IMMUNOPERU 2025

INTERPLAY BETWEEN THE ENVIRONMENT AND THE IMMUNE SYSTEM

October 5 - 11, 2025

Señorial Hotel
567 Jose Gonzales, Miraflores,
Lima, Peru

IUIS International Union of Immunological Societies

ALACI LATIN AMERICAN AND CARIBBEAN ASSOCIATION OF IMMUNOLOGY

Peruvian Society for Immunology

immunopaedia.org

CONCYTEC CONSEJO NACIONAL DE CIENCIA, TECNOLOGÍA E INNOVACIÓN TECNOLÓGICA

ProCIENCIA

UNIVERSIDAD PERUANA CAYETANO HEREDIA

About IMMUNOPERU 2025:

This IUIS-ALACI-PSI course has brought together a diverse group of students, immunologists and experts to share their distinct perspectives, skills and expertise. The focus was on a variety of endemic and emerging diseases related to environmental and climate change.

The goal was to catalyze the development of novel concepts, methods and approaches in addressing these emerging challenges.

MAIN TOPICS

The course has addressed the Impact of environmental exposures on immunity in infectious disease, chronic inflammation and cancer with particular attention to:

Changes in microbial communities and their metabolites that drive inflammatory disease (eg. effects of antibiotics, dietary and other factors)

Environmental cues and pollutants linked to the development of hematologic malignancies.

The impact of climate change on endemic infectious diseases (eg. Tuberculosis, Dengue Fever, Chagas Disease, and others).

Local Organizers:

Dr. Liz Veramendi
Dr. Iris Goyzueta
Dr. Rosario Inocente
Dr. Iskra Tuero
Dr. Marie Lazo
Dr. Cecilia Diaz

International organizers:

Dr. Yanet Valdez
Dr. Kelly McNagny
Dr. Rosana Pelayo
Dr. Clive Gray
Dr. Guillermo Docena
Dr. Roslyn Kemp

Faculty:

Dr. Michael Schnoor
Dr. Mónica Guzman
Dr. Stella Hartinger
Dr. Gabriel Núñez
Dr. Caroll Beltrán
Dr. Manuela Verastegui
Dr. Mónica Pajuelo
Dr. José Ignacio Larco
Dr. Cesar Galván
Dr. Jule Vázquez
Dr. Olivia Rodriguez
Dr. María Antonieta Quispe
Mag. Christian Campos
Dr. Cesar Ramal
Dr. Amy Morrison
Dr. Eduardo Verne
Dr. Carlos Vera
Dr. Pilar Suguimoto

FUNDINGS:

International Union of Immunology Societies – IUIS

IMMUNOPAEDIA

Asociación Latinoamericana y Caribeña de Inmunología - ALACI

Sociedad Peruana de Inmunología – SPI

CONCYTEC – PROCIENCIA

Universidad Peruana Cayetano Heredia - UPCH

MONDAY OCTOBER 6TH: OPENING TALKS

CHAIR: DR. YANET VALDEZ

7:00–7:30h	BREAKFAST
8:30h	BEYOND BORDERS: CHAMPIONING RESPECT AND INCLUSION IN IMMUNOLOGY RESEARCH Drs. Yanet Valdez, Kelly McNagny and Mónica Guzman
10:00h	OPENING TALK"CLIMATE CHANGE AND INFLUENCES HEALTH" Dr. Stella Hartinger Peña
10:30h	Q&A/COFFEE/TEA BREAK

SCIENTIFIC SESSION 1: " THE IMMUNE SYSTEM IN RESPONSE TO ENVIRONMENTAL PRESSURES "

11:00h	CLIMATE CHANGE AND YOUR HEALTH: "THE IMMUNE CONNECTION" Dr. Clive Gray
11:20h	HOW IT IS THOUGHT THAT ENVIRONMENTAL EXPOSURES MAY IMPACT CLONAL HEMATOPOIESIS AND THUS THE IMMUNE CELLS AND PREDISPOSITION TO OTHER ILLNESSES OR CONDITIONS Dr. Mónica Guzmán
11:40h	Q&A AND DISCUSSION WITH THE SPEAKERS
12:00h	LUNCH BREAK Dinning room

PANEL DISCUSSION ON TECHNOLOGY DEVELOPMENT FOR EVALUATING IMMUNE RESPONSES

14:00h	SPECTRAL CYTOMETRY, CYTOF, HYPERION, O-LINK, HUPROT, SPATIAL TRANSCRIPTOMICS AND ANALYSIS Dr Kelly McNagny, Dr. Rosana Pelayo, Dr.Gabriel Nuñez, Dr. Michael S. & Dr. Clive Gray (TBC)
	Q&A AND DISCUSSION FROM THE STUDENTS Moderador: Dr. Mónica Guzmán
15:00h	HANDS ON EXERCISE: FACULTY MEMBERS CREATE A PROPOSAL OUTLINE & SPECIFIC AIMS ON THE SPOT (IMMUNOHACKATHON). STUDENTS CHOOSE TOPICS. FACULTY WEARS THEIR SOCCER COUNTRY T-SHIRT.
16:00h	COMFORT BREAK
16:15h	1ST GRANT PROPOSAL BRAINSTORMING SESSION EACH TEAM GOES WITH THEIR MENTORS AND ESTABLISH THEIR WORKING PROJECTS IUIS Team and mentors
17:30h	FIND YOUR TEAM MATES All
18:00h	POSTER SESSION DAY 1
19:30h	ICE BREAKER ACTIVITY / DINNER

TUESDAY OCTOBER 7TH : SCIENTIFIC SESIONS

CHAIR: DR. KELLY MCNAGNY

SCIENTIFIC SESSION 2: "ENVIRONMENTAL EXPOSURES: ALLERGIC AND METABOLIC DISEASE"

7:00–7:30h	BREAKFAST
8:30h	THE GUT MICROBIOTA: ROLE IN HEALTH AND DISEASE Dr. Gabriel Nuñez
9:00h	THE IMMUNE SYSTEM IN ALLERGIES Dr. Kelly McNagny
10:00h	STRESS AND CHRONIC URTICARIA, WHAT COMES FIRST Dr. Jose Ignacio Larco
10:30h	EXPLORING THE RELATIONSHIP BETWEEN ALLERGIC SENSITIZATION AND REGIONAL CLIMATE CLASSIFICATIONS IN PERU Dr. Cesar Galván
	Q&A INTEGRATED WITH COFFEE BREAK

SCIENTIFIC SESSION 3: RESEARCH IN MICROBIOME IN AUTOINFLAMMATORY DISEASES: CROH'S COLITIS, IBS

11:30h	STRESS, MICROBIOTA AND LIVER PATHOLOGY Dr. Caroll Beltrán
12:00h	UNDERSTANDING COLITIS INDUCED BY IMMUNE CHECKPOINT BLOCKADE IN CANCER THERAPY Dr. Gabriel Nuñez
12:30h	CLIMATE CHANGE, IMMUNOLOGY AND INFERTILITY Drs. Liz Veramendi & Rubén Motrich
13:00h	MICROBIOTA AND INTESTINAL FIBROSIS Dr. Yanet Valdez/ Dr. Kelly McNagny
	Q&A AND DISCUSSION WITH THE SPEAKERS
13:30h	LUNCH BREAK

CHAIR: DR. ROSANA PELAYO

SCIENTIFIC SESSION 4: "ENVIRONMENTAL EXPOSURES: CANCER & LEUKEMIAS"

15:00h	ENVIRONMENTAL EXPOSURE IN NORMAL AND MALIGNANT LYMPHOPOIESIS Dr Rosana Pelayo
15:30h	SOCIO-ENVIRONMENTAL DETERMINANTS AND RISK MAPPING IN LEUKEMIA Dr Juan Carlos Nuñez
16:00h	TARGETING CANCER STEM CELLS IN LEUKEMIA Dr Monica Guzman
16:30h	IMMUNOTHERAPY FOR THE TREATMENT ACUTE LYMPHOBLASTIC LEUKEMIA Dr. Jule Vazquez - Peru
17:00h	Q&A AND DISCUSSION WITH THE SPEAKERS All
17:30h	COFFEE BREAK
18:00h	SECOND GRANT WRITING WORKSHOP & GROUP WORK IUIS Team and mentors
19:00h	POSTER SESSION DAY 2
20:00h	DINNER

WEDNESDAY OCTOBER 8TH : SCIENTIFIC SESIONS

CHAIR: DR. ISKRA TUERO

SCIENTIFIC SESSION 5: "CLIMATE CHANGE AND IMPACT ON ENDEMIC DISEASES"

7:00–7:30h	BREAKFAST
8:00h	APPLICATIONS OF IMMUNOINFORMATICS IN THE DEVELOPMENT OF MULTI-EPITOPE ANTIGENS FOR VACCINES AND IMMUNODIAGNOSTICS Dr. Mirko Zimic
8:30h	BREAKING PARADIGMS IN TUBERCULOSIS: CAN ANTIBODIES CHANGE THE COURSE OF THE DISEASE? Dr. Iskra Tuero
9:00h	NEUROCYSTICERCOSIS AND THE NEUROINFLAMMATION Dr. Manuela Verastegui
9:30h	CHAGAS IMMUNOLOGY Dr. Olivia Rodriguez Morales
10:00h	VACCINES RESEARCH AND DEVELOPMENT IN VECTOR-BORNE VIRAL AND PARASITIC DISEASES Dr. Emilio Malchiodi
10:30h	MICRO-RNA ROLE FOR CHAGAS DISEASE CONGENITAL TRANSMISSION Dr. Monica Pajuelo
11:00h	THE HUMORAL IMMUNE RESPONSE, THE DIFFICULTY OF SEROLOGICAL DIAGNOSIS OF TEGUMENTARY LEISHMANIASIS ASSOCIATED WITH THE NUTRITIONAL STATUS OF PATIENTS. Dr Maria Quispe Ricaldi
11:30h	Q&A AND DISCUSSION WITH THE SPEAKERS

11:45h TEA/COFFEE BREAK (AT THE RESTAURANT)

11:45h POSTER SESSION DAY 3

13:00h LUNCH BOX AND BUS BOARDING (SOCIAL EVENT: SIGHTSEEING MUSEUM VISIT)

19:45h ARRIVAL TO THE HOTEL

20:30h DINNER
MULTICULTURAL NIGHT
(A table will be available to place snacks and other items you have brought from your country to share)

THURSDAY OCTOBER 9TH : SCIENTIFIC SESSIONS AND GRANT PROPOSAL

CHAIR: DR. IRIS GOYZUETA

SCIENTIFIC SESSION 7

6:30h–7:30h BREAKFAST

8:00h BIRD VIEW
Dr. Iris Goyzueta

8:30h ACTUAL SITUATION OF THE CLIMATE CHANGE AND METAXENIC DISEASES TRANSMISSION: ONGOING RESEARCH IN LORETO REGIONAL HOSPITAL – zoom
Dr. Cesar Ramal (Creating a Research facility from scratch)

8:50h WHY DON'T WE HAVE MUCH CHIKUNGUNYA VIRUS IN PERU? SORTING IT OUT USING A ONE-HEALTH RESEARCH APPROACH
Dr. Amy Morrinson
UCDavis - AB PRISMA

LESSONS LEARNED FROM LONGITUDINAL COHORT STUDIES ON DENGUE IN IQUITOS, PERU. WHAT ARE THE IMPLICATIONS FOR VACCINATION?
Dr. Amy Morrinson
UCDavis - AB PRISMA

9:30h TEA/COFFEE BREAK

10:00h DENGUE 1 VS DENGUE 2 MMUNOLOGICAL PROFILE IN DENGUE: HOW DO ENVIRONMENT AND IMMUNITY INFLUENCE THE CLINICAL PROGRESSION OF THE DISEASE?
Moises Apolaya (MINSA) Dengue I
Mag. Christian Campos (UNTRM) Dengue 2

11:00h PEDIATRIC RESPONSE
Dr. Eduardo Verne

11:30h IMMUNOSENESCENCE – SPECIFIC RESPONSE
Dr. Carlos Vera

12:40h DIAGNOSTIC KITS – MALARIA
Dr. Pilar Suguimoto

13:00h Q&R

13:30h THE FUTURE OF WORK IN THE HEALTH SECTOR: INNOVATION, JUST TRANSITION, AND GREEN JOBS FOR A CLIMATE-RESILIENT FUTURE
Mg. Fiorella Davero Guevara

14:00h LUNCH

14:35h 3RD GRANT PROPOSAL BRAINSTORMING SESSION
IUIS Team and mentors/panels

17:30h TEA BREAK (INDOOR)

18:30h RECAP

18:30h END OF DAY 5

19:00h DINNER

FRIDAY OCTOBER 10TH : GROUP PRESENTATIONS, FEEDBACK AND DISCUSSION

CHAIR: DRS. CLIVE AND MICHAEL

GROUP PRESENTATIONS, FEEDBACK AND DISCUSSION

7:00–7:30h BREAKFAST

9:00h GRANT PROPOSAL PRESENTATION BY GROUPS AND FEEDBACK

10:30h TEA/COFFEE BREAK

10:45h GENERAL DISCUSSION ON COURSE AND FEEDBACK FROM STUDENTS

13:00h LUNCH BREAK

14:00h ROUNDTABLE: HOW CAN WE MOVE FORWARD AS LATIN AMERICAN IN IMMUNOLOGY? SPECIFIC AIMS FOR THE FUTURE?
ACTION ITEMS: AS SCIENTISTS WHAT CAN WE DO TO MINIMIZE CLIMATE CHANGE?
IMMUNOPERU FOR THE WORLD:
TIMING OF THE MIRAFLORES COLLABORATION AGREEMENT

15:20h AWARDS FOR POSTER PRESENTATIONS AND GRANTS

19:00h FAREWELL EVENT

SATURDAY OCTOBER 11TH : SPECTRAL FLOW CYTOMETRY SESSION. THEORY AND PRACTICE AT CAYETANO HEREDIA UNIVERSITY (UPCH)

6:00h–7:00h BREAKFAST

7:00h STUDENTS LEAVE TO CAYETANO HEREDIA UNIVERSITY (UPCH) FOR CLASS

13:00h END OF THE COURSE

14:30h LUNCH

IUIS-ALACI-SPI IMMUNOPERU-2025

INTERPLAY BETWEEN THE ENVIRONMENT & THE IMMUNE SYSTEM

SEPTEMBER 2ND-OCTOBER 11TH , 2025
HOTEL SEÑORIAL 567 JOSÉ GONZALES, MIRAFLORES 15074, LIMA, PERU

PRE-COURSE ON-LINE SESSION 1: SEPTEMBER 2ND

15:00–16:30h SESSION 1: PICTURE A SCIENTIST
Dr. Yanet Valdez

PRE-COURSE ON-LINE SESSION 2: SEPTEMBER 5TH

15:00–16:30h ZOOM MEETING 2 – PRESENTATION ON GRANT WRITING
Dr. Clive Gray and mentors

PRE-COURSE ON-LINE SESSION 3: SEPTEMBER 9TH

15:00–16:30h ZOOM MEETING 3 – BREAKOUT ROOMS WITH FACULTY
Dr Clive Gray and mentors

PRE-COURSE ON-LINE SESSION 4: SEPT 15TH /17TH

15:00–16:30h SESSION 4: PRESENTATIONS ON GRANT WRITING 3
Dr. Tracey Lamb

SUNDAY OCTOBER 5TH: OPENNING CEREMONY

18:00h WELCOME AND INTRODUCTIONS
Drs. Liz Veramendi, Iskra Tuero, Iris Goyzueta, Marie Angelique Lazo, Rosario Inocente and Cecilia Díaz

18:30h KEYNOTE ADDRESS
Dr. Sixto Enrique Sánchez Calderón - President National Council of Science, Technology and Innovation (CONCYTEC)
Dr. Clive Gray - IUIS
Dr. Iskra Tuero - SPI/Local Committee

19:00h PISCO SOUR WELCOME DRINK & OPENNING DINNER RECEPTION

Decoding the Language of Tumor-Immune Communication: The Role of Extracellular Vesicles in Melanoma

Ercole Agustina [1], *Ana Carolina Donadío* [2], *María Julia Lamberti* [1,3]

[1] INBIAS-CONICET-UNRC, Rio Cuarto, Córdoba, Argentina.
[2] CIBICI-UNC, Argentina.
[3] Departamento de Biología Molecular, Facultad de Ciencias Exactas, Físico-Químicas y Naturales, UNRC, Argentina.

Ultraviolet (UV) radiation, a major environmental risk factor, plays a central role in the development of cutaneous melanoma—a highly aggressive cancer characterized by a high mutational burden. Beyond initiating malignant transformation, UV exposure also shapes the tumor microenvironment (TME), influencing immune surveillance and inflammation. Immunotherapies have shown promise in melanoma treatment, yet a significant proportion of patients remain unresponsive, underlining the need to better understand tumor-immune dynamics influenced by environmental factors.

Extracellular vesicles (EVs) released by tumor cells are emerging as key mediators of intercellular communication, carrying bioactive molecules that impact immune function, inflammation, angiogenesis, and therapy resistance. To investigate these mechanisms, we developed a novel melanoma model using murine B16-F10 cells genetically engineered to express CD63-GFP, allowing fluorescent tracking of EVs.

Cells were transfected with a pCD63-GFP plasmid using polyethylenimine (PEI), and stable clones were selected via G418 antibiotic resistance and confirmed by fluorescence microscopy. This model enables us to visualize EV release and uptake in real time, providing a tool to explore how environmental stressors such as antitumor therapies influence EV-mediated immune modulation.

Ongoing studies focus on how melanoma-derived EVs affect dendritic cells, key regulators of adaptive immunity, and whether stress-induced changes in EV cargo can promote antitumor or immunosuppressive responses. This approach aims to illuminate new therapeutic pathways at the intersection of environmental exposure, immune regulation, and cancer progression.

The effect of lead (Pb) on the immune response and working memory of children and adults from Huautla, Morelos

Aída Elizondo García [1], *Christian G. Curiel Guerrero* [1], *Paula Licona Limón* [2], *Fernanda Reyes Mojica* [3], *J. Quetzalli Trujillo Domínguez* [3], *Marcela Osorio Beristain* [4], *Jaqueline García Hernández* [5] *& Isaac G-Santoyo* [3]

[1] Institute of Ecology, Mexico City, México.
[2] Institute of CellularPhysiology, Mexico City, México, UNAM.
[3] Faculty of Psychology, Mexico City, México, UNAM; [4]CIByC, UAEM,Cuernavaca, Morelos, México; [5]CIAD, Guaymas, Sonora.

In the Sierra de Huautla Biosphere Reserve in Morelos, Mexico, significant mining waste containing heavy metals such as Pb has accumulated. Pb can directly affect the central nervous system by entering the brain, disrupting neuronal communication, and modulating the immune system (IS), including the proliferation of IS cells and cytokine expression. These effects may also influence brain regions involved in working memory. However, the interaction between these systems in human populations remains poorly understood.

This study aims to assess the impact of Pb exposure on cytokine expression and the phenotypic profile of IS cells, as well as to evaluate working memory performance in children and adults living in Huautla, Morelos. Pb concentrations were measured in hair samples using voltammetry. Working memory was assessed using the Neuropsychological Battery of Executive Functions Frontal Lobes, and serum cytokines were quantified through a multiplex assay (IL-1β, IFN-α, IFN-γ, TNF-α, IL-6, IL-10, IL-12p70, IL-33, IL-4, IL-23, IL-18, IL-17A, IL-8, and MCP-1). Peripheral blood mononuclear cells were isolated, cryopreserved, and later stimulated for flow cytometry analysis of T lymphocyte.

Preliminary findings revealed significantly higher Pb concentrations in adult males (n=42) compared to females (n=78; Mann–Whitney U test), and higher working memory scores in females (n=15) than in males (n=10; Student's t-test). These sex differences may result from cultural and physiological factors, including hormonal influences. Using general linear models and generalized least squares, Pb concentrations in hair were found to be negatively associated with serum levels of IL-1β, IFN-α, IFN-γ, TNF-α, IL-6, IL-10, IL-12p70, and IL-33. For some cytokines, such as IL-1β and TNF-γ, this relationship was sex-dependent, appearing only in boys.

These preliminary results suggest that chronic Pb exposure is associated with altered cytokine expression in a dose-dependent manner. High Pb levels appear to be linked to immunosuppression, while low doses may trigger immune activation, possibly influenced by Pb itself or by other environmental factors. Ongoing analyses aim to further characterize the effector and activator phenotypes of immune cells and their possible relationship with working memory performance.

Role of Bcl-3 and senescence in Colorectal Cancer

A. Cassana [1,2,3,4,5], *R. Maldonado-Agurto* [6,7], *G. Landskron* [6,7], *M. De La Fuente* [6,7], *I González* [6,7], *B. Gárate PdT* [2], *M. Abedrapo M* [1,8], *F. López-Köstner* [9], *C.J. Beltrán* [2,10].

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[6] Universidad Finis Terrae, Center of Biomedical Research, Santiago de Chile, Chile.
[7] Clinica Las Condes, Santiago de Chile, Chile.
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[9] Clinica Universidad de Los Andes, Santiago de Chile, Chile.
[10] Universidad de Concepción, Clinical Biochemistry and Immunology Department, Concepción, Chile.

Introduction: Colorectal cancer (CRC) is a leading cause of cancer worldwide. Cellular senescence has been implied in its carcinogenesis and could be promoted for environmental factors; activating the NF-κB signaling pathway. Bcl-3 protein is a key factor in the regulation of this pathway, whose levels are elevated in CRC, and has been considered as a poor prognostic marker. It is unknown the role of the senescence and Bcl-3 in CRC. **Objectives:** To evaluate the Bcl-3 expression and the presence of cellular senescence (p16 expression) in the intestinal mucosa of healthy and pathological tissue of patients with CRC, and subsequently establish the correlation between them and the disease's clinical stage. **Methods:** CRC patients from three Chilean centers were included. In tumoral tissue (TU) and adjacent non-tumoral tissue (non-TU) from the surgical piece, the expression of Bcl-3 and p16 were determined by immunohistochemistry, QuPath for image analysis [Positivity index (PI) and H-score (H)]. Wilcoxon, Mann Whitney U, Kruskal Wallis, and Spearman correlation were used for comparison and correlation, respectively; significance: $p<0.05$. **Results:** Twenty-four patients were included. Twenty-five TU and 24 non-TU samples were analyzed. Bcl-3 and p16 expression were significantly higher in TU compared to non-TU tissue, both in the epithelium and glandular area (Bcl-3:PI p=0.053; H p=0.0242 - p16:PI p=0.001 – H p=0.011) as in lamina propria and stromal area (Bcl-3:PI p=0.006; H p=0.002 - p16:PI p=0.001 – H p=0.001); mainly in the epithelium. Bcl-3 and p16 cytoplasmic expression had a positive correlation in the epithelium of TU (PI:r=0.570, p=0.011; H:r=0.498, p=0.029). There was a positive correlation between Bcl-3 expression in TU and metastasis (r=0.474, p=0.040); likewise, between p16 expression in TU and clinical stage (PI:r=0.528, p=0.020; H:r=0.460, p=0.048), tumor size (r=0.479, p=0.038), lymph node involvement (r=0.528, p=0.020), and metastasis (PI:r=0.580, p=0.009; H:r=0.606, p=0.006). **Conclusion:** The higher expression of Bcl-3 and p16 and the cytoplasmic correlation in TU suggests an interaction between senescence and Bcl-3 pathway in CRC.

Assessing Cytotoxic mediators secreted by Immune Cells in Patients with Drug-Sensitive Active Pulmonary Tuberculosis Undergoing Treatment

Alessia Piamonte [1], *Sandra Palma Albornoz* [1], *Iskra Tuero* [1]

[1] Laboratorio de Inmunobiología de Infecciones- Facultad de Ciencias e Ingeniería, Universidad Peruana Cayetano Heredia, Lima- Perú.

Tuberculosis (TB) remains a critical public health threat in Peru and Latin America. Although, there are drugs available for TB treatment the lack of efficient monitoring tools hinders effective control. This study provides valuable insights into the immunological dynamics of TB by analyzing cytotoxic immune responses throughout the six-month anti-TB treatment. By evaluating the behavior of circulating immune cells—CD8+ T cells, NK cells, B cells, granulocytes, and iNKT cells—and their production of cytotoxic molecules (perforin and granzyme B). We assess the different immune cell populations and the cytotoxic molecules by flow cytometry. We obtained total blood from active TB patients before initiating treatment, at 2 and 6 months of treatment. We observed distinct functional patterns associated with immune recovery and pathogen clearance. NK and T cells showed progressive restoration of cytotoxic activity during treatment, suggesting a reactivation of protective immune responses. iNKT cells demonstrated early perforin production, potentially contributing to initial pathogen control. Meanwhile, neutrophils showed reduced perforin production as bacterial burden decreased, reaffirming their role in early defense. B cells exhibited a dichotomous response, shifting from cytotoxic activity to adaptive functions, such as potential antibody production. These findings emphasize the importance of monitoring immune responses during TB treatment, not only to understand disease progression but also to identify potential biomarkers of therapeutic response. Ultimately, this knowledge can help transform the clinical approach to tuberculosis by enabling more precise diagnosis, personalized treatment strategies, and the development of novel immunotherapies and vaccines. Understanding the immune landscape of TB is not only vital for regional public health but represents a critical step forward in the global fight against one of the world's deadliest infectious diseases.

Risk assessment in the hematological and biochemical profile of patients suspected or confirmed with Zika, Dengue or Chikungunya in Valencia, Venezuela

Angel Fernandez [1,2], *Sarah Bethencourt* [1], *Adriana Tami* [1,3]

[1] Faculty of Health Sciences, University of Carabobo, Valencia, Venezuela.
[2] Department of Physiological Sciences, Faculty of Health Sciences, University of Carabobo, Valencia, Venezuela.
[3] Department of Medical Microbiology, University Medical Center Groningen, Groningen, Netherlands.

The epidemic caused by Dengue (DENV), Zika (ZIKV) and Chikungunya (CHIKV) constitutes a public health problem in Venezuela. The objective of the study was to analyze blood samples from patients older than 5 years who presented acute febrile syndrome suspected of arboviral infection and to characterize the laboratory risk profile, during the co-circulation of DENV, ZIKV and CHIKV in Valencia, Venezuela. Acute (day of illness 1-5) and follow-up (day of illness ≥6) blood samples were collected from 367 symptomatic patients enrolled in a multicenter study of febrile patients recruited between 2012 and 2016. The samples were analyzed by RT-PCR for the three arboviruses and the findings were related to hematological and biochemical parameters. Statistical analysis showed that decreased platelet count (p=0.004) and total cholesterol levels (p=0.004), as well as increased alanine aminotransferase (p=0.005) and creatine kinase levels in blood (p=0.017), were significant independent risk factors for DENV infection. On the other hand, decreased white blood cell count (p=0.025) and lactate dehydrogenase levels (p<0.001), as well as reduced blood albumin concentration (p=0.001), are significant and independent risk factors for CHIKV and ZIKV, respectively. Laboratory characterization is imperative for the timely diagnosis of infected patients. Hematological and biochemical risk parameters can complement clinical findings to make a timely diagnosis in patients with undifferentiated febrile syndrome.

Cellular exhaustion in T cell subsets and IgG (anti-Spike) antibody response in people vaccinated against the SARS-CoV-2 Virus

Camila Arlet Aronés Santayana [1,2], *Ivan Lozada-Requena* [1]

[1] Laboratorio de Inmunología, Departamento de Ciencias Celulares y Moleculares, Facultad de Ciencias e Ingeniería, Universidad Peruana Cayetano Heredia, Lima- Perú.
[2] Centro de Investigación de Virología, Universidad de San Martín de Porres, Lima- Perú.

Introduction: Vaccination against SARS-CoV-2 has significantly reduced the effects of the pandemic; However, it is important to know the effects on post-vaccination immunological components to know how they can be affected. **Objectives:** Determine percentage changes in the population of total lymphocytes, T cells (TC) and their subsets; evaluate the level of cellular exhaustion of TC CD4+ and CD8+ and determine IgG (anti-spike) antibodies level in different vaccination platforms. **Methodology:** We isolated PBMC and serum from 51 vaccinated and 15 unvaccinated participants to measure the percentages and MFI of lymphocyte populations and the concentration of IgG antibodies, respectively, by flow cytometry and ELISA. Statistical data were analyzed with GraphPad Prism 9. **Results:** Vaccination with 3P+1M+1P induced a lower %CD3+ than 3P+1M; lower %CD8+ than 3P and 3P+1M, but higher %CD4+ than 3P+1M. All groups vaccinated or not presented a negative correlation in which the higher the %CD8+ the lower the %CD4+. Cellular exhaustion in CD4+PD1+ from 3P+1M was greater than in all CD8+PD1+ from all vaccination platforms including non-vaccinated, except 3P and CD4+PD1+ vaccinated or unvaccinated platforms. No significant differences were found in the production of IgG (anti-spike) in the vaccination platforms. **Conclusion:** Homologous or heterologous vaccination platforms starting with 3 doses do not modify the production of IgG (anti-spike) antibodies; However, they improve LTCD8+ values, which are the most important subset for the antiviral response against SARS-CoV-2.

Characterization of B Cell Populations in Malaria Caused by Plasmodium vivax Using Single- Cell RNA Sequencing (scRNA-seq)

Julian Torres Flores [1,2], *Katherine Torres, PhD* [1], *Joseph M. Vinetz, MD* [3], *Elizabeth Villasis, PhD* [2], *Fabiola Díaz Soria, MSc* [2]

[1] Department of Cellular and Molecular Sciences, Universidad Peruana Cayetano Heredia (UPCH), Lima, Peru.
[2] Laboratorio de Referencia Regional de Loreto (LRRL), Dirección Regional de Salud Loreto, Iquitos, Peru.
[3] Division of Infectious Diseases, Department of Internal Medicine, Yale School of Medicine, New Haven, CT, USA.

Plasmodium vivax is the most geographically widespread cause of human malaria, often leading to recurrent and chronic infections due to its ability to form dormant liver stages (hypnozoites). Despite its public health impact, the immune mechanisms underlying *P. vivax* infections—particularly those governing humoral responses—remain poorly understood. B cells play a pivotal role in the adaptive immune response to malaria, not only through antibody production but also via antigen presentation and immunomodulation. However, the phenotypic and transcriptional diversity of B cell subpopulations during P. vivax infection is yet to be fully characterized.

In this study, we employed single-cell RNA sequencing (scRNA-seq) to profile peripheral blood mononuclear cells (PBMCs) from individuals with *P. vivax* malaria, both symptomatic and asymptomatic, as well as from uninfected controls in an endemic region of the Peruvian Amazon. High-resolution transcriptomic analysis allowed us to identify distinct B cell subsets, including naïve, memory, atypical memory, and plasmablast populations, and to evaluate their gene expression signatures and clonal relationships.

We observed significant shifts in the distribution and activation states of B cells during active P. vivax infection. Atypical memory B cells—often associated with chronic antigen exposure— were markedly expanded in symptomatic individuals. Gene expression analysis revealed upregulation of inhibitory receptors, altered metabolic pathways, and transcriptional programs consistent with immune exhaustion and dysregulated humoral immunity.

These findings provide novel insights into the immunological landscape of *P. vivax* infection and highlight potential targets for therapeutic and vaccine strategies. Our data underscore the importance of single-cell approaches in uncovering the complexity of host immune responses in malaria and contribute to a better understanding of B cell-mediated immunity in neglected tropical diseases.

Seropositivity of four Serological Tests for *Strongyloides spp.* Detection in a Retrospective Cohort in community of the Peruvian Amazon

César David Martel Serrubio [1,2]

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Strongyloides spp. is a soil-transmitted helminth endemic in tropical regions, where diagnosis remains challenging due to its often asymptomatic presentation and low larval output in stool samples. Serological testing has emerged as a reliable alternative; however, variability in diagnostic performance among different assays remains a concern. This study aimed to compare the seropositivity rates of four serological assays used to detect anti-Strongyloides IgG antibodies.A retrospective cohort of 500 plasma samples from individuals residing in the community of Zungarococha, Loreto (Peruvian Amazon), was analyzed. The evaluation included two ELISA tests—one using the recombinant NIE antigen and another employing a crude larval antigen—as well as two qualitative rapid tests. Frequencies of seropositive and seronegative results were compared among the four assays. Additionally, Fleiss's Kappa was used to assess agreement among the tests, and Fisher's exact test was applied to identify statistically significant differences.The ELISA based on recombinant NIE antigen yielded the highest seropositivity rate (61.9%), followed by the ELISA with crude antigen (42.8%). In contrast, the two rapid tests showed markedly lower detection rates. Fisher's exact test indicated a significant difference between the NIE-based ELISA and the crude antigen ELISA ($p < 0.05$), supporting the superior sensitivity of the recombinant antigen. In conclusion, the recombinant NIE-based ELISA demonstrated enhanced performance in detecting anti- Strongyloides antibodies. These results support its potential utility in serological screening and epidemiological surveillance, especially in endemic areas where conventional parasitological or molecular tools may be inaccessible. Incorporating recombinant antigens into diagnostic strategies could improve detection rates and facilitate early treatment in affected populations.

C- reactive protein levels in paraguayan patients infected with Chikungunya virus

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Chikungunya virus (CHIKV) is an alphavirus from the Togaviridae family, transmitted by Aedes aegypti and Aedes albopictus mosquitoes. In recent decades, it has caused several outbreaks around the world and continues to spread rapidly to new regions, partly driven by climate change and globalization.

Infection with this virus causes a febrile illness accompanied by joint pain and myalgia, along with other symptoms such as arthritis, skin rash and headache. Although the disease is self-limiting and not associated with high mortality, it can lead to severe, chronic and disabling arthritis, representing a burden on healthcare systems.

During the acute phase, CHIKV infects macrophages and fibroblasts in synovial joints. This infection is characterized by high viremia and a strong immune response, mainly involving the production of antiviral IFN-alpha, as well as many pro-inflammatory cytokines such as IL-6 and TNF-alpha, and chemokines, which trigger the sudden onset of fever and joint inflammation typical of the disease.

C-reactive protein (CRP) is an acute-phase protein whose levels increase in response to pro-inflammatory cytokines such as IL-6, and is therefore considered a biomarker of inflammation. CRP has been reported as a prognostic marker in CHIKV infection, with higher levels observed in viremic compared to non-viremic patients.

The inflammatory response to CHIKV is not yet fully understood; therefore, this study measured CRP levels in paraguayan patients diagnosed with Chikungunya disease. CRP levels were measured by immunoturbidimetry in 150 serum samples from paraguayan patients of both sexes, with confirmed Chikungunya infection by RT-qPCR.

We observed an elevation of CRP levels during the acute viremic phase of Chikungunya disease in the paraguayan population. CRP levels were negatively correlated ($p<0.01$) with Ct values obtained through virus-specific qPCR analysis.

Further studies are needed, including additional inflammatory mediators such as pro- inflammatory cytokines, to identify potential biomarkers of CHIKV disease.

Pediatric STAT3 Hyper-IgE Syndrome: A case series

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Introduction: STAT3 hyper-IgE syndrome (HIES), also known as Job syndrome, is a rare inborn error of immunity (IEI) characterized by a constellation of symptoms related to increased infection susceptibility, eczema, elevated serum IgE levels (>2,000 IU/ml), craniofacial anomalies, and recurrent bone fractures. **Objectives:** We aimed to evaluate the spectrum of clinical and immunological features in pediatric patients with HIES at a national pediatric tertiary hospital. **Methods:** We retrospectively reviewed the cases of five pediatric patients with STAT3-HIES followed at the Instituto Nacional de Salud del Niño from May 2023 to January 2025. We analyzed clinical presentations, immunological evaluations, genetic testing, and treatment. **Results:** This study comprised five male patients, the median age at diagnosis was 7 years, with a median diagnostic delay of 3 years. Four (80%) patients suffered from necrotizing pneumonia with empyema, and one (20%) had chronic mastoiditis. Among the bone anomalies, we found thoracic scoliosis (2/5) and genu valgum (1/5). Mucocutaneous manifestations included eczema (3/5), recurrent abscesses (2/5), and oropharyngeal candidiasis (2/5). Predominant pathogens were Candida albicans, Pseudomonas sp., and Staphylococcus aureus, each identified in two patients. Hypogammaglobulinemia was observed in two patients, and four patients presented with mildly reduced CD4+ T and CD19+ B cell counts. Genetic analysis revealed two pathogenic STAT3 gene variants: c.1144C>T (3/5) and c.1909G>A (2/5). Finally, intravenous immunoglobulin therapy was administered to one patient. **Conclusion:** The common clinical features of the patients were recurrent sinopulmonary and mucocutaneous infections, and eczematoid skin lesions. Further investigation is required to advance our comprehension of HIES and formulate focused treatment strategies to improve the quality of life for affected patients. This represents the initial Peruvian case series on STAT3-HIES.

Activated PI3K Delta Syndrome in a Pediatric Patient: A Case Report on Diagnosis and Management

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Background: Activated PI3K Delta Syndrome (APDS) is a rare inborn error of immunity caused by pathogenic variants in the PIK3CD or PIK3R1 genes. It presents with recurrent infections, lymphoproliferation, autoimmunity, and an increased risk of malignancy. Without prompt diagnosis and treatment, APDS can result in severe complications. **Aim:** To diagnose and manage a child with chronic diarrhea and failure to thrive, using a multidisciplinary approach to uncover the underlying cause and initiate therapy. **Results:** The patient exhibited chronic diarrhea, significant growth retardation, and generalized weakness. On physical examination, hepatomegaly and splenomegaly were noted. Laboratory analysis revealed anemia and thrombocytopenia, as well as T CD4 lymphopenia with normal serum immunoglobulin G, A, and M levels. Imaging studies, including ultrasound and CT, revealed hepatomegaly, splenomegaly, and an abdominal tumor of unknown etiology. MRI findings were pending at the time of this report. Biopsy of the ileum and colon demonstrated malakoplakia, an unusual histopathological finding that may suggest underlying immune dysregulation. Genetic sequencing revealed a heterozygous pathogenic variant, in the PIK3CD gene, confirming the diagnosis of APDS. Based on the clinical and paraclinical findings, treatment included monthly intravenous immunoglobulin, everolimus to control lymphoproliferation, and antibiotic prophylaxis. The patient is under evaluation for hematopoietic stem cell transplantation, a potentially curative option. **Conclusions:** APDS is a challenging condition to diagnose due to its variable presentation. This case highlights the importance of genetic testing in patients with unexplained immune dysfunction. The finding of malakoplakia in this patient is notable and underscores the spectrum of immune dysregulation associated with APDS. HSCT remains the only curative therapy for APDS, but it is associated with significant risks. Our team at Hospital Nacional Edgardo Rebagliati Martins remains committed to advancing the diagnosis and management of inborn errors of immunity.

Temporal study of inflammation and its relation to the progression of axonal damage in an animal model of neurocysticercosis

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Introduction: Neurocysticercosis (NCC) is a helminthic infection of the central nervous system (CNS) caused by the larval stage of *Taenia solium* (cysticercus). It is endemic in Latin America, with an estimated prevalence ranging from 4.9% to 22.6%, and between 10% and 20% in Peru. The presence of cysticerci in the CNS triggers a chronic inflammatory response that contributes to neuronal damage. Glial cells, particularly microglia and astrocytes, play a key role in neuroinflammatory processes associated with neurodegenerative diseases. In conditions such as Alzheimer's, Parkinson's, and multiple sclerosis, chronic microglial activation—combined with inefficient phagocytosis and impaired communication with neurons—has been shown to contribute to neuronal damage. However, this mechanism has not been well studied in NCC. This study aims to provide evidence on how inflammatory responses, including microglial activation, may contribute to the progression of neuronal damage in NCC.

Results: An animal model of NCC was used, with five groups corresponding to 1.0, 1.5, 3.0, 6.0, and 12 months post-infection (mpi). Distinct inflammatory patterns were observed across disease stages. In early phases, macrophage infiltration occurred without fibrosis, whereas by 3 mpi, macrophages were associated with fibrotic tissue, in both parenchymal and meningeal cysts. Fibrosis staining revealed a shift in collagen type: type III predominated early, while type I became more prevalent at later stages. Microglial activation increased over time, with distinct morphologies (amoeboid, hypertrophic, dystrophic) observed at different stages.

Conclusions: Cellular infiltration, fibrosis, and collagen type vary over time and depend on cyst localization, reflecting a complex inflammatory dynamic associated with progressive axonal damage.

Deciphering the environmental impact on the leukemic niche: a redox imbalance upon acute exposure to heavy metals

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Background: Increasing environmental pollution worldwide has been linked to a rise in non-communicable diseases, including childhood leukemia (CL). Regions with high pollution levels, such as the Alto Atoyac Basin (CAA, acronym in Spanish) that covers Puebla and Tlaxcala, Mexico has been exhaustively studied by our group from the epidemiology perspective, demonstrating an association between CL and toxicant as heavy metals. However, the underlying mechanisms remain poorly understood.

Aim: To explore the biological mechanisms involved in pro-leukemogenic development in bone marrow (BM hematopoietic niches.

Material and Methods: Three-dimensional BM-like organoids were structured by using mesenchymal stromal cells (MSCs) and leukemia blasts from BM aspirates of CL patients, followed by experimental exposure to heavy metals $CdCl_2$ and As_2O_3 to evaluate their biological effects. ROS production, cell cycle, cell proliferation, and proteins involved in signaling pathways activation (pNFkB, pSTAT1, pAKT, ASC, IL-1b, TLR4), along with cytokines and chemokines (CXCL12, CXCL10, CXCL11, CXCL8, CXCL5) relevant to hematopoiesis, and the receptor CXCR7 were investigated by flow cytometry. DNA damage was analyzed using comet assays.

Results and conclusions: Metal exposure increased proinflammatory proteins such as CXCL8, CXCL10, CXCL11, CXCL12, pSTAT1, and pNFκB, as well as ROS levels, both total and mitochondrial, primarily by cadmium. Leukemic cells showed a higher population in G0/G1 phase and increased undivided cells following cadmium treatment. Comet assays confirmed DNA damage. These findings suggest cadmium and arsenic modify the microenvironment by inducing oxidative stress, activating damage response pathways, generating a positive feedback loop between ROS and inflammation and promoting cell cycle arrest as an adaptative response. Since leukemic cells exhibited compromised DNA repair systems, DNA mutations can arise. We propose that oxidative stress, DNA damage and inflammatory pathways (e.g. NF- κB) collectively lead to DNA mutations and altered signaling pathways related to cell survival, proliferation, and inflammatory response, contributing to the leukemia ecosystem.

Use of polyclonal Antibodies for the detection of circulating Trypanosoma cruzi antigens in clinical Samples

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Chagas disease, caused by the protozoan *Trypanosoma cruzi*, is a parasitic infection that affects millions of people, primarily in Latin America. It is estimated that between 6 and 10 million individuals are infected worldwide, with thousands of deaths reported annually. The disease progresses through three clinical phases: acute, indeterminate, and chronic. During the acute phase, in addition to serological tests, molecular methods can be used to confirm active parasitic infection. In the indeterminate and chronic phases, diagnosis relies mainly on serological detection of specific antibodies. However, these tests can yield false positives due to cross-reactivity with other diseases such as leishmaniasis, and cannot distinguish between past and active infections, as antibodies may persist even after successful treatment.

To overcome these limitations, the direct detection of circulating T. cruzi antigens in body fluids such as serum and urine has emerged as a promising diagnostic alternative, as it provides direct evidence of active infection. To address this, a two-stage project was designed. In the first stage, antigenemia and antigenuria were experimentally evaluated in infected guinea pigs. In the second stage polyclonal antibodies were produced in alpacas, rabbits, and chickens immunized with different T. cruzi antigens (excreted/secreted, membrane, trypomastigote lysate, and recombinant 1F8 protein). These antibodies were used to develop a capture ELISA for detecting circulating antigens in clinical samples (serum, plasma, and urine) from seropositive patients.

The results were encouraging: 55% of the seropositive samples were also positive in the antigen-capture ELISA, with consistent detection in matched plasma and urine samples (10.1371/journal.pntd.0006069). These findings support the potential of polyclonal antibodies to enhance Chagas disease immunodiagnostic, particularly as a tool to confirm active infection. As a next step, further characterization of the detected antigens using techniques such as Western blot in both serum and urine is proposed. This will enable more precise identification of circulating antigens, aid the development of more sensitive and specific diagnostic tools, and facilitate their implementation in laboratories located in endemic areas.

Airway administration of OM-85 bacterial lysate mitigates *Pseudomonas aeruginosa* susceptibility but aggravates inflammation and tissue damage in a preclinical cystic fibrosis model.

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Pseudomonas aeruginosa is a gram-negative bacterium frequently associated with severe infections in cystic fibrosis (CF) patients. Its ability to colonize the lungs fosters persistent infections that are difficult to eradicate, leading to progressive lung function decline and increased morbidity and mortality. This study evaluated the prophylactic efficacy of the bacterial lysate OM-85 in a preclinical CF model and its impact on P. aeruginosa infection. C57BL/6 mice were induced into a CF model, nasally administered 1mg of OM-85, and subsequently infected with the virulent PA14 strain. Quantitative PCR analysis revealed that OM-85 modulated the lung microbiota, reducing Bacteroidetes and Gammaproteobacteria while increasing Firmicutes. In the CF model, Bacteroidetes and Firmicutes were predominant. Upon infection, OM-85-treated mice exhibited lower bacterial burden but heightened immune activation, with increased pulmonary levels of IL-17 and IFN-γ and reduced IL-10. Flow cytometric analysis demonstrated an increased influx of $CD11^{+}CD86^{+}$, $CD4^{+}IFN\text{-}\gamma^{+}$, and $CD4^{+}IL\text{-}17^{+}$ immune cells in the lungs. Histopathological analysis showed pronounced tissue damage in OM-85-treated and PA14-infected mice, including septal thickening, alveolar collapse, and leukocytic infiltration. Liver tissue from PA14-infected groups exhibited hepatic parenchyma expansion, sinusoidal capillary collapse, and increased interstitial cellularity, correlating with elevated serum AST and ALT levels. These findings suggest that while OM-85 prophylaxis enhances immune defense against P. aeruginosa, it also exacerbates tissue damage, warranting further investigation into its long-term effects in CF patients.

Temporal Analysis of Axonal Mitochondrial Transport Disruption in a Murine Model of Neurocysticercosis”

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Neurocysticercosis is a parasitic infection of the central nervous system caused by the larval stage of *Taenia solium.* It remains a significant public health issue in endemic regions and is a leading cause of acquired epilepsy worldwide. The pathogenesis of neurocysticercosis involves complex interactions between biological and immunological factors, leading to multifactorial neuronal damage, including inflammation, gliosis, and neural tissue alterations. Among the affected processes, axonal transport is crucial for the proper distribution of mitochondria along the axon, which is essential for neuronal survival and function. This study investigate the disruption of mitochondrial transport in a murine model of neurocysticercosis at different time points (1, 1.5, 3, 6, and 12 months), comparing it with an uninfected control group. Immunohistochemistry and immunofluorescence techniques were used to analyze the expression and distribution of key molecular markers: cytochrome c (mitochondrial marker), neurofilament (axonal integrity), and KIF5A (a kinesin involved in axonal transport). Quantitative image analysis revealed abnormal accumulation of both cytochrome c and KIF5A in axonal swellings adjacent to the parasitic cysts, with the highest accumulation observed at 6 and 12 months. No significant changes were found in the control group. These findings suggest a novel mechanism by which neurocysticercosis may lead to neuronal damage, potentially through the interference with mitochondrial transport along the axon. This study offers new insights into how parasitic infections affect neurons over time and highlights the potential of targeting intracellular transport processes in future treatments. Further research is required to identify the specific biological mechanisms behind mitochondrial transport disruption and its contribution to neuronal damage.

Stromal factor-driven modulation of dendritic cell activation in the melanoma tumor microenvironment

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Melanoma continues to represent a major public health issue due to its elevated mortality rate among skin cancers. Despite advancements in immunotherapy, treatment resistance and non-responsiveness remain major clinical challenges, largely due to the tumor's ability to evade immune detection. The tumor microenvironment (TME) plays a pivotal role in directing immune responses, particularly by inhibiting the activation of dendritic cells (DCs). Recent evidence suggests that melanoma-associated fibroblasts (MAFs) contribute significantly to immune evasion. This study investigates how the melanoma TME modulates DC activation.

To replicate melanoma TME, we developed in vitro models using homotypic and heterotypic 3D spheroids, via the Liquid Overlay technique. These spheroids combined B16 melanoma cells and NIH-3T3 fibroblasts in varying ratios. JAWS-II DCs were co-cultured with these spheroids under basal and lipopolysaccharide (LPS)-stimulated conditions. Additionally, VEGF, a key stromal-derived immunosuppressive factor, was tested for its role in DC modulation. DC activation was assessed by flow cytometry.

Our results show that spheroids with higher fibroblast proportions exhibited reduced size and increased compaction. In contrast, homotypic melanoma spheroids failed to form compact structures, rapidly disaggregated, and showed extensive cell death. LPS stimulation induced significant DC activation, which was suppressed by co-culture with heterotypic spheroids, whereas homotypic fibroblast spheroids had no effect. Notably, DCs co-cultured with homotypic melanoma spheroids exhibited reduced viability, suggesting the release of death- associated signals that could negatively impact DC viability.

Furthermore, VEGF treatment reversed LPS-induced DC activation, reinforcing its role as a key immunosuppressive factor primarily secreted by MAFs.

Based on these findings, we hypothesize that the suppression of DC activation in the melanoma TME may result from the immunosuppressive effects of VEGF, predominantly secreted by stromal cells, which may reinforce MAF-mediated DC inhibition.

Our ongoing studies aim to dissect these processes, with a focus on identifying key mediators and potential therapeutic targets to counteract TME-induced immunosuppression.

Biofilm Formation as a Factor Associated with Antimicrobial Resistance in Clinical Isolates of *Pseudomonas aeruginosa*

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Pseudomonas aeruginosa is an opportunistic pathogen that poses a significant challenge in hospital settings due to its ability to form biofilms and its resistance to multiple antimicrobials. Biofilm formation acts as a protective barrier that facilitates evasion of antimicrobial activity and the host immune response.

This project aims to evaluate the association between biofilm-forming capacity, related genes (algD, pslD, and pelF), and the antimicrobial resistance profile in clinical strains of *P. aeruginosa.* Biofilm formation will be quantified using the crystal violet assay in 96-well microplates, with absorbance measured at 570 nm using a spectrophotometer. Results will be interpreted according to the criteria of Ansari et al. (OD570 < 0.12: weak producers; OD570 = 0.12–0.24: moderate producers; OD570 > 0.24: strong producers). Genes related to biofilm formation will be detected by polymerase chain reaction (PCR) using primer sets specific for algD, pslD, and pelF. Antimicrobial susceptibility will be assessed using the disk diffusion method, following CLSI guidelines. Statistical analysis will be performed using the Chi-square test to evaluate the association between biofilm-forming capacity, the presence of biofilm- related genes, and antimicrobial resistance; a Pvalue < 0.05 will be considered statistically significant.

The results of this project will provide valuable insights into the mechanisms of phenotypic antimicrobial resistance and their relationship with biofilm formation and associated genes in

P. aeruginosa. In addition, it will contribute local data on relevant clinical strains in Peru, enriching both the regional and national scientific landscape. This study will also lay the groundwork for future research involving transcriptomic analysis or the sequencing of virulence and resistance genes, and will support the development of more effective therapeutic strategies and improved control of persistent infections in clinical settings.

Environmental Exposure and Bone Marrow Immune Microenvironment in Pediatric Acute Leukemia in Mexico

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Acute leukemia is the most common cancer in childhood. In Mexico, both incidence and mortality rates exceed global averages, particularly in the central states of Puebla, Oaxaca, and Tlaxcala (POT), where over 60% of the population lives in poverty. The relationship between environmental toxicants and the increasing incidence of disease within this region has led to the identification of a Sanitary Environmental Emergency Zone (RESA).

While pediatric leukemia outcomes have improved globally, children in low- and middle- income countries, including Mexico, remain 4–7 times more likely to die from the disease, largely due to treatment failure and early relapse. We hypothesize that environmental exposures may influence the bone marrow (BM) immune microenvironment, making it permissive to leukemia progression and relapse.

Here, we analyzed BM aspirates and biopsies from pediatric acute leukemia patients at diagnosis and follow-up using mass cytometry (MC) and imaging mass cytometry (IMC). Data were processed using FlowJo™, MCD Viewer, HistoCAT, CellProfiler, and visualized with R and Python.

Our findings from BM samples show a substantial increase in expression levels of chemokine receptors CXCR3 and CXCR7 in leukemia compared to healthy conditions. Patients who responded favorably to treatment and did not develop detectable measurable residual disease (MRD), showed pro-inflammatory microenvironments enriched in CXCL8 and CXCL10, whereas non-responders (detectable MRD) exhibited immunosuppressive signatures marked by CD39, Galectin-9, and PD-1. Of note, patients residing near the RESA had higher levels of detectable MRD.

Our findings suggest that environmental exposures may shape the BM immune niche, influencing treatment outcomes. This study supports microenvironmental profiling as a tool for risk stratification and highlights potential therapeutic targets. It also underscores the critical interplay between environmental toxicity, immune dysregulation, and cancer progression, aligning with the course's themes on environmental impact and immunity in chronic disease and malignancy.

Perfil sérico mineral en vacas Holstein en etapa de transición y su relación con las enfermedades de la producción, Chiclayo 2021

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Se evaluó el perfil sérico mineral (calcio, fosforo y magnesio) en vacas Holstein en etapa de transición y su relación con las enfermedades de la producción, Chiclayo 2021, realizado en el establo Agropecuaria del Rosario E.I.R.L – Chiclayo. Se examinaron veinte vacas (primíparas y multíparas) en etapa de transición, criadas de manera intensiva con las mismas condiciones de manejo y alimentación. Se extrajo 7 ml. de sangre de la vena coccígea media, recolectados en tubos sin anticoagulante previamente rotulados, colocados en cajas de Tecnopor con hielo, y transportados al laboratorio para su respectivo análisis. Se encontraron niveles bajos ($p<0.01$) de calcio, fosforo y magnesio en el segundo día posparto, para luego regularizarse desde el día siete hasta el día veintiuno postparto. Las vacas multíparas (segundo y tercer parto) presentaron al segundo día postparto los niveles más bajos ($p<0.01$) de calcio y fosforo, así como también el 65 % de vacas multíparas presentaron enfermedades de la producción; mientras que en las primíparas solo se presentó en un 35%, existiendo una relación significativa; para luego normalizarse a los 21 días postparto en un 50%.

COMPARISON OF THE TUBERCULIN SKIN TEST AND QUANTIFERON-TB GOLD FOR DETECTING LATENT TUBERCULOSIS INFECTION IN POPULATIONS EXPOSED TO ENVIRONMENTAL FACTORS IN THE PERUVIAN AMAZON

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Latent tuberculosis infection (LTBI) remains a critical public health challenge in high-burden regions like the Peruvian Amazon. Diagnostic tools such as the tuberculin skin test (TST) and interferon-gamma release assays (IGRAs, e.g., Quantiferon-TB Gold) may be influenced by host immunity and environmental factors like biomass smoke, overcrowding, and humidity.Compare TST and Quantiferon performance in LTBI detection and assess environmental/immunological impacts on results. A cross-sectional study in two rural Amazonian communities included participants aged ≥5 years. Both TST and Quantiferon tests were administered. Environmental variables (biomass fuel use, indoor air quality, overcrowding) and nutritional status were recorded. A subgroup underwent IFN-γ and IL-2 level analysis. Statistical analyses included Cohen's kappa (agreement) and logistic regression (associations). **Results:** Preliminary data revealed moderate agreement between tests (κ = 0.45). Discordant results were more common in individuals exposed to biomass smoke or showing immunosuppression (e.g., malnutrition). Quantiferon demonstrated higher specificity in BCG-vaccinated participants, while TST showed frequent positivity in environments with non-tuberculous mycobacteria.

Conclusion: Environmental factors (indoor air pollution, nutrition) and immunological profiles significantly influence LTBI test accuracy. Quantiferon offers superior specificity in BCG- vaccinated populations, but local ecological conditions (e.g., mycobacterial exposure) must inform test selection. Integrating environmental and immunological data could optimize LTBI detection strategies in vulnerable Amazonian communities.

Comparative Evaluation of Active and Latent Tuberculosis Detection Using the GeneXpert System and the QuantiFERON Test: Implications for Diagnosis and Clinical Management in Endemic Settings

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Tuberculosis (TB) remains a major public health challenge in endemic regions. This study evaluates the diagnostic performance of two key tools: GeneXpert, a rapid molecular assay for detecting *Mycobacterium tuberculosis* and rifampicin resistance in sputum, and QuantiFERON, an immunological test that identifies latent TB infection through interferon-gamma release. Conducted in a high-risk populatio including individuals with respiratory symptoms, HIV, healthcare workers, and close TB contacts his research aims to assess the accuracy and concordance of both tests in identifying active and latent TB. Sputum and blood samples will be collected accordingly, and patients will be followed to detect possible TB progression. Sensitivity, specificity, and predictive values will be calculated to determine diagnostic efficacy. The expected outcome is to inform clinical strategies by highlighting the value of early detection, especially of latent TB, in preventing future active disease.

PRELBAC: Evaluation of the Efficacy and Safety of Bacterial Lysate OM-85 in Preventing Recurrent Respiratory Infections in Children Treated at the Guillermo Almenara Irigoyen National Hospital, Lima. A Retrospective Cohort Study (2019-2023)

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Background: Recurrent respiratory infections (RRIs) in children represent a major global public health issue, particularly in low- and middle-income countries, where they cause high pediatric morbidity, burden healthcare systems, and contribute to the overuse of antibiotics. OM-85, a bacterial lysate derived from multiple respiratory pathogens, has shown mucosal immunostimulant effects by enhancing both innate and adaptive immune responses in the respiratory tract. Objective: To evaluate the efficacy and safety of OM-85 in preventing RRIs in pediatric patients treated at the Guillermo Almenara Irigoyen National Hospital (HNGAI), Lima, during the period 2019–2023.

Methods: A retrospective cohort study will be conducted by reviewing medical records of children aged 1 to 14 years diagnosed with RRIs and treated at HNGAI between 2019 and 2023. Two groups will be analyzed: one treated with OM-85 and a control group without treatment. Relevant clinical data will be collected and statistically analyzed using Stata v18. Descriptive and inferential statistics will be applied, including Student's t-test, Wilcoxon test, McNemar test, chi-square test, logistic regression, and Cox regression models, with a significance level of $p<0.05$.

Expected Results: It is expected that the use of OM-85 will be associated with a significant reduction in the frequency and severity of RRIs, a favorable safety profile, improved respiratory-related quality of life, and lower healthcare costs.

Conclusion: This protocol aims to generate local evidence on the effectiveness of OM-85 as a preventive immunomodulatory intervention for pediatric RRIs. The findings may support updates to national clinical guidelines and contribute to global strategies aimed at reducing the burden of these infections in vulnerable populations.

Environmental exposome and immune infiltrates in Glioblastoma: A preliminary study linking heavy metal exposure to tumor immunity in Peruvian patients

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Introduction: Glioblastoma multiforme (GBM) is a highly immunoresistant brain tumor characterized by a profoundly immunosuppressive microenvironment. Emerging evidence suggests that environmental exposures—particularly to heavy metals such as arsenic, cadmium, and lead—may shape immune responses within tumors, yet their impact on brain tumor immunity remains poorly explored.

Objective: To explore the association between immune cell infiltration and potential chronic exposure to heavy metals in GBM patients, with a regional focus on populations from environmentally burdened areas in Peru.

Methodology: We performed immune deconvolution using CIBERSORT on transcriptomic data from public GEO datasets (47 GBM cases and 25 non-tumoral brain tissues from European and Asian cohorts). Concurrently, we are conducting an exploratory validation in Peruvian GBM cases from the National Institute of Neoplastic Diseases (INEN), focusing on M2 macrophages and γδ T cells. Gene expression validation is being carried out via qPCR, alongside immunofluorescence staining of tumor sections. Quantification of heavy metals in tumor tissues is being performed using atomic absorption spectroscopy (AAS).

Results: Transcriptomic analysis revealed a significant increase in M2 macrophages and γδ T cells in GBM tissues compared to controls. Preliminary data suggest that patients from highly contaminated regions in Peru exhibit similar immune patterns. Median overall survival was approximately 7 months. Measurement of arsenic, lead, and cadmium in tumor samples is ongoing to establish individual exposure profiles.

Conclusion: Our findings point to a potentially underrecognized axis between environmental exposures and tumor immunity in GBM. This work sets the stage for functional studies and supports the integration of environmental, immunological, and genomic data. The development of a CNS tumor biobank within INEN would be a valuable step toward personalized interventions in exposed populations.

Neutrophil/lymphocyte ratio associated with mortality in patients with stage 5 chronic kidney disease starting hemodialysis in a public hospital.

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Objetive: To determine the association of the neutrophil lymphocyte neutrophil index (NLI) with mortality in patients with chronic kidney disease stage 5 (CKD-5), prevalent in hemodialysis, between the years 2015-2016, in a public Hospital.

Methods: Cohort, observational and analytical design, the sampling was non-probabilistic and by convenience. We evaluated 250 records of patients with CKD-5 in ambulatory hemodialysis for at least 3 months, which started hemodialysis at the Hospital Nacional Arzobispo Loayza (HNAL) between the years 2015-2016, then were referred to external dialysis centers and had subsequent follow-up in the nephrology service of the HNAL, the observation ended on December 31, 2019. Multiple regression using generalized linear models was used in the analysis. The exposure variable was INL (≥3.5 and < 3.5) and the outcome variable was vital status at the end of the observation.

Results: The median age was 65 years with interquartile range (IQR) from 57 to 71, the percentage of deceased was 24% and the median observation time was 3.8 years IQR (2.8 - 3.9). In multivariate analysis, patients with NLI ≥ 3.5 had higher mortality (RR: 2.85, 95%CI: 2.17- 8.96, p = 0.033), adjusted for sex, age, neutrophil level, lymphocytes, platelets, C-reactive protein, ferritin, platelet-lymphocyte index, and Kt/V. The increase in 0.1 units of Kt/V was associated with a 9.7% decrease in mortality (95%CI: 0.02 - 0.08) p < 0. 001.

Conclusion: NLI ≥ 3.5 was associated with increased mortality in patients with CKD stage 5 on chronic hemodialysis.

Does Involving Parents in Soil Sampling Identify Causes of Child Exposure to Lead? A Case Study of Community Engagement in Mining-Impacted Towns in Peru

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Over a million people in Peru may be exposed to lead (Pb) due to past or present mining- related activities; however, neither soil Pb nor blood Pb are routinely monitored throughout the country. Because little is known about Pb contamination in smaller mining-impacted towns, soil Pb was mapped in four such towns with a portable X-ray fluorescence analyzer in 2015. The roadside mapping delineated hotspots of highly contaminated soil (1,000–6,000 mg/kg Pb) in two of the towns. The local health department, provided with a LeadCare II analyzer, then measured blood-Pb levels >5 in 65% and >10 µg/dL in 15% of children (n = 200) up to 6 years of age in these same four communities. There were no clear relations between child blood-Pb levels and Pb levels in soil samples collected inside (n = 50) or outside the home (n = 50). Increased child blood Pb was associated with decreased level of cleanliness of parent clothing (n = 136) and shoes (n = 138), linking a possible behavioral factor for transferring contaminated soil and dust to children. In order to explore individual exposure and variations in soil Pb, 10 parents of children with blood Pb >10 µg/dL and 10 parents of children with blood Pb <5 µg/dL were invited to collect soil samples in areas where their children play and screen it for Pb using a color-based field procedure. Importantly, parents identified a new hotspot of Pb contamination that had been missed by the previous portable X-ray fluorescence soil mapping. The findings highlight the feasibility and value of involving families impacted by environmental contamination to identify and reduce environmental health risk.

Activin A cooperates with the Actin-binding Protein Cortactin to Promote B-cell Acute Lymphoblastic Leukemia Progression

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B-cell acute lymphoblastic leukemia (B-ALL) is the most common childhood malignancy worldwide. B-ALL cells capitalize on interactions with bone marrow (BM) niches for malignant progression and the capacity of B-ALL cells to escape therapy-induced death. Developing treatments that target both cell-intrinsic factors and the leukemic BM microenvironment is crucial.

Factors that enable the migration and establishment of B-ALL cells in protective bone marrow niches enhance the invasiveness of leukemic cells. The actin-protein cortactin and the growth factor activin A are known for controlling cell migration and adhesion. Both proteins are overexpressed in the leukemic BM compared with healthy individuals; and we recently showed that cortactin overexpression in B-ALL cells promotes extravasation, BM colonization, and organ invasion. However, it remains unknown whether activin A targets cortactin to promote the invasiveness of leukemic B cells and their establishment in protective niches, where those cells could hide and later trigger relapse.

In this study, we investigated the joint roles of cortactin and activin A in B-cell acute lymphoblastic leukemia. We found that activin A enhances CXCL12-driven migration across the HUVEC monolayer and supports BM organoid colonization by B-ALL cells. Mechanistically, these processes are driven by increased expression of surface CXCR4 in B-ALL cells and increased actin polymerization. Notably, activin A-induced migration and BM organoid colonization were significantly abrogated in cortactin-depleted B-ALL cells. Activin A did not regulate cortactin expression in B-ALL cells, but inhibition of ERK1/2, which is known to phosphorylate cortactin, abrogated activin A-induced migration. We are currently determining whether activin A-induced phosphorylation of cortactin through ERK1/2 is the underlying reason for the observed invasive capabilities.

Together, our data suggest that activin A activates cortactin to enhance actin filament formation, migration, and invasiveness of B-ALL cells. Thus, targeting activin A signaling could be a novel treatment strategy to improve B-ALL disease outcomes.

Molecular Characterization of CTX-M Group Genes in Clinical *Escherichia coli* Strains Isolated from Pediatric Patients at a Referral Hospital in Lima

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Pediatric infections caused by *Escherichia coli* resistant to third-generation cephalosporins are of particular concern due to their impact on therapeutic efficacy, as they limit conventional treatment options. One of the main enzymes responsible for this resistance is the CTX-M-type extended-spectrum β-lactamase (ESBL). Therefore, the objectives of this study focus on the identification of CTX-M group genes (CTX-M1, CTX-M2 and CTX-M9), along with genotypic typing in clinical E. coli strains isolated from pediatric patients at a referral hospital in Lima. This is a descriptive, cross-sectional study with an exploratory approach. Polymerase chain reaction (PCR) will be used to identify CTX-M group genes, and genotypic typing will be performed using repetitive extragenic palindromic PCR based on the BOX-A1R primer (BOX- PCR). The results will be analyzed using the GelJ software. The study aims to identify and molecularly characterize CTX-M group genes, with the goal of contributing to a better understanding of their dissemination in pediatric patients.

Role of small extracellular vesicles induced by *Helicobacter pylori* in the promotion of in vitro angiogenesis

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Gastric cancer is the fifth most common cancer in terms of incidence and mortality worldwide. Its etiology is multifactorial; however, colonization of the gastric mucosa by *Helicobacter pylori* has been associated with the development of chronic inflammation and immune processes that can trigger multiple gastric pathologies, including adenocarcinoma. A hallmark of this cancer is the promotion of angiogenesis, a complex process in which new capillaries grow from pre-existing vessels. This process is orchestrated by multiple factors, including Vascular Endothelial Growth Factor-A and Angiopoietin-2, which counteracts the anti-angiogenic activity of the microRNA Mir-34a. The study of small extracellular vesicles (sEVs) has been enhanced by the discovery of their fundamental role in cell communication and signaling mechanisms. Previously, it has been shown that *H. pylori* infection can modify the expression of pro-angiogenic factors, but the role of sEV-mediated pro-angiogenic signaling has not been elucidated. To determine the presence of angiogenic factors in sEVs derived from *H. pylori*- infected gastric epithelial cells and their potential role in promoting angiogenesis, sEVs will be isolated in vitro by differential centrifugation and ultracentrifugation, and characterization experiments will be performed using electron microscopy, Western blotting, and RT-qPCR. Finally, the pro-angiogenic capacity of sEVs will be analyzed in a HUVEC multicellular spheroid model using live-cell imaging.

Genetic Patterns of Immune-Evasive and Carbapenem-Resistant *Pseudomonas aeruginosa* in a Clinical Environment

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Introduction: *Pseudomonas aeruginosa* is a major opportunistic pathogen responsible for a wide range of hospital-acquired infections, particularly in immunocompromised patients. Its notable genetic plasticity, intrinsic resistance to antibiotics, and ability to evade host immune defenses make it a critical focus of biomedical research. The emergence of multidrug-resistant and virulent clones in clinical settings highlights the urgent need to better understand the molecular mechanisms that underlie both antimicrobial resistance and immune evasion in this pathogen.

Objectives: This study will aim to characterize the genetic diversity of *P. aeruginosa* clinical isolates and to detect the presence of key carbapenem resistance and virulence genes associated with immune evasion.

Methodology: Clinical isolates of *P. aeruginosa* will be collected from a referral hospital in Peru. Genomic DNA will be extracted and analyzed using ERIC-PCR to assess clonal diversity and genetic relatedness among the isolates. Conventional PCR will be performed to detect carbapenemase-encoding genes (blaOXA, blaKPC, blaVIM, and blaIMP) and virulence genes (lasA, lasB, toxA). The selected virulence genes are known to play roles in immune evasion, including the degradation of immunoglobulins and complement proteins, inhibition of phagocytosis, and disruption of host cellular functions.

Expected results: It is anticipated that several isolates will harbor both resistance and virulence genes, indicating the presence of high-risk clones capable of both antimicrobial resistance and immune modulation. The study may reveal genetic groupings with enhanced survival advantages in clinical environments.

Importance of the work: This research is expected to contribute valuable insights into the molecular epidemiology of P. aeruginosa and its adaptation strategies in hospital settings. By linking genetic resistance profiles with immune-related virulence traits, this work may support the development of improved infection control and therapeutic approaches against multidrug- resistant pathogens.

Particulate matter impairs immune system function by upregulating inflammatory pathways and decreasing the pathogen response, which impact SARS-CoV-2 pathogenesis

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Currently, a decrease in air quality has been observed. Airborne coarse-particulate matter (PM10) has been linked to human pathologies including, increased susceptibility to infectious diseases. High levels of PM10 have been associated with increased COVID-19 morbidity/mortality. However, the molecular mechanisms induced by PM in immune cells have not been systematically integrated.

Our aim was to evaluate the effect of PM10 on viral replication and the inflammatory response triggered by SARS-CoV-2 in human immune cells (PBMCs). The production of proinflammatory cytokines and antiviral factors was quantified by RNA-seq, qPCR and ELISA. In addition, the viral replication was evaluated in A549 cell line, previously exposed to PM10.

It was found that SARS-CoV-2 stimulation increased the production of proinflammatory cytokines, such as IL-1beta, IL-6 and IL-8. Besides, the PM10 was able to reprogram the expression of 1,196 genes in immune cells, including activation of a proinflammatory state with an increase in cytokines/chemokines (especially those involved in neutrophil and monocyte recruitment), while NK cell-recruiting chemokines were repressed. PM10 exposure also reduces the expression of antimicrobial factors. Additionally, PM10 induces the release of IL-1beta in a coculture of epithelial cells and PBMCs exposed to SARS-CoV-2. Also, increased viral replication of SARS-CoV-2 was observed in response to PM10. In vivo, PM10 induces the recruitment of inflammatory cells to the lung, with a significant increase in polymorphonuclear cells. Furthermore, PM10 increases gene expression of genes involved in the inflammatory response, such as NLRP3, IL-1β, and IL-18, in lung tissue.

Our analysis across gene regulatory and signaling pathways suggested that preexposure to PM10 plays a role in the dysregulation of immune cell functions, which are relevant for antiviral responses and general host defense against SARS-CoV-2 and even other pathogens.

Antibiotic resistance genes in aquatic environments in Iquitos: impact on public and environmental health

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The alarming increase in bacterial resistance to antibiotics globally has diluted sources other than the hospital and community, where water has taken on great importance. The aquatic environment is the source and natural habitat of a large number of microorganisms, including antibiotic-resistant bacteria, as well as being considered one of the main receptors for antimicrobials, resistant bacteria and antibiotic resistance genes from human activities. Contamination of water with these emerging contaminants has serious implications for human health related to the spread of bacterial resistance and the emergence of new resistance mechanisms.

Antibiotics are probably the most successful family of drugs developed to date to improve human health, to prevent and treat infections. It was found that the use and sale of them around the world revealed that in general, there is a systematic lack of data, which allows an effective intervention and the proposal of mitigation strategies to the environmental problem of antibiotic-resistant bacteria; there is a strong relationship between antibiotic residues in ecosystems and the increase in antibiotic-resistant bacteria in the environment; But at present, there is not enough information to reach a definitive conclusion on the importance and impact of the presence of these bacteria that would allow the assessment of potential risks to ecosystems and human health. It is hypothesized that the use of antibiotics for purposes other than antibiotic therapy can enrich the population of resistant bacteria capable of infecting humans.

The study will be conducted at the Tropical and Infectious Diseases Research Laboratory (LIEIT) Sampling will be carried out in December (three replications on different dates)

Analysis of physical-chemical parameters and heavy metals

All samples will be analyzed to determine the mandatory control parameters in accordance with Peruvian regulations: physical-chemical (turbidity, residual chlorine, temperature, conductivity and pH) and heavy metals (Ni, Pb and Cr).

DNA extraction: The PowerWater® DNA Isolation Kit (MO BIO Laboratories, Inc., 2746 Loker Ave West, Carlsbad, CA, USA) will be used following the manufacturer's recommended protocol. The quantification of the DNA concentration will be carried out under the basic photometry procedure using a biospectrometer

Determination of resistance genes: The determination of resistance genes will be carried out by conventional PCR, using the corresponding primers and established conditions. In each case, a negative result (ultrapure water instead of DNA sample) to detect any contamination by reagents or tampering. marA, ermC, amp, QEP and qEmarA were selected due to their local and global relevance.

Multivalent vaccine candidate from conserved immunogenic peptides in entry or exit proteins of Orthopoxvirus genus

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Orthopoxvirus (OPXV) genus includes several emerging and re-emerging zoonotic viruses that pose significant global health threats and affect a wide range of animal species. Among them, smallpox caused pandemics in the 20th century, Borealpox was responsible for the first recorded death in Alaska, and Monkeypox (Mpox), classified as a public health emergency by the World Health Organization in 2022, had its alert level updated in 2024 due to the emergence of a new Clade Ib variant. The lack of therapies for these viruses, combined with the limitations of live-attenuated vaccines underscores the need for new preventive strategies. This study focuses on developing a multiepitope vaccine targeting all viruses within the OPXV genus. To achieve this, proteins involved in viral entry and exit were extracted from the National Center for Biotechnology Information's virus database. A total of 160 sequences from all OPXV viruses were analyzed to identify conserved epitopes using the Immune Epitope Database. After excluding transmembrane regions and N-glycosylation sites, the remaining epitopes were concatenated to create a multiepitope chimeric protein, which was combined with β-defensin and PADRE adjuvants. The resulting construct, containing eight conserved epitopes covering all OPXV viruses (including Mpox Clade Ib), was assessed for antigenicity, allergenicity, and structural stability. Furthermore, the proposed multiepitope vaccine demonstrated a favorable interaction with the TLR2 receptor and promising predictions for inducing both humoral and cellular immune responses after three doses of the vaccine candidate. These findings suggest that the vaccine could offer a novel multivalent approach for combating zoonotic viruses within the OPXV genus. The candidate protein shows strong potential for further in vitro and in vivo studies, and if its efficacy is confirmed, it could provide an effective solution for preventing diseases caused by these pathogens, as well as for the development of immunodiagnostic tests based on the identified epitopes.

Impact of Active Pulmonary TB Treatment on the Diversity of Circulating NK cells

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Introduction: Tuberculosis, caused by *Mycobacterium tuberculosis*, is a highly contagious disease, and one of the main causes of death worldwide. Despite the existence of a treatment, tools to monitor treatment progress have limitations due to the lack of sensitivity or access to the population. M. Tuberculosis has several strategies to evade the immune response, including infection of macrophages by restricting the immune system. Natural Killer (NK) cells are fundamental components of the innate immune system, kill infected cells and collaborate with adaptive immune system cells. Our objective is to study NK cells' behavior in patients undergoing antituberculosis treatment.

Methods: 21 blood samples were collected from tuberculosis patients before and after six months of treatment, and peripheral blood mononuclear cells (PBMC) were isolated. Using flow cytometry, we evaluated the different populations and subpopulations of NK cells expressing CD56 and CD16, also evaluated their ability to produce IFN-ɣ and perforin after stimulation via FcɣRII and NKG2D MICA/B receptors.

Results: CD56+CD16+ and CD56+CD16- NK cell subpopulations increased at the end of treatment and the CD56++CD16++ subpopulation decreased. In addition, the levels of perforin and IFN-ɣ produced by NK cells decrease.

Conclusion: Antituberculosis treatment impacts NK cells phenotypes and function.

Menin as therapeutic target for multiple myeloma

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Multiple myeloma (MM) is a genetically heterogeneous plasma cell malignancy with limited curative treatment options. Many patients often relapse or develop resistant recurrence. Recent studies have identified a secreted protein bleurin, encoded by BLEUR1, as a promising therapeutic target in hematologic malignancies, specifically in leukemia. While its role in leukemia appears well established, the function of bleurin in multiple myeloma remains largely unexplored.

To address this gap, we analyzed publicly available DepMap CRISPR knockout screens, which revealed that BLEUR1 is an essential gene in MM cell lines, suggesting that MM cells rely on bleurin for survival.

To substantiate this, we developed a flow cytometry-based assay for single cell quantification of bleurin and observed variable expression patterns among the cell lines, which were confirmed through western blot analysis. To determine its subcellular localization, we performed cell fractionation and immunofluorescence, both of which confirmed the presence of bleurin in the nucleus of MM cells. Notably, upon treatment with bleurin inhibitors, MM cell lines exhibited sensitivity to the small molecules resulting in reduced cell viability and lower bleurin expression.

Together, these findings provide insight into the function of bleurin in MM and support its potential as a therapeutic target. Ongoing studies with in vivo models and primary patient samples aim to further evaluate the translational potential of bleurin inhibition in MM. Ultimately, the goal of this project is to uncover the role of bleurin in MM and assess the viability of a novel treatment strategy for patients.

Association between segmented filamentous bacteria (SFB) colonization and the use of antibiotics in the gut immune response of TNFR1-/- mice

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Segmented filamentous bacteria (SFB) are potent microbial stimuli of the gut mucosal immune system, including IgA and IL-17 production. In the ileum of mice, SFB appear shortly after weaning, and then quickly decreases. Antibiotic use has been shown to create an imbalance in the intestinal microbiota, called dysbiosis, which induces inflammation that can lead to several chronic pathologies. TNF receptor 1-deficient (TNFR1-/-) mice develop reactive arthritis (ReA) after oral infection with Yersinia enterocolitica (Ye) serotype O:3. This study aimed to evaluate the association between SFB colonization and antibiotic treatment on the intestinal immune response in TNFR1-deficient mice. First, we confirmed the presence of SFB in the mice in our laboratory. For this purpose, SFB determination was carried out by qPCR in fecal samples. In addition, SFB presence was analyzed by Gram staining in the ileum lavage of 21 to 35-day-old (weaning time) male C57BL/6 wild-type (WT) and TNFR1-/- mice. Then, we compared the number of IgA-producing cells in the intestinal lamina propria by immunofluorescence. Finally, lymphocytes, neutrophils, total macrophages and CX3CR1+ macrophages (cells that maintain gut homeostasis) were evaluated in mesenteric lymph nodes (MLN) by flow cytometry. qPCR results were positive for SFB in fecal DNA extracts. In addition, Gram staining showed high number of SFB in both WT and TNFR1-/- mice at the weaning time. We observed higher number of IgA+ cells in lamina propria of TNFR1-/- mice ($p<0.05$, compared with WT mice). Slight increase of CX3CR1+ macrophages was detected in TNFR1-/- mice ($p<0.05$). After the treatment of the mice with antibiotic (vancomycin), macroscopic changes (inflammation) were observed in the ileocecal valve (ViC) of WT mice. In addition, we observed a decrease of IgA+ cells in both groups of mice ($p<0.05$) and an increase of the difference between TNFR1-/- and WT mice ($p<0.0001$). Similar to WT mice, significant increases of neutrophils, macrophages, CX3CR1+ macrophages, total T lymphocytes, CD4+ T lymphocytes and CD8+ T lymphocytes were detected in the MLN of antibiotic-treated 35-day- old TNFR1-/- mice compared with TNFR1-/- mice without antibiotic treatment ($p<0.01$). Our results demonstrate that both the lack of TNF receptor 1 and antibiotic treatment impact on the development of the intestinal immune response. More results are needed to understand the mechanism behind these effects.

Factors associated with the transmission of congenital Chagas disease in the Hospital de la Mujer Dr. Percy Boland.

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Introduction: Vertical transmission of *Trypanosoma cruzi* infection accounts for an increasing proportion of new cases of Chagas disease. Thus, better stratification of associated risk factors is needed to predict which types of women are most likely to transmit the infection to neonates.

Methods: For this study we conducted surveys and used data already established at the Hospital de la Mujer Dr. Percy Boland in Santa Cruz, Bolivia, collecting maternal gynecological- obstetric data and serological status in relation to Chagas disease, in addition to clinical data of the newborn and the results of Micromethod and qPCR; and finally, housing data, observation of vinchuca, family history in relation to Chagas disease and its origin.

Results: Among 2455 women enrolled, 302 (12.3%) tested positive for Chagas disease. Household conditions, coming from a department considered endemic, and a history of living in a rural area were significantly associated with higher odds of maternal infection. Factors influencing vertical transmission included cesarean delivery and family history of the disease. Of the 302 neonates of seropositive mothers, 18 (6%) were diagnosed with congenital Chagas disease, by various methods, where 6 (2%) were by micromethod, and 13 (4.3%) were by qPCR.

Conclusion: Although improved access to screening and qPCR increased the number of infants diagnosed with congenital Chagas disease, many infants remain undiagnosed. Better understanding of risk factors, improved access to highly sensitive and specific diagnostic techniques, and working together consciously with mothers on treatment may help improve regional initiatives to reduce the burden of disease.

Association between Chagas disease in pregnant women and premature births in a public hospital in Santa Cruz, Bolivia

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Introduction: Chagas disease is caused by the flagellate protozoan *Trypanosoma cruzi* (*T. cruzi*). While newborns can acquire the infection through vertical transmission during pregnancy. The extent to which Chagas disease contributes to premature births remains unclear. This study aims to determine the association between Chagas disease in pregnant women and prematurity in their newborns.

Methods: This study utilizes data from a prospective cohort. A secondary cross-sectional analysis was conducted on 3971 mothers with and without Chagas disease. The multinomial regression model was employed to assess the association, adjusting for maternal age, party, socioeconomic Prematurity was defined as [definition of prematurity, e.g., gestational age less than 37 weeks.

Results: Among 3791 births since 2017 and part of 2021, 19.07 % were from mothers with Chagas disease, The prevalence of low birth weight (defined as <2500 grams according to WHO guidelines) was 15.01%. Congenital Chagas infection was observed in 1.08% of children, 23.02 % of the mothers had a history of spontaneous abortions, 12.44 % of the births were low birth weight and premature but 22.56 % have normal weight being premature. Mothers with Chagas had higher risk (still not significant) of preterm birth with low birth weight compared to mothers without Chagas disease (adjusted odds ratio:0.66 95% CI: 0.51-0.85) (p=0.002). No significance associations were found between Chagas disease and other birth outcomes, including low birth weight with term delivery and preterm birth with normal birth weight.

Discussion: In population of newborns born to mothers with and without Chagas disease, maternal age was significantly associated with preterm births and low birth weight (p<0.001). Mothers 35 years older had 1.68 times higher odds of preterm births to mothers younger than 17 years. However, mothers with Chagas disease have only 1.87-fold increase in the odd's preterm births (ic%0.50-0.85). Other studies have identified a numerous risk factor for preterm birth, including i) previous history of preterm birth, low birth weight, ii) obesity, diabetes, hypertension, iii) smoking, iv) infections, v) maternal age (under 17 or over 40), vi) genetics, vii) multiple pregnancy (twins, triplets

or older), and pregnancies that are too close together. However, the interplay between these and other environmental and social factors is not fully understood. This study confirmed an association between of prematurity and mothers aged 35 years or older.

Unusual case of de novo psoriasis in the setting of leukocyte adhesion deficiency post hematopoietic stem cell transplantation: A case report.

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Background: Leukocyte adhesion deficiency type I (LAD I) arises from alterations in the ITGB2 gene, therefore the adhesion and migration of leukocytes is altered, treatment is the transplant of hematopoietic progenitors (HSCT), patients undergo prior conditioning; then the injector infusion is performed and immune reconstitution is awaited. However, when immune reconstitution is abnormal, can generate multiple clinical complications: serious infections, autoimmune diseases, to injectable versus host disease (GVHD).

GVHD and psoriasis have shared immunological mechanisms. Psoriasis is an inflammatory skin disease, which mainly includes the Th 17 cell pathway, the risk factors are genetic and environmental.

Abstract: A 16 years old female patient diagnosed with LAD I since June 2013, underwent conditioning with busulfan, antithymocyte globulin and fludarabine; followed by HSCT on 11- 29-2018, with her mother as donor.

She received GVHD prophylaxis with cyclosporine and methotrexate. On 01-02-2019, she developed grade II acute GVHD affecting skin and liver. She had semiliquid stools, raising suspicion of GVHD reactivation, for which corticosteroid doses were increased. She showed a favorable response, and steroids were gradually tapered.

On 01-14-2025, she was diagnosed with guttate psoriasis, confirmed by skin biopsy, with negative antistreptolysin titers and throat secretion cultures. Currently, she presents intermittently appearing, mildly scaly plaques on the upper and lower limbs.

Conclusions: The development of de novo psoriasis in patients with LAD I following HSCT is an exceptional finding, with few cases reported in the literature. The likely pathophysiology involves dysregulated immune reconstitution, in which the interplay between autoreactive T cells, proinflammatory cytokines such as IL-17 and IL-23, and environmental factors may trigger a psoriasiform cutaneous inflammatory response.

In this case, the diagnosis of guttate psoriasis was confirmed histologically, with no evidence of associated streptococcal infection, which supports the hypothesis of a post-transplant immune-mediated etiology rather than an infectious one.

Production of two recombinant proteins from *Helicobacter pylory*: CagA and HopQ as antigenic targets for a serological test prototype

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Introduction: *Helicobacter pylori* is a gram-negative bacterium that colonizes the stomach of half of the world's population, and its chronic infection represents an important risk factor for the development of gastric cancer. The serological response against the virulence factors CagA and HopQ has been used as a biomarker, given that these proteins are relevant in the pathogenesis of gastric pre-neoplastic lesions induced by *H. pylori.* Hence, the aim was to produce H. pylori CaqA and HopQ recombinant proteins for the development of a homemade ELISA test that enables anti-HopQ and anti-CaqA IgG antibodies detection in serum samples.

Methodology: We designed two expression plasmids: one for CagA and one for HopQ, and the proteins were expressed in E. coliBL21. The antigens were purified by Ni-NTA affinity chromatography. Serum samples from *H. pylori* positive patients were tested for specific IgGs with an in-house ELISA test using the recombinant CagA and HopQ proteins as antigens. A concentration range from 16 to 0.25 µg/mL was tested for each protein. The CagA protein identity was achieved by tandem mass spectrometry (MS/MS).

Results: A saturation curve was performed with the different dilutions for each antigen, and itshowed the optimal concentrations for the ELISA test were 2 ug/mL for CagA and 4 ug/mL for HopQ. In a production volume of 350 mL, we obtained 900 µg for CagA and 600 µg for HopQ.

Conclusion: The detection of IgG antibodies against CagA and HopQ was successful for *H. pylori* positive serum samples, demonstrating that these recombinant antigens could be used for serological tests in the screening for pre-neoplastic lesions. The efficiency of antigen production is within the expected range for a small scale, which determines the possibility of upscaling this process to obtain a greater amount of the protein product. Also, we were able to identify CagA antigen by MS/MS mass spectrometry whose peptide masses matched the predicted masses.

In Silico Screening of Molecules Targeting TIP60-FOXP3 Interaction Inhibition as a Strategy to Block Treg Cell Modulation in the Tumor Microenvironment

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Introduction: The acetylation of FOXP3 by TIP60 (TIP60–FOXP3 interaction) plays a crucial role in the activation of regulatory T cells (Tregs) and the maintenance of immune tolerance. However, within the tumor microenvironment, Tregs suppress the activity of effector immune cells, allowing tumor cells to evade immune surveillance and invade surrounding tissues. To counteract this effect, small molecules such as MG149 have been investigated as potential inhibitors of the TIP60–FOXP3 interaction, aiming to suppress Treg function and restore anti- tumor immunity. Despite promising results, MG149 remains in preclinical stages. Therefore, this study explores the potential repurposing of approved drugs from the DrugBank database to identify new TIP60–FOXP3 interaction inhibitors.

Results: An in silico pharmacophore model was designed using PHARMIT based on the structural features of MG149. The model included one aromatic ring, one hydrogen bond donor, one hydrogen bond acceptor, and two hydrophobic features. This screening yielded 28 initial hits. Applying Lipinski's Rule of Five reduced the pool to six candidate molecules, all derivatives of penicillin: Cloxacillin, Dicloxacillin, Flucloxacillin, Imidafenacin, Nafcillin, and Ritodrine. Molecular docking using AutoDock Vina revealed that MG149 had a binding affinity of –7.4 kcal/mol, while the six candidates showed an average binding energy of –7.45 ± 0.29 kcal/mol, indicating comparable binding strength to that of MG149. An additional challenge was to assess whether these molecules could permeate the cell membrane to reach their intracellular target. The lipophilicity, expressed as LogP, was evaluated for each molecule. The six candidates showed an average LogP of 2.46 ± 0.22, which falls within the optimal range (1– 3) for passive membrane permeability, suggesting a high likelihood of effective cellular uptake.

Conclusions: This in silico screening identified six penicillin-derived molecules with potential to inhibit the TIP60–FOXP3 interaction. Their docking scores were comparable to MG149, and their LogP values suggest favorable membrane permeability. These findings support the potential repositioning of these compounds as immunomodulatory agents in cancer therapy. Future studies should validate these results in vivo, focusing on their capacity to reduce tumor growth by suppressing Treg activity and enhancing immune-mediated tumor clearance.

Ivermectin impairs the microbicidal capacity of macrophages in vitro by binding to the TLR- 4/MD2 complex, but is beneficial in acute pneumonia in TLR-4 knockout mice.

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Toll-like receptor-4 (TLR-4) is a pattern recognition receptor (PRR) widely distributed in macrophages, recognizing pathogen-associated molecular patterns (PAMPs). The MD2 complex integrates with TLR-4, both of which are necessary for the recognition of lipopolysaccharides found in the outer membrane of Gram-negative bacteria, such as Pseudomonas aeruginosa. Studies have shown that antiparasitic ivermectin treatment improves the survival of mice after receiving a lethal dose of lipopolysaccharides, although the mechanisms of action in this process remain unclear. Therefore, were conducted in silico studies using molecular docking, and it was found that ivermectin binds to the MD2 complex of TLR-4. To verify whether this binding would interfere with the immunofunctional activity of macrophages, bone marrow-derived macrophages (BMDMs) were stimulated with ivermectin and infected with Pseudomonas aeruginosa PA14. It was observed that treatment with ivermectin did not alter cell viability, impaired bacterial clearance, decreased NO and TNF-α secretion, in addition to increasing NF-κB activation in Raw 264.7 macrophages when challenged with LPS. All these results were reversed in vitro when the MD2 complex was inhibited in these BMDMs or Raw 264.7. To verify the in vivo repercussions, C57BL/6 WT or C57BL/6 TLR-4 KO mice were treated with ivermectin or PBS intraperitoneally for 5 days and infected with PA14 (CEUA 23/2021). Following treatment, ivermectin decreases the recovery of viable bacteria in the lungs of TLR-4 KO mice. Furthermore, the treatment decreased the inflammatory infiltrate, the secretion of IL-6 and TNF-α, and increased the secretion of IL-17 and IFN-γ in the lungs of infected mice. Thus, it was demonstrated in silico that ivermectin binds to the MD2 portion of the TLR4/MD2 complex, which reduced the microbicidal capacity of macrophages. Despite this, ivermectin treatment showed benefits, especially in TLR-4 KO mice in the recovery of viable bactéria, histopathological patterns and in the modulation of cytokines.

Early - onset multiple sclerosis: a case report

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A child male 3 y.o presented 8 days before admission diarrhea that was self-limited in 3 days, followed by progressive muscle weakness that made walking difficult. The day of admission hyporexia, sickness, drowsiness and irritability were added. The neurological examination revealed flaccid quadriparesia, decreased tone in limbs and generalized hyperreflexia with bilateral aquilian clonus and abnormal plantar response on the both foots.

During his hospitalization he presented a seizure, the EEG showed background activity associated with diffuse slow waves and epileptiform abnormalities in left hemisphere. Valproic acid was started. His brain TEM showed multiple low-density areas periventricular and subcortical white-matter lesions in both cerebral hemispheres. CSF and blood analytical were normal. Diagnosis of acute disseminated encephalomyelitis (ADEM) was made. He received methylprednisolone and IVIG. His Brain MRI showed multiple lesion enhancing hypointense in T1, hyperintense in T2 and FLAIR in the deep white matter of both cerebral hemispheres. The cervical spine showed diffuse increased signal in T2 that erases habitual gray and white substance configuration. Visual evoked potential showed bilateral prolonged latency of P100. Two years later he was admitted to the hospital for right sixth cranial nerve alteration.

A repeat brain MRI revealed demyelination zone of the white matter of both cerebral hemispheres and two lesions that enhancing. Oligoclonal bands was detected in the CSF and Anti NMO-IgG was negative and the diagnosis of multiple sclerosis was confirmed.

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