as antigenic presentation, phagocytosis, production of proinflammatory cytokines and release of metalloproteinases (destroyers of the BBB); conditioning systemic responses that exacerbate brain damage. However, and like the personality of the God Janus in Greek mythology, the activation of this cell has two sides, one "opens" inflammatory pathways and the other "closes" the process, activating signaling responsible for resolution. The aim of the present work is to know the role of microglia in the development of the inflammatory process and its resolution in IHD. During the acute phase of HD, the phenotypic activation of microglia presents a proinflammatory profile that perpetuates damage leading to cell death. While, in the resolution phase, differentiation will produce an anti-inflammatory phenotype, aiding repair. Microglial profile activated during EHI depends on the microenvironments that promote their differentiation in the different phases of the disease, which will be described in depth.

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Resumen corto

Study of the inhibition of breast cancer cells viability via chemo-phototherapy with photoactive polymeric nanoparticles

Villanueva-Briseño, A. A. *[1], Sevilla-Rivero, R. [1], Navarro-Real, M. [1], Quintero-Ramos, A. [1], Del Toro-Arreola, A. [1], Topete-Camacho, A. [1], Daneri-Navarro, A. [1]

[1]Departamento de Fisiología, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, Guadalajara, Jalisco, México. adrian.villanueva@alumnos.udg.mx

Breast Cancer (BC) is the most mortal cancer that affects women, which had an incidence of 24.5% and a mortality of 15.5% of all cancers. BC treatment is mainly focused on the receptors that the tumors overexpress, however, conventional therapies (chemotherapy, radiotherapy, surgery, etc.) have severe side effects in patients, and BC can overwhelm those treatments by the developing resistance, leading to poor prognosis. Regarding this, nanomedicine can overcome the limitations that conventional therapies have. Implementation of photoactivable nanoparticles (NPs) shows advantages like controlled dose liberation, minimal invasion, fewer side effects, well tolerated by patients, and can be personalized. In this work, we evaluated the viability inhibition capability of photoactivable polymeric nanoparticles in BC cells (MCF7 and HCC1954 cell lines). NPs synthesis was made via double-emulsion solvent evaporation and were characterized with UV-vis spectrophotometry, dynamic light scattering and Doppler laser microelectrophoresis. BC cell viability was measured with spectrophotometry using a water-soluble tetrazolium salt (CCK-8) to quantify the number of live cells. We found that the viability of BC cell lines is inhibited when NPs and phototherapy were applied than without light stimulus, showing that our NPs can be internalized in BC and have a triple effect by means of doxorubicin, photothermal therapy, and photodynamic therapy. This multitherapeutic approach will be further studied with in vivo models to elucidate its potential clinical use in BC patients.

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Resumen corto

Encapsulation of Asparaginase into Virus-like particles of Brome Mosaic Virus

Villanueva-Flores, F. [1,2,3*], Pastor, A.R. [2], Palomares, L.A. [2], Huerta-Saquero, A. [1]

[1]Departamento de Bionanotecnología, Centro de Nanociencias y Nanotecnología, Universidad Nacional Autónoma de México. Km. 107 carretera Tijuana-Ensenada. 22860. Ensenada, BC. México. [2]Departamento de Medicina Molecular y Bioprocesos, Instituto de Biotecnología, Universidad Nacional Autónoma de México. Ave. Universidad 2001. Col. Chamilpa. 62210. Cuernavaca, Morelos, México. [3]Tecnologico de Monterrey, Escuela Nacional de Medicina y Ciencias de la Salud. Ave. Heroico Colegio Militar 4700, Nombre de Dios, 31300. Chihuahua, Chihuahua, México.

Asparaginase (ASNase) is a widely used drug to treat Acute Lymphoblastic Leukemia (LLA). ASNase often triggers severe immunogenic responses in pediatric patients which may lead to discontinuation of treatment. Plant-derived virus-like particles (pVLPs) have emerged as promising nanocarriers due to their lack of infection capability for humans, immunostimulatory properties to fight cancer cells, and high loading capacity. In this work, we encapsulated a commercial ASNase into Brome Mosaic Virus-like particles (BMV-VLPs) to form stable ASNase-BMV nanobioreactors. Encapsulation was performed taking advantage of electrostatic interactions between ASNase and VLPs proteins. ASNase-BMV nanobioreactores showed increased enzymatic activity and thermal stability in comparison with other similar encapsulation systems. Moreover, we observed that ASNase-BMV nanobioreactors had similar cytotoxicity against MOLT-4 and Reh cells than the commercial drug. A higher specific anti-ASNase IgG response in the mice group immunized with ASNase encapsulated into BMV VLPs compared with IgG anti-ASNase titers measured in the free ASNase mice group was observed. We detected a high and specific IgG response against BMV capsids but, interestingly the IgG response was lower with filled capsids (BMV+ASNase) compared with empty BMV capsids. BMV-VLP nanobioreactors demonstrated being a tool to stimulate the immune response. As far as we know, this is the first work where ASNase is encapsulated into pVLPs and is proposed as a novel formulation for LLA treatment.

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Resumen corto

Evaluation of the effect of neonatal *Candida albicans* infection on the distribution of mast cells in meninges

Villarreal-Rivota, B. *[3,4], Estrada-Parra, S. A. [1], González-González, G. M.[2], Chacón-Salinas, R. [3], Becerril-García, M. A.[4]

[1]Laboratorio de Inmunología Molecular I/Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Departamento de Microbiología, Facultad de Medicina, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México. [3]Laboratorio "Dr. Sergio Estrada Parra" /Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [4]Laboratorio de Inmunología Neonatal/Departamento de Microbiología, Facultad de Medicina, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México.
berenice.villarreal.rivota@gmail.com

Disseminated candidiasis to the brain is an important cause of morbidity and mortality, particularly in neonates, in whom it reaches a mortality rate of up to 90%. The control of the infectious agent in the central nervous system is mainly associated to the microglia cells. However, evidence indicates that mast cells (as immune cells present in meninges) generate a rapid response to brain damage in inflammatory or infectious contexts and that their activation precedes that of microglia. *In vitro* it has been demonstrated that MC can be activated with *Candida albicans* by degranulating, producing pro-inflammatory cytokines and releasing extracellular traps, but there´s a lack of *in vivo* evidence. In this work groups of adult and neonatal BALB/c mice were intravascularly infected with 1 x 10^5 CFU of *Candida albicans*. The development of neuroinfection was assessed by fungal load and metachromatic cell analysis by meningeal histopathology at different post-infection times. The brain fungal load showed the effective development of neuroinfection; while the number of meningeal metachromatic cells increased gradually during the course of the infection in both age groups, it was higher at the early neonatal stage. Additionally, the metachromatic cells that were activated in neonates increases during the infection; contrary to what is observed in adults, who maintain minimal levels of activation. Their higher activation could be related to a greater inflammatory environment during the development of neuroinfection in the neonatal phase vs. adult life, as well as to differences in the expression of cellular receptors during this stage.

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Resumen corto

IL-22 binding protein (IL-22BP) concentration and its correlation with clinical variables in patients with spondyloarthritis

Villavicencio-Arzaluz, R. * [1,2], Bernal-Alferes, B. [1,2], Meza-Olguín, G. [3], Casasola-Vargas, J. [3], Burgos-Vargas, R. [3], Domínguez-López, M. L. [2], Romero-López, J. P. [1,2].

[1]Laboratorio de Patogénesis Molecular, Red MEDICI, Carrera de Médico Cirujano, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla, Estado de México, México [2]Laboratorio de Inmunoquímica 1, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México. [3]Departamento de Reumatología, Hospital General de México "Dr. Eduardo Liceaga", Ciudad de México, CDMX, México. Contact: ricardovilla2809mail.com

Axial spondyloarthritis (axSpA) are rheumatic inflammatory diseases that share genetic triggers and environmental factors that promote inflammation. The inflammatory mechanisms are altered by the type 3 immune effector response, mediated by IL-17 and IL-22-producing cells. It is possible that the mechanisms that regulate type 3 immunity are altered in these patients. Our aim was to determine if type 3 effector cytokines are altered in SpA. We included 19 patients with SpA, and registered clinical and radiological variables. We measured the concentrations of IL-22BP, calprotectin, of IL-1β, IL-10, IL-8, IL-6 and IL-8 concentration is increased in axSpA patients' serum when compared to healthy controls (p=0.03). IL-22BP is diminished in axSpA patients (p=0.04) and serum calprotectin is higher (p=0.002). Serum calprotectin concentrations are higher in patients with high disease activity (ASDAS) (ANOVA p=0.01) and on the contrary, a higher activity was related to low IL-22BP levels. Patients with high calprotectin levels have higher concentrations of IL-1β, IL-10 and IL-8 (p=0.03, 0.0007, 0.007, respectively). IL-8 and IL-6 concentrations are increased in the synovial fluid, meanwhile IL-22BP is decreased. A clear correlation exists between type 3 cytokines with disease activity and imaging studies. IL-1β, IL-6, IL-8 and IL-10 have higher serum concentrations in axSpA patients, while IL-22BP levels are decreased. The concentration of these cytokines is correlated with activity scores, imaging findings, and serum calprotectin levels.

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Resumen corto

Characterization of lymphocyte subpopulations in lymphoma dogs

Vinagre-Ruiz, J. [1]*, Cobos-Marín, L. [1], Muñoz-Duarte, A. I. [1], Olguín-Alor, R. [4], López-Mejía, E. [4], Rodríguez-Cortés, O. [5], Cervantes-Arias, A. [3], Ramírez-Díaz, G.[2]

[1]Departamento de Microbiología, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Av. Universidad #3000, Edificio3, Colonia, C.U., Coyoacán, 04510 Ciudad de México, México. [2]Departamento de Patología, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Av. Universidad #3000 Edificio 1, Colonia, C.U., Coyoacán, 04510 Ciudad de México, México.[3]Hospital Veterinario de Especialidades, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Av. Universidad #3000, Colonia, C.U., Coyoacán, 04510 Ciudad de México, México.[4]Laboratorio Nacional de Citometría de Flujo, Instituto de Investigaciones Biomédicas, UNAM Circuito Escolar S/N, Ciudad Universitaria, Colonia, C.U Coyoacán, 04510 Ciudad de México, México.[5]Laboratorio de Inflamación y Obesidad, Sección de Estudios de Posgrado e Investigación, Escuela Superior de Medicina, Instituto Politécnico Nacional. Salvador Díaz Mirón y plan de San Luis. Col. Santo Tomás, Ciudad de México, México.
mvzvinagre@gmail.com

Non-Hodgkin lymphoma (NHL) is the seventh most common cancer in humans and represents 4.3% of all malignancies. In dogs, canine lymphoma occurs in approximately 6% of all malignant neoplasms in the dog, and comprises 80-90% of neoplasms of hematopoietic origin. Changes in the immune response are crucial to its development because it can deplete or promote its development. In this research the objective was to evaluate the changes in the different lymphocyte subpopulations in peripheral blood of dogs with lymphoma. Lymphocyte subpopulations were evaluated, using the flow cytometry technique, in 10 healthy dogs and three dogs newly diagnosed multicentric lymphoma with non-treatment. In Healthy dogs, the obtained percentages were : T lymphocytes 61.52 ± 11.9%, T helper lymphocytes 32.62 ± 8.3%, cytotoxic T lymphocytes 20.87 ± 7.1%, T regulatory cells 0.90 ± 0.2%, NK-like cells 14.11 ± 8.2%, B lymphocytes 25.33 ± 7.1 and a CD4/CD8 ratio of 1.5, in contrast with lymphoma dogs, whose percentages were: T lymphocytes 30.83 ± 28.63%, T helper lymphocytes 51.80 ± 17.09%, cytotoxic T lymphocytes 26.72 ± 20.57%, T regulatory cells 8.5±8.5%, NK-like cells 6.0±2.2% and B lymphocytes 46.8±45.1% and a CD4/CD8 ratio of 1.9. Changes in lymphocyte populations in lymphoma patients compared with healthy dogs, such as decreased NK-like cells and increased T regulatory cells, could have clinical relevance, so more studies must be conducted with a bigger number of dogs with lymphoma. This research was made at the National Flow Cytometry Laboratory.
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Resumen corto

Role of Macrophage Migration Inhibitory Factor (MIF) in the development of diabetic retinopathy

Zacarias-García, M. [1*], Juárez-Avelar, I. [2], Reyes-Hernández, J. L. [3], Ramos-Montes, O. A. [1], Rodríguez-Hernández, T. [1], González-González, M. I. [3], Vázquez-Mendoza, A.[1]

[1]Laboratorio de Enfermedades Inflamatorias Oculares, Carrera de Optometría, Facultad de Estudios Superiores Iztacala UNAM, Tlalnepantla de Baz, Estado de México, México. [2]Laboratorio de Inmunidad Innata, UBIMED, Facultad de Estudios Superiores Iztacala UNAM, Tlalnepantla de Baz, Estado de México, México. [3]Laboratorio de Inmunología Experimental y Regulación de la Inflamación Hepatointestinal UBIMED, Facultad de Estudios Superiores Iztacala, UNAM, Tlalnepantla de Baz, Estado de México, México.
*Autor correspondencia: aliciavm@ired.unam.mx

Diabetic retinopathy (DR) results from progressive damage to the retinal microvasculature as a consequence of the sustained hyperglycemic state, oxidative stress, and inflammatory process. Altogether, these events promote changes in the permeability of the blood-retina barrier, progressive loss of vascular endothelial cells, activation of microglia, and neovascularization, leading to decreased visual acuity and blindness. Clinical studies reported increased levels of IL-1β, IL-6, TNF-α and macrophage migration inhibitory factor (MIF) in vitreous and serum samples from RD patients. MIF is constitutively expressed in human cornea and rat iris, retina and ciliary epithelium, and it has been demonstrated that MIF indeed aggravates pathologies in the posterior eye segment, like vitreoretinopathy and uveítis. However, information about its role in the development of ocular inflammatory diseases such as DR is limited. We aimed to determine if MIF promotes the development of RD. Type II diabetes was induced in male 7-week-old, wild-type (WT) and MIF genetically deficient mice ($Mif^{-/-}$), through the intraperitoneally administration of two doses of streptozotocin (100mg/kg weight) at 2-day intervals. We observed that at 8 weeks of Diabetes induction, $Mif^{-/-}$ mice presented lessened tissue injury as evidenced in retina sections as compared to WT mice. Also, in absence of MIF, decreased infiltrating cells were observed in the inner plexiform and ganglion cell layers of retina as compared to WT mice. These observations were associated with lower blood glucose concentration and VEGF transcripts in retinal tissue. Our results show that MIF is a key player during the development of DR.

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Resumen corto

TGF-β controls the proliferation and survival of CD8⁺ T cells in a Trim33-dependent way

Zambrano-Romero, J. D. *[1], Contreras-Castillo, E. [1], Ramos-Baldera, J. L. [1], Licona-Limón, P[1].

[1]Departamento de Biología Celular y del Desarrollo, Instituto de fisiología Celular, Universidad Nacional Autónoma de México, Mexico City, Mexico. jromero@ifc.unam.mx

CD8⁺ T cells are essential players in the defense against infections elicited by viruses and bacteria, as well as for killing transformed cells during cancer. Transforming growth factor β (TGF-β) is a potent immunosuppressive cytokine known to regulate several CD8⁺ T cell functions. It restrains the expression of IFN-γ, granzyme B, and perforin, which are essential for CD8⁺ T cell effector functions. Additionally, TGF-β elicits cell cycle arrest and apoptosis in effector CD8⁺ T cells. Unfortunately, the exact mechanisms by which TGF-β carries out these effects in CD8⁺ T cells remain unknown. Trim33 is an E3 ubiquitin ligase that can be activated downstream of TGF-β signaling; however, the role of Trim33 in CD8⁺ T cell functions has not been studied. Here, we focused on elucidating the TGF-β-dependent function of Trim33 in CD8⁺ T cells. We found a reduced TGF-β anti-proliferative capacity in activated Trim33$^{-/-}$ CD8⁺ T cells compared to WT CD8⁺ T cells. In addition, there was increased survival of Trim33$^{-/-}$ CD8⁺ T cells in the presence of TGF-β in vitro. Using a melanoma mouse model and an acute infection mouse model with OVA-expressing Listeria monocytogenes, we observed that Trim33$^{-/-}$ CD8⁺ T cells proliferate better than their WT counterparts in the tumor and during the clonal expansion phase, respectively. These data suggest that Trim33 could regulate CD8⁺ T cell proliferation and survival in a TGF-β-dependent manner.

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Resumen corto

Bone marrow mesenchymal stromal cell immunophenotyping predicts MRD in childhood acute lymphoblastic leukemia

Zamora-Herrera, G. *[1,2], Alberto-Aguilar, D. [1], Gaspar-Mendoza, P. A. [1,3], Torres-Pineda, L. [1,4], Romo-Rodríguez, R. [1], López-Blanco, J. A. [1], Ayala-Contreras, K. A. [1], Trejo-Pichardo, C. O. [1], Balandrán, J. C. [5], Ramírez-Ramírez, D. [1], Casique-Aguirre, D. [1], Monjaraz, E. [2], Pelayo, R. [1,6]

[1]Laboratory of Oncoimmunology and Cytomics of Childhood Cancer, CIBIOR-IMSS, Puebla, México. [2]Physiology Institute, Benemérita Universidad Autónoma de Puebla, Puebla, México. [3]Bachelor of Biomedicine, Benemérita Universidad Autónoma de Puebla, Puebla, México. [4]Bachelor of Biotechnology, Benemérita Universidad Autónoma de Puebla, Puebla, México. [5]Laboratory of Dr. Iannis Aifantis, Department of Pathology, NYU, NY, USA. [6]Education and Research Unit, Mexican Institute of Social Security, CDMX, Mexico.
gabriela.zamorah@alumno.buap.mx

B-Acute Lymphoblastic Leukemia (B-ALL) is a global health priority due to the high incidence and mortality rates. B-ALL is characterized by high proliferation of blast cells that emerge and progress in bone marrow (BM) niches, where normal hematopoiesis is blocked and their niches are hijacked and progressively reconfigured. Mesenchymal stromal cells (MSC) are key components of the BM niche for normal hematopoiesis and exhibit important immunomodulatory properties. We have previously shown that MSC contributed to B-ALL pathogenesis by generating a pro-inflammatory microenvironment followed by exhaustion of hematopoietic stem and progenitor cells (HSPCs) and/or immunosuppression, supporting tumoral progression. By RNA seq approach, we also demonstrated the activity of at least two niches supporting leukemogenesis. In this work, we aim to explore a MSC-based patient risk stratification by evaluating the MSC phenotypic profile through multidimensional flow cytometry in primary MSC derived from B-ALL pediatric patients. 50 primary MSCs cultures were evaluated for 21 cell surface markers, showing apparent MSCs profiles associated to disease evolution endowed with the expression of CD39, Galectin-9, VCAM1, IDO1, NFkB, CXCL11 and a number of inflammatory and immunosuppressive molecules whose expression levels change from debut to MRD monitoring. Of note, CD39 appears as a marker of leukemia maintenance niches supporting malignant clones with aberrant expression of CD66c. For the first time, our results show the importance of MSCs phenotypic signatures to predict outcomes and propose innovative targets for concomitant therapies focused on the tumor microenvironment.

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Resumen corto

Determination of immunological endotypes in the pathogenesis of atopic dermatitis

Zumaya-Pérez, L. C. *[1], Velazquez-Samano, G. [2], Valerio-Gómez, V. I. [2], Mondragón-García, D. [2], Pastelin-Palacios, R. [1], Moreno-Eutimio, M. A.[1]

[1]Laboratory of Immunobiology, Department of Biology, Faculty of Chemistry, National Autonomous University of Mexico, Mexico City, CDMX, Mexico. [2]Allergy and Immunology Service, HGM "Eduardo Liceaga", Mexico City, CDMX, Mexico. zumachao@gmail.com

Atopic dermatitis (AD) is a common chronic inflammatory skin disease with a prevalence of 20% in children and 5% in adults in developed countries. T-cell response, especially T helper cells of type Th2, is important in AD. However, recent research has found that Th1 and Th17 responses are present in some endotypes, and the role of T cytotoxic response is unclear. T-cell response also differs between ethnic groups. The CLA molecule, CCR4, and CCR10 chemokine receptors are important in AD immunopathology. The study aimed to determine CLA, CCR4, and CCR10 in T cells by flow cytometry in 25 AD patients and 15 healthy controls in the Mexican population. Results showed more expression of CLA and CCR4 but not CCR10 in Th cells of severe AD patients compared to healthy controls. In vitro production of IFN-γ is less in CD8+ T cells of AD patients. There were no differences in IL-4 and IL-17 production. In summary, T helper cells of severe AD patients express more CLA and CCR4 than healthy controls in the Mexican population. In vitro production of IFN-γ is less in CD8+ T cells of AD patients. These results contribute to proposing immunological endotypes in AD and could have implications for developing personalized treatments.

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Resumen corto

Proof-of-concept of an antigenic protein against SARS-CoV-2

Zúñiga-Hernández, M. E. *[1], Reyes-Barrera, K. L. [1,2], Abraham-Juárez, M. J. [1,3], Guzmán-López, J. A. [1,3], Alpuche-Solís, A. G. [1]

[1]División de Biología Molecular, Instituto Potosino de Investigación Científica y Tecnológica, A.C., San Luis Potosí, San Luis Potosí, México. [2]Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, CDMX, México. [3]Laboratorio Nacional de Genómica para la Biodiversidad (LANGEBIO), Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV), Irapuato, Guanajuato, México.
melvin.zuniga@ipicyt.edu.mx

Severe acute respiratory syndrome 2 (SARS-CoV-2), caused by a coronavirus, is responsible for more than 6.9 million deaths worldwide. The best alternative to avoid severe cases is vaccination. The different platforms for vaccine production have been improved to reduce costs, secondary effects and to improve the immune response. However, production costs remain high. Therefore, we expressed and purified in a bacterial system, the receptor binding domain (RBD) of the SARS-CoV-2 spicule protein as a proof of concept of mice immunization. To elucidate the immune response of RBD, we set up an immunization program using a subcutaneous route in BALB/c mice, and testing 5 and 7.5 µg of RBD and adjuvant. We collected serum samples, tracheopulmonary and intestinal lavages and we evaluated immunoglobulins by indirect ELISA. Immunization of the RBD antigenic protein generated a strong immune response, obtaining high IgG titers after the 3rd immunization in serum samples. On the other hand, the IgG antibody titer was maintained until day 60 after the first immunization for both treatments. We observed that the treatment with 7.5 µg of RBD generated a high IgG production in lung and intestinal lavage samples, moreover, both treatments presented IgA production in these mucouse membranes. Additionally, we detected neutralizing antibodies against RBD in serum samples in both treatments, therefore, the results are promising for future challenge in mice.

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