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Abstracts
A01-A118

Abstracts of the XLIII Annual Meeting Sociedad de Biología de Cuyo

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Mendoza - Argentina

IN MEMORIAN

Dra. Amira Ponce Zunino (1931-2024)

Dr. Amira Ponce Zunino (1931–2024) built a distinguished academic career that culminated in her appointment as Consulting Professor at the National University of Cuyo (UNCuyo) and as an Independent Researcher at CONICET.

Her arrival in Mendoza from her native Entre Ríos coincided with the beginning of academic activities at the UNCuyo School of Medical Sciences, around 1951. By 1953, she had begun to develop her dual vocation—teaching and science—at the Institute of Physiology (FCM-UNCuyo), a workplace guided by the renowned Dr. Fasciolo, a disciple of Nobel laureate Bernardo Houssay. From that year until her last participation in a scientific publication in 2022, she remained a permanent member of the Physiology faculty and sustained her academic activity for more than six decades—an unparalleled example of dedication.

As an emblematic figure of the UNCuyo School of Medical Sciences, her scientific career focused on cardiovascular research. Her first scientific work, recorded in 1962, was titled “Isolated Cat Heart in Anoxia and Alkalosis: Mechanical Activity and Coronary Flow.” In the later stages of her career, her research focused on the search for natural products to mitigate oxidative stress associated with ischemia–reperfusion in cardiac tissue. She stood out for her mastery in the use of diverse research models, ranging from isolated cells and tissues to the isolated and perfused heart, becoming a leading figure in the field.

Her commitment extended to the scientific community, as she was an active member of various societies and promoted scientific communication and discussion within multidisciplinary teams. Her legacy, marked by academic excellence, lives on through her many disciples, professionals, teachers, and researchers.

Dr. Amira Ponce Zunino was included in the book *“History of Medicine Through Its Women,”* which highlights the life stories of the first women physicians in Mendoza, emphasizing the challenges they faced at that time and the remarkable acceptance these women achieved within the academic and medical fields.

IN MEMORIAN

Dr. Fernando Daniel Saravi (1955-2025)

Professor Dr. Fernando Daniel Saraví (1955–2025) devoted 50 years of his life to an outstanding career in teaching and research in Physiology at the Institute of Physiology, School of Medical Sciences, National University of Cuyo (UNCuyo). His extensive trajectory, which began as an ad honorem student assistant in the 1970s, coincided with the reestablishment of the Cuyo Society of Biology.

Dr. Saraví stood out for his pedagogical talent and his ability to synthesize complex concepts, clearly reflected in his open-access virtual textbook on Physiology and Biophysics. Through this work, he brought students closer to the forefront of knowledge and to the integration of scientific disciplines.

A key milestone in his career was his leadership—while still an undergraduate student—in organizing the First Conference on Research Initiation at the FCM-UNCuyo in 1980. This initiative was revived in 2014, inspiring the creation of the Scientific Association of Health Students (ACES) at UNCuyo, consolidating a legacy that continues today with the incorporation of Research Methodology courses into undergraduate curricula.

After graduating as a physician in 1981, Dr. Saraví's career became an exceptional example of successfully integrating three dimensions: teaching, research, and clinical practice. This vision was reflected in his research focus on digestive physiology and bone physiology. His doctoral thesis initially centered on digestive physiology, particularly transepithelial transport in the colon. His work explored the biophysics and bioenergetics of this process, emphasizing the functional differences between the proximal and distal regions of the intestine, and addressing concerns related to human colonic diseases such as colorectal cancer, colitis, and constipation.

Dr. Saraví served as Head of the Bone Densitometry Service at the School of Nuclear Medicine (1995–2025). Among his achievements were contributions to the development of a pediatric body composition reference database and to the study of bone density, including research on the effects of yerba mate consumption in postmenopausal women.

His career stands as a testament to the successful integration of science, education, and clinical practice, leaving a profound legacy at the FCM-UNCuyo.

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Abstracts
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OPENING LECTURE

A01

MAGNETIC HYBRID NANOMATERIALS APPLIED TO THE REMEDIATION OF MINING EFFLUENTS: TOWARD EFFICIENT AND SUSTAINABLE PROCESSES

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Metallic mining generates liquid effluents containing high concentrations of heavy metals and toxic species. These wastes represent a critical challenge to the sustainability of the activity, given their environmental impact and the costs associated with their treatment.
In this context, nanotechnology emerges as a disruptive alternative. In particular, magnetic hybrid nanomaterials constitute an innovative platform for effluent remediation, as they combine the high adsorption capacity of their functionalized surfaces with the possibility of being rapidly recovered through magnetic separation.

INTERNATIONAL SYMPOSIUM 1

A02

TECHNOLOGIES FOR THE EXTRACTION AND ENCAPSULATION OF ESSENTIAL OILS: CHALLENGES AND SOLUTIONS FROM AN APPLIED CHEMISTRY PERSPECTIVE

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Plant-derived essential oils (EOs) possess robust antimicrobial, antioxidant, analgesic, and antineoplastic properties. These traits are highly effective for treating oral conditions like candidiasis and supporting local cancer therapies by reducing microbial load, managing pain, and promoting mucosal tissue recovery. However, direct clinical application of raw EOs is unfeasible due to significant physicochemical limitations. EOs are highly hydrophobic, volatile, and prone to rapid thermal and photodegradation. Furthermore, high free concentrations cause severe local irritation and an overwhelmingly intense taste, which narrows their therapeutic window and compromises patient compliance. To overcome these barriers, encapsulation technologies serve as a vital tool to stabilize volatile compounds, modulate release kinetics, and enhance biocompatibility. Researchers prioritize traceable, edible species—such as *Origanum vulgare*, *Lavandula dentata*, and *Mentha suaveolens*—extracting their EOs via controlled hydrodistillation in a Clevenger-type apparatus to prevent thermal degradation.For the delivery matrix, the formulation utilizes emulsification and ionic gelation to create hybrid alginate–gelatin networks. Alginate rich in G-blocks cross-links with calcium ions (\(\text{Ca}^{2+}\)) to provide structural integrity and diffusion control, while gelatin imparts elasticity and crucial mucoadhesive properties. This system is structurally reinforced by Pickering emulsions stabilized by solid nanoparticles (calcium carbonate, starch nanocrystals, or cellulose nanocrystals) that form a rigid physical barrier at the oil-water interface, preventing droplet coalescence.The synergy of these technologies yields a high encapsulation efficiency, protects the oil from oxidation, and eliminates initial cytotoxic irritation peaks. By delivering a tunable, sustained release, this platform maintains stable, sub-cytotoxic local concentrations over extended clinical periods. This optimized delivery profile preserves the therapeutic efficacy of EOs, supports tissue healing, and mitigates the risk of selecting for microbial resistance in the oral cavity.

A03

DEVELOPMENT OF ESSENTIAL OIL–LOADED HYDROGELS FOR THE TREATMENT OF DENTURE STOMATITIS THROUGH AN INTERDISCIPLINARY APPROACH

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Candida albicans biofilms are responsible for recurrent and resistant infections, such as denture stomatitis, one of the most common fungal infections affecting humans. Currently available drugs are ineffective against biofilms and, consequently, denture stomatitis exhibits high resistance and chronicity, impairing patients' quality of life, especially in older adults who wear removable dentures. Available antifungal agents cannot penetrate the biofilm matrix; therefore, innovative alternatives for their eradication must be explored.Essential oils stand out as promising alternatives due to their well-recognized antimicrobial activity. Preliminary data from our group demonstrate that the essential oil of *Origanum vulgare* inhibits biofilms of reference strains of *C. albicans*.However, their high volatility represents a limitation that must be overcome in order to formulate a preparation aimed at the treatment of denture stomatitis. Through the incorporation of the essential oil into hydrogel matrices, it was possible to obtain formulations capable of inhibiting the growth, adhesion, proliferation, and viability of early and mature *C. albicans* biofilms, both in reference strains (ATCC 90019 and 10231) and in clinical isolates from patients with denture stomatitis.
Nevertheless, factors such as seasonality must be considered, since the harvesting period can significantly affect the composition of essential oils as well as their biological activity, as we were able to observe in the compositional profiles obtained by GC/MS.
Our results demonstrate that the incorporation of essential oils into a hydrogel matrix is an innovative alternative for obtaining formulations with antibiofilm activity; however, it is essential to consider their development from an interdisciplinary perspective, which enables a more comprehensive approach to understanding, developing, and evaluating natural products.

A04
EVOLUTIONARY BIOCHEMISTRY: AN APPROACH TO UNDERSTANDING THE ORIGIN AND THE EMERGENCE OF ENZYMATIC FUNCTIONS

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Evolutionary Biochemistry constitutes an interdisciplinary framework that combines phylogenetic analyses, ancestral sequence reconstruction, and biochemical and biophysical characterization of proteins, with the aim of elucidating the molecular mechanisms underlying the emergence of new enzymatic functions (1). Its main strength lies in the possibility of experimentally accessing extinct ancestral proteins, which makes it possible to recreate in the laboratory evolutionary trajectories that connect functional divergences throughout the history of diverse protein families.

Over the past decade, this approach has driven a paradigm shift in the study of enzymes: from a reductionist view toward a systemic conception, in which enzymatic function is understood as the emergent result of multiple concurrent physicochemical phenomena.

In this context, our work has focused on the study of the origin and evolution of nucleotide-dependent enzymes. Through the reconstruction of ancestral sequences from different families of flavin monooxygenases, we identified the physicochemical determinants associated with their catalytic activity and characterized the functional transitions that led to the acquisition of new traits over the course of evolution. These findings reinforce the notion that enzymatic function is an intrinsically multicausal phenomenon and provide a conceptual framework for understanding processes of molecular innovation and highly complex biological transitions.

INTERNATIONAL SYMPOSIUM 2

IODINE NUTRITION, THYROID HORMONES AND REPRODUCTION

A05
IODINE DEFICIENCY AND ITS IMPACTS ON FEMALE REPRODUCTIVE PERFORMANCE

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Iodine is a trace element vital to human health, particularly for reproductive health in women. Found in various chemical forms—both inorganic (e.g., iodide and iodate) and organic (e.g., methyl iodide)—iodine compounds are ubiquitous in the environment, influencing nutrient cycling and biological processes. Its bioavailability is critical for the synthesis of thyroid hormones, which play an integral role in regulating metabolic processes, growth, and development. Iodine deficiency remains a global health issue, affecting women of reproductive age across both low- and high-income nations. Evidence suggests that even mild to moderate iodine deficiency can impair thyroid function in women of reproductive age, potentially leading to reproductive complications, including infertility, miscarriages, and neurological impairments in offspring. Research indicates that low urinary iodine concentration (UIC) is associated with delayed conception, underscoring the need for a dietary iodine threshold for optimal reproductive health. Additionally, thyroid hormones interact with gonadal tissues, thereby affecting menstrual function and fertility. Conditions such as polycystic ovary syndrome (PCOS) and thyroid disorders frequently coexist, complicating diagnosis and treatment. Recent findings highlight that women with PCOS exhibit a significantly higher prevalence of subclinical hypothyroidism, which shares symptoms with and may intensify reproductive dysfunctions.From a physiological perspective, iodine deficiency may trigger protective mechanisms that inhibit pregnancy during conditions unfavorable for fetal development. The metabolic disturbances associated with iodine deficiency have been linked to reproductive irregularities, underscoring the need for careful monitoring and intervention. Public health initiatives, such as iodization of salt, are effective strategies for improving iodine status; however, in iodine-deficient regions, systematic monitoring of iodine intake in women of reproductive age is crucial. Ensuring adequate iodine levels is essential to improving reproductive health outcomes and ultimately promoting maternal and child health in affected populations. Future research must clarify the intricate associations among iodine status, thyroid function, and reproductive health to develop targeted interventions that ensure reproductive health in our community.

A06
IMPACT OF IODINE NUTRITION AND THYROID HORMONES DURING PREGNANCY: FROM FUNDAMENTALS TO CLINICAL PRACTICE

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Adequate iodine availability and optimal thyroid function are essential during pregnancy, as hormonal demands increase significantly to support fetal development, especially of the central nervous system (CNS). Iodine deficiency and hypothyroidism, whether clinical or subclinical, have been associated with a higher risk of pregnancy loss, hypertension during pregnancy, and neurodevelopmental problems. In Chile, several studies have shown a high prevalence of thyroid dysfunction in women with no prior history, highlighting the importance of updating surveillance in nutrition and endocrinology. Our studies indicate that a hypothyroxinemic environment drives macrophages to adopt an inflammatory M1 phenotype, as evidenced by increased expression of HLA-DR and CD80, elevated production of IL-6 and TNF-α, and increased reactive oxygen species (ROS). These changes point to a pro-inflammatory microenvironment that could potentially affect initial implantation processes and maternal-fetal immune modulation. Proteomic analysis of serum from pregnant women with hypothyroxinemia identified altered proteins related to oxidative stress pathways, immune response, and metabolism. Finally, preliminary data from a cross-sectional study conducted between 2019 and 2024 at a Family Health Center in southern Chile are presented, where TSH levels were measured in 598 pregnant women. The prevalence of thyroid disease reached 16.6%, consistent with previous national studies. Significant relationships were observed between thyroid alterations, gynecological-obstetric history, and some perinatal outcomes. Overall, these findings demonstrate that thyroid dysfunctions and the possible reemergence of iodine deficiency remain public health challenges, emphasizing the importance of strengthening iodine nutritional monitoring, updating diagnostic ranges, and promoting timely screening during pregnancy.

A07

IMMUNOLOGICAL ALTERATIONS INDUCED BY HYPERTHYROIDISM DURING PREGNANCY AND LACTATION

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Thyroid dysfunction leads to metabolic, angiogenic, and developmental alterations that cause reproductive complications. Currently, immune regulation by thyroid status has not been well characterized. The objective of this study is to evaluate how hyperthyroidism (hyperT) modulates immune and morphological aspects of the placenta and mammary gland. Control and hyperthyroid Wistar rats (induced by a daily subcutaneous injection of 0.25 mg/kg T4) were mated 8 days after starting treatment and sacrificed on days 19 (G19) and 20 (G20) of gestation and day 2 of lactation. We observed that hyper increases fetal number, fetal weight, and placental weight on G19. In addition, hyper induced an endocrine imbalance with higher serum corticosterone and changed placental morphology, specifically the basal zone and decidua. These changes were accompanied by increased mRNA expression of the glucocorticoid receptor and monocyte chemoattractant protein-1 and increased CD45+ infiltration. On day 2 of lactation, HiperT mothers had more implantation sites and offspring and a higher offspring mortality rate than controls. The HiperT offspring had lower weight on days 1 and 2, lower weight gain, and decreased length and head circumference. T4 and prolactin levels in the HiperT group increased in mothers but T4 levels decreased in offspring. The HiperT group had increased the percentage of CD45+ cells and the percentage of CD3+/µl cells compared to the control, while the number of CD11 b/c+ cells was decreased. No changes were observed in the resident immune cells of the mammary gland. Finally, through in vitro assays, we demonstrated that TH induced the activation of immune cells. From a maternal clinical perspective during pregnancy, we work in the Department of Perinatology at Lagomaggiore Hospital, Mendoza, Argentina. Of the 3,426 patients admitted to the Department of Perinatology between June 1, 2024, and May 31, 2025, only 9 had hyperthyroidism, representing a prevalence of approximately 2 per 1,000 mothers. Of these, 82 participated in this study and 63 were healthy controls (76.8%), 11 had hypothyroidism (13.4%), and 8 had hyperthyroidism (9.7%). Gestational age at delivery revealed a lower median in the hyperthyroidism group compared to the hypothyroidism and control groups. The assessment of breast development indicated normal breast trophism and milk secretion in mothers with hyperthyroidism. Birth weight, length, and weight-to-length ratio were lower in newborns of mothers with hyperthyroidism compared to those of mothers with hypothyroidism and healthy controls. It should be noted that a high frequency of Apgar 1 scores below 7 and Apgar 5 scores below 9 was strongly associated with maternal hyperthyroidism. In summary, we demonstrate that hyperthyroidism affects the immunological and morphological aspects of the placenta and induces fetal phenotypic changes, which could be related to the premature labor observed in hyperthyroidism. These results suggest that T4 affects the development of offspring in early lactation. Although further research is needed to determine the precise impact of hyperthyroidism on newborn growth, these findings underscore the importance of specialized clinical monitoring of newborns of mothers with this condition.

SYMPOSIUM ON EXPERIMENTAL RADIOBIOLOGY

A08

EXPLORING RADIOPHARMACEUTICAL STRATEGIES FOR AGGRESSIVE SOLID TUMORS

Oglio R, Nevares N, Miranda J, Dores Y, Zapata M, Perona M, Carpano M, Rodriguez C, Lopez Bularte C, Pozzi O, Juvenal G, Thomasz L.
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The development of targeted radionuclide therapies represents one of the most promising strategies in modern oncology, enabling the selective delivery of ionizing radiation to tumors while minimizing exposure to healthy tissues. In this context, our laboratories have development two therapeutic radiopharmaceuticals with potential applications in aggressive and poor prognosis neoplasms: ^{131}I-delta-iodolactone (^{131}I-ILδ) and [^{1}77Lu]Lu-PSMA-617. Delta-iodolactone (IL-δ) is an iodinated derivative of arachidonic acid, identified as 6-iodo-5-hydroxyeicosatrienoic delta-lactone. This molecule has attracted growing interest due to its role in thyroid autoregulation and its potent antitumor effects. IL-δ has shown antineoplastic activity beyond the thyroid gland, in models of breast cancer, neuroblastoma, glioblastoma, melanoma, lung carcinoma, and colon cancer. In our laboratories, we successfully developed the synthesis of this iodinated lipid and its radiolabeling with ^{131}I. ^{131}I may enhance its therapeutic potential by promoting tumor-selective energy deposition. In parallel, [^{1}77Lu]Lu-PSMA-617, an FDA-approved therapeutic radioligand for PSMA-positive metastatic castration-resistant prostate cancer (mCRPC), was evaluated for its potential application beyond prostate cancer. Specifically, we assessed its therapeutic efficacy in a murine model of triple-negative breast cancer (TNBC) and in a human colorectal cancer model. In TNBC, treatment with 74 MBq of [^{177}Lu]Lu-PSMA-617 inhibited tumor growth by 72% and significantly extended survival, while maintaining good systemic tolerance. This response was accompanied by reduced vascular density and increased leukocyte (CD45) infiltration. In colorectal cancer, tumor inhibition was moderate (30%), suggesting that therapeutic efficacy may depend on vascular density, PSMA expression levels and tumor microenvironment. In summary, ^{131}I-ILδ and [^{1}77Lu]Lu-PSMA-617 represent two distinct therapeutic approaches based on different biological mechanisms to achieve tumor control and demonstrate the potential for future clinical translation of locally developed radiopharmaceuticals.

A09

RADIOSENSITIZATION OF HYPOXIC TUMOR CELLS USING ILLUMINATED PHOTOSYNTHETIC MICROALGAE AND DOSIMETRIC CONSIDERATIONS IN RADIOBIOLOGICAL EXPERIMENTS

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La hipoxia tumoral es uno de los principales desafíos en radioterapia, ya que está asociada a la radioresistencia de las células tumorales. Este fenómeno es frecuente en tumores sólidos y se vincula de manera consistente a un peor pronóstico clínico. Aunque diversas estrategias han sido exploradas para mitigar la hipoxia, ninguna se aplica de forma rutinaria en la práctica clínica. En esta presentación se mostrarán resultados experimentales obtenidos con células tumorales de la línea MCF-7 sometidas a condiciones hipóxicas, en los cuales se evaluó el potencial radiosensibilizador de microalgas fotosintéticas biocompatibles bajo iluminación controlada como una alternativa innovadora para compensar la escasez de oxígeno. Además, se discutirá la relevancia de una dosimetría precisa en estudios radiobiológicos y se presentará la metodología dosimétrica empleada, incluyendo un análisis sobre posibles mejoras a los protocolos establecidos para irradiadores de rayos X de kilovoltaje utilizados en experimentación radiobiológica.

A10

BIOLOGICAL RESPONSE TO RADIATION: TRANSLATIONAL AND MULTIDISCIPLINARY PERSPECTIVES

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The study of the biological response induced by ionizing radiation is essential for its use and optimization in medical applications. In this presentation, the activities of the Radiobiology and Biodosimetry Laboratory of Fundación Intecnus will be described, organized around three main pillars with a translational and multidisciplinary approach. First, we will discuss advances in biodosimetry, highlighting the need for rapid methods such as the development of gene expression biomarkers to estimate absorbed doses. We will also address how this technology can be used in radiotherapy treatments to identify radiosensitivity biomarkers that guide personalized protocols. Finally, research in Nuclear Medicine will be presented, aiming to characterize the radioinduced biological response to radiopharmaceuticals used in Nuclear Medicine therapy and their potential contribution to internal dosimetry. Taken together, these lines of work reflect how the integration of biology, physics, and clinical practice can drive translational radiobiology, strengthen therapeutic precision and improve patient safety.

SYMPOSIUM WINE AND SOCIETY

A11

WHAT WE TALK ABOUT WHEN WE TALK ABOUT MALBEC? A CULTIVAR WITH MULTIPLE PERSONALITIES

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Biotechnology applied to the wine industry encompasses a wide range of techniques and scientific developments, from fundamental studies of recombinant DNA technology, bioinformatics, genomics, proteomics, metabolomics, and other "-omics." In this regard, the role that Next-Generation Sequencing (NGS) and gene editing technologies are assuming for the functional study and potential modification of the grapevine plant is crucial. Using various genetic and genomic tools (including NGS techniques), our group has initiated several projects related to the study of phenotypic and genetic variation in the grapevine for different quality-related traits: biosynthesis of color-determining compounds or nutraceuticals, berry shape and size, among others. We study the diversity present among different grapevine varieties and, in particular, within the Malbec variety, both in its evolution during the selection process since its arrival in the country more than 170 years ago and in the variety's potential adaptation to climate change conditions. Recently, our research team has deciphered the complete diploid genome of Malbec, providing a clearer perspective on the genetic interaction between its two parental varieties, Prunelard and Magdeleine Noire des Charentes. We achieved a detailed and precise assembly of the haploid complements that make up the Malbec diploid genome, with exceptionally low error rates. Likewise, with the aim of conducting functional studies of the grapevine genes we identified in our genomic and transcriptomic experiments or performing genetic modifications to adapt the plant to stress conditions, we are developing transformation and gene-editing experiments using "DNA-free" CRISPR/Cas9 technology.

A12

RESVERATROL AS A THERAPEUTIC MOLECULE IN THE 21ST CENTURY

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Resveratrol (3,5,4′-trihydroxystilbene) is a natural polyphenolic phytoalexin widely investigated for its potential therapeutic actions since its association with the ‘French Paradox’. The trans isomer, considered the biologically active form, exhibits a broad spectrum of molecular effects despite its low systemic bioavailability. Its pharmacological profile includes anti-inflammatory, antioxidant, metabolic, cardioprotective and epigenetic actions mediated by multiple converging pathways. At the inflammatory level, resveratrol selectively inhibits COX-1 activity and suppresses COX-2–induced prostaglandin synthesis, while downregulating NF-κB in a dose- and time-dependent manner. These mechanisms contribute to decreased cytokine production and attenuation of chronic inflammatory signalling. Resveratrol also activates SIRT1 and the AMPK/PGC-1α axis, promoting mitochondrial biogenesis, enhancing ATP production and modulating cellular responses to energetic stress. These effects extend to improved mitochondrial turnover through stimulation of mitophagy, particularly via pathways involving Sirt1/Sirt3 and BNIP3, with significant implications for endothelial protection during hyperlipidemia and ischemia/reperfusion injury. Antioxidant activity is further mediated by the p62–Keap1/Nrf2 signalling cascade, resulting in enhanced expression of SOD-1, CAT, glutathione peroxidase and heme oxygenase-1, and inhibition of pro-oxidant enzymes such as caspase-3. In metabolic regulation, resveratrol promotes browning of white adipose tissue through SIRT1/AMPK-dependent mechanisms, reducing lipid accumulation and improving insulin sensitivity. Cardiovascular studies demonstrate that resveratrol supports endothelial nitric oxide synthase activity, improves vascular autonomous function, reduces oxidative stress in erythrocytes, mitigates blood pressure elevation in hypertensive models and prevents atherosclerotic plaque progression through anti-inflammatory and anti-thrombotic actions. At the epigenetic level, clinical evidence suggests that consumption of resveratrol-enriched wine can reverse epigenetic aging by modulating DNA methylation profiles, histone modifications and nucleosome positioning. Additional clinical data indicate improvements in hippocampal connectivity, glucose metabolism and memory performance in older adults receiving daily resveratrol supplementation. Despite a favourable safety profile at doses below 2 g/day and positive results in approximately two-thirds of clinical trials, substantial variability persists across studies due to differences in formulation, population characteristics,
baseline health, treatment duration and dose. A major limitation remains its inherently poor bioavailability, which has driven the exploration of novel delivery systems and metabolite profiling, including the contribution of microbiota-derived compounds such as lunularin. Current evidence underscores the therapeutic promise of resveratrol but highlights the need for large, well-designed randomized trials and optimized formulations to translate its robust preclinical effects into consistent clinical outcomes.

CLOSING LECTURE

A13

HOW THE OXIDATIVE STRESS RESPONSE OF *STREPTOCOCCUS PNEUMONIAE* IMPACTS ON ITS INTRACELLULAR SURVIVAL IN HOST CELLS

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Streptococcus pneumoniae is a gram-positive, aerotolerant bacterium that naturally colonizes the human nasopharynx. It is responsible for various infections, including sinusitis, otitis, pneumonia, and meningitis, making it a major cause of morbidity and mortality worldwide. While *S. pneumoniae* is considered a typical extracellular pathogen, emerging evidence indicates that it plays a significant role in its replication and survival within host cells, contributing to disease progression and pathogenesis. This bacterium produces high levels of H_2O_2 to eliminate other microorganisms present in the respiratory tract microbiota. However, it also triggers an oxidative stress response to endure these challenging conditions. Moreover, this self-defense mechanism is beneficial for tolerating the oxidative stress imposed by the host's immune response. In our laboratory, we have reported that two-component systems play a crucial role in the pneumococcal stress response to oxidative conditions and the intracellular survival of *S. pneumoniae* in host cells. Furthermore, we have provided evidence that influenza infection enhances the intracellular survival of *S. pneumoniae* within pneumocytes. We have demonstrated that the SirRH signal transduction system controls the expression of genes involved in the oxidative stress response, which *S. pneumoniae* requires to increase its intracellular survival in influenza A-infected pneumocytes. Recently, we reported the first mechanism of antibiotic persistence in *S. pneumoniae*, particularly against fluoroquinolones, which is induced by the oxidative stress imposed by host cells during its transient intracellular life. These findings regarding the role of the oxidative stress response during the intracellular phase of the pneumococcus, including coinfection with influenza A and the induction of antibiotic persistence in host cells, contribute to our understanding of pneumococcal pathogenesis and its implications for secondary bacterial infections in influenza patients, as well as the potential negative impacts on fluoroquinolone treatment for pneumococcal diseases.

GENERAL, CELLULAR AND MOLECULAR BIOLOGY

A14

RADIATION-INDUCED EFFECT OF ADIPOSE TISSUE ON RENAL CANCER PROGRESSION

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Radiotherapy (RT) is a common cancer treatment aimed primarily at killing tumor cells. However, RT also affects the tumor microenvironment, influencing tumor growth, spread, and tumor control. In renal cancer, conventional RT has shown limited effectiveness. In contrast, stereotactic ablative radiotherapy (SABR), which uses high doses in fewer sessions, has demonstrated better tumor control in both primary and metastatic renal cancer, along with improved patient quality of life. As a result, SABR is gaining global relevance, especially for patients unable to undergo surgery or with small tumors. Despite its growing use, the mechanisms by which SABR affects tumor behavior and the microenvironment remain poorly understood. This study begins to explore the effect of SABR on the MT; specifically, we evaluated if soluble factors released by irradiated normal (hRANi) and tumor (hRATi) perirenal adipose tissue modulates the proliferation, migration and adhesion of human renal epithelial cell lines. It also aims to identify soluble components present in the different conditioned media (CMs) from hRANi and hRATi. Fragments of normal (hRAN) and tumor (hRAT) perirenal adipose tissue were collected from kidney donors and renal cancer patients, respectively. These tissues were irradiated with X-rays at doses of 0, 2, and 10 Gy, and then incubated for 24 hours to generate CMs. Protein expression of adiponectin, leptin, perilipin 1, and FABP4 was analyzed by Western blot. Additionally, human renal epithelial cell lines—tumor (786-O) and non-tumor (HK-2)—were treated with the CMs to assess cell proliferation (MTT assay), adhesion, and migration (wound healing assay). hRAT irradiated with 2 Gy showed a significant decrease in the expression of leptin (pro-tumorigenic adipocytokine) and FABP4 (elevated in patients with renal cancer) compared to non-irradiated hRAT. When evaluating changes in the biological activity of cells incubated with the different CMs, we observed that hRATi-CMs 10 Gy significantly lost its ability to stimulate proliferation of HK-2 and 786-O cells at 24 and 48 h ($p<0.05$) compared to hRATi-CMs at 0 Gy and 2 Gy, and/or the control medium. We found the adhesion capacity of both cell lines incubated with hRATi-CMs 10 Gy decreased compared to those incubated with hRATi-CMs 0 and 2 Gy ($p<0.05$). Finally, we observed that 786-O cells incubated with hRATi-CMs 10Gy showed a significantly reduced migration capacity at 6 and 12 h *vs.* hRATi-CMs 0 and 2 Gy ($p<0.05$). In conclusion, radiation alters the behavior of the peritumoral renal adipose tissue, and the irradiated adipose tissue, at high doses, can reverse at least in part the tumor features.

A15

LIQUID BIOPSIES AND KIDNEY CANCER: SEARCH FOR BIOMARKERS

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Renal cell carcinoma (RCC) is one of the most common and deadliest urological tumors worldwide. In this context, liquid biopsies emerge as a promising alternative for the detection and monitoring of biomarkers in biological fluids such as blood and urine, offering a non-invasive and repeatable method. This study aimed to identify and validate potential biomarkers for RCC by combining experimental and bioinformatics approaches. Tissue, plasma, and urine samples from patients and healthy controls were analyzed using qRT-PCR and Western blot techniques, evaluating the expression of VEGF, AQP1, AQP2, PLIN1, PLIN2, adiponectin, NF-κB, Hsp27, and PCNA. Simultaneously, *in silico* analyses were performed using data from The Cancer Genome Atlas (TCGA) and bioinformatics tools to corroborate and validate the experimental results. The findings revealed differential gene and protein expression profiles between patients and controls, highlighting the increased expression of VEGF, AQP1, PLIN2, and Hsp27, along with the decreased expression of PLIN1 and adiponectin in RCC patients. These results suggest the involvement of multiple molecular pathways related to angiogenesis, lipid metabolism, cell proliferation, and stress resistance, reinforcing the potential of these markers for early detection and prognosis of the disease. In conclusion, integrating liquid biopsies with bioinformatics analysis offers a multidimensional approach to the study of RCC, providing strong evidence for the future development of biomarker panels applicable in clinical practice and personalized medicine.

A16

PRIMER VALIDATION FOR CIRCADIAN GENE EXPRESSION ANALYSIS IN SPLENIC MACROPHAGES

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Circadian rhythms align physiology and behavior with the 24-hour solar cycle, an adaptive process orchestrated by the molecular clock. In mammals, the suprachiasmatic nucleus (SCN) functions as the master pacemaker, synchronizing peripheral clocks through sympathetic and hormonal cues. Preliminary evidence from our laboratory suggests that norepinephrine (NE), released by sympathetic innervation, sustains BMAL1 rhythmicity in splenic macrophages (MΦ), thereby linking circadian regulation to immune function. To further explore clock–immune interactions in the spleen, we focused on the expression of *Rorα*, *Rev-erbα*, and *Per1/2*, key transcriptional regulators of the molecular clock. Quantitative PCR (qPCR) offers a wide dynamic range, sensitivity, and accuracy, but requires careful optimization and validation to ensure reproducibility and biological relevance. Therefore, our aim was to validate primer pairs for robust and specific amplification of these circadian genes. Primers were designed using PrimerQuest™ Tool and subjected to rigorous *in silico* evaluation, including analyses of specificity, splicing variants, predicted amplicon size, and the absence of secondary structures. This was followed by empirical optimization, in which cDNA input and primer concentrations were titrated. Reliable amplification was obtained using 300 nM primer concentrations with 100 ng template. Amplification specificity was confirmed by capillary electrophoresis sequencing (CES), which verified the identity of the PCR products. With optimized conditions, the validated primers displayed high sensitivity and reproducibility, enabling the detection of temporal expression changes in *Rorα*, *Rev-erbα*, and *Per1/2* in splenic MΦ. These results demonstrate that the selected primer sets are suitable for quantitative assessment of circadian gene expression and provide a robust methodological framework for future studies. The validated qPCR primers constitute a reliable tool for investigating circadian gene expression in splenic MΦ. This methodological advancement establishes the basis for studying how NE and the SCN–spleen axis shape immune rhythmicity, thereby contributing to our understanding of neuro-immune circadian regulation.

A17

PROSTATE CANCER CELLS MODULATE ADIPOKINE AND HORMONE RECEPTOR EXPRESSION IN PERIPROSTATIC ADIPOSE TISSUE

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Epithelial–stromal interactions are crucial for normal tissue homeostasis and cancer development. In prostate cancer (PCa), obesity is associated with worse outcomes, highlighting the role of adipose tissue as a stromal regulator. We have previously demonstrated that peritumoral adipose tissue influences tumor cell behavior. Here, we investigated the reverse dialogue, assessing how PCa cells affect periprostatic adipose tissue (PPAT). Normal PPAT from retropubic adenomectomies were incubated for 24 h with conditioned media (CMs) from three PCa cell lines with different hormonal dependence and aggressiveness (LNCaP, DU145, PC3). Morphology, lipid content, and the expression of adipokines and hormone receptors were evaluated. No major morphological or lipid content changes were detected. However, all tumor-derived CMs increased leptin expression, a pro-tumorigenic adipokine linked to proliferation, migration, and angiogenesis. Notably, LNCaP-CM (hormone-sensitive) upregulated aromatase, androgen receptor (AR), and estrogen receptor α (ERα). Since AR and ERα are associated with tumor growth in hormone-sensitive PCa, these results suggest that LNCaP cells induce PPAT to enhance peripheral aromatization and hormone supply. In contrast, DU145- and PC3-CMs (both hormone-insensitive) only reduced ERβ, a receptor with proposed antiproliferative roles. In conclusion, prostate tumor cells actively reprogram PPAT in a hormone phenotype–dependent manner, supporting its role as an active partner in PCa progression.

A18

STRUCTURAL CHARACTERIZATION OF THE INTERACTION BETWEEN CYCLOOXYGENASE 1 AND 2 WITH FLAVONOIDS

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Cyclooxygenase (COX) is a key enzyme involved in the synthesis of prostanoids, including prostaglandins, prostacyclin and tromboxane, through the conversion of arachidonic acid to prostaglandin H2, which is the rate-limiting step in prostanoid production. There are two principal isoforms of COX which are named as COX-1 and COX-2. COX-2 isoform is believed to be responsible for biosynthesis of prostaglandins PGs that are associated with inflammation. COX inhibition is one of the targets of non-steroidal anti-inflammatory drugs (NSAIDs), the most widely used drugs for the treatment of various inflammatory diseases and relieving pain. Traditional NSAIDs work by inhibiting both COX-1 and COX-2 isoforms, while "COXIBs" exert their biological effects by inhibiting COX-2. Both groups of drugs present adverse effects, so the search for other types of

compounds with anti-inflammatory activity is of interest. Flavonoids have demonstrated anti-inflammatory and gastrointestinal protective activity in animal models, and in previous studies we have analyzed their binding to COX. Our objective was to compare the binding of flavonoids, 7-O-methyleriodictiol, nepetin, 7-O-methylsudachitin and quercetin, at the binding sites of the COX-1 and COX-2 enzymes. Although COX-1, and COX-2 isoforms are highly similar in structure, there is a notable structural difference in the active site (catalytic domain) of COX-2. For this purpose, structural data for the human COX-1 (AY3C) and COX-2 proteins (5IKR) deposited in the Protein Data Bank (PDB) were used. The Autodock Vina and Chimera bioinformatic tools were used to perform *in silico* docking assays of the compounds to the COX-1 and 2 enzymes. The binding of the compounds to the enzyme was observed and evaluated using the Pymol and Chimera programs. The results suggest that flavonoids bind to two binding sites on the surface of both enzymes with high affinity. One of these sites is the active site of each enzyme, where flavonoids show high affinities compared to the indomethacin control. The flavonoid 7-O-methyleriodictyol shows the highest binding affinity for the COX-2 active site. The results suggest that flavonoids could have anti-inflammatory effects by binding these compounds to cyclooxygenase proteins, regulating their metabolic functions.

A19

ANTITUMOR EFFECT OF EXTRACTS OBTAINED FROM DIFFERENT TYPES OF GRAPES AND OLIVE POMACE ON RENAL CANCER

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Wine and olive oil productions are two of the main agri-food economic activities in Mendoza, and grape and olive pomace are by-products resulting from this production. These pomaces are sources of bioactive phenolic compounds that could be used for tumor prevention. Initially, bioactive extracts from different pomaces were obtained and characterized: 1) conventional Malbec (CM), 2) organic Malbec (OM), and 3) olive pomace (O) using: a) Natural Deep Eutectic Solvents (NADES) and b) acidified water (AQ, conventional procedure). In this work, we evaluated the effect on cell proliferation, viability, adhesion, and migration of seven serial dilutions (from 50 mg/mL to 0.78 mg/mL) of each of the six extracts on tumor (786-O and ACHN) and non-tumor (HK-2) human renal epithelial cell lines. Proliferation was assessed at 24 and 48 h by MTT, viability by Trypan blue, adhesion by MTT, and migration by Wound healing. CM and OM extracts significantly decreased the proliferation and viability of the three cell lines in a dose- and time-dependent manner ($p<0.05$), while extract A also did so, but only at high concentrations. The CM-, OM-, and A-NADES extracts produced a stronger reduction in the proliferation and viability of the three cell lines than the corresponding aqueous (CM-, OM-, and A-AQ) extracts ($p < 0.05$). The effect on proliferation and viability was significantly greater in tumor cell lines than in non-tumor cell lines ($p<0.05$). Likewise, the extracts significantly decreased cell adhesion of the 786-O line ($p<0.05$), with CM- and OM-NADES being more efficient than the respective AQ extracts. Finally, CM-, OM-, and O-NADES extracts decreased cell migration of both 786-O and ACHN ($p<0.05$). However, 786-O (primary tumor cells) was much more sensitive to the extracts than ACHN (metastatic site cells). In conclusion, 1) NADES extracts showed a greater antitumor effect than AQ; 2) CM and OM extracts presented a greater antitumor effect than O; 3) finally, tumor renal cell lines were more sensitive to the extracts than non-tumor cell lines.

A20

EXPLORING THE THERAPEUTIC POTENTIAL OF SYNTHETIC COMPOUNDS AGAINST Leishmania amazonensis

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Leishmaniasis is a parasitic zoonotic disease on the rise in South America and is considered by the WHO as a neglected tropical disease, disproportionately affecting low-income populations with limited access to health services. Globally, an estimated 700,000 to 1 million new cases are reported each year. Transmission occurs through the bite of infected sand flies, and the clinical manifestations—cutaneous, mucocutaneous, or visceral—depend largely on the infecting species. In Argentina, the disease mainly affects the northern region, where its incidence has steadily increased over the past two decades. Current therapies remain unsatisfactory due to their toxicity, high cost, difficult administration, and the emergence of drug-resistant strains. These limitations highlight the urgent need for new therapeutic strategies. In this context, synthetic compounds have gained attention as potential sources of novel antileishmanial agents. Here, we evaluated the therapeutic efficacy of two synthetic compounds, LL-PA-075 and APC-1-109, in an *in vivo* model of cutaneous leishmaniasis. Male BALB/c mice (8–10 weeks) were infected in the right footpad with 1×10^4 *Leishmania amazonensis* promastigotes and treated locally once a week for 10 weeks. LL-PA-075 treatment resulted in a marked reduction in footpad swelling, accompanied by a significant decrease in parasite burden and splenic index, as well as a downward trend in total IgG levels. In contrast, APC-1-109 did not exhibit significant therapeutic effects. It even seems to exacerbate the infection since the parameters analysed increase in mice treated with APC-1-109. Taken together, these findings highlight LL-PA-075 as a promising candidate for the development of new therapies against *L. amazonensis* and cutaneous leishmaniasis.

A21

EFFECT OF ESTROGEN AND PROGESTERONE ON THE REGULATION AND INTRACELLULAR TRANSPORT OF CATHEPSIN D AND ITS RECEPTORS IN A HUMAN ENDOMETRIUM-DERIVED CELL LINE

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The endometrium is a key tissue for reproduction. The steroid hormones estrogen (E2) and progesterone (P4) regulate morphological and functional transformations during the menstrual cycle, converting the endometrium into a receptive state, highlighting the importance of intracellular trafficking to allow implantation. Impaired adhesive capacity of the endometrial luminal epithelium leads to inadequate blastocyst adhesion and implantation failure. Defective endometrial adhesion is a major cause of infertility-related implantation failure but the mechanisms contributing to this remain poorly defined. In recent years, the involvement of Lysosomes have been recognized for their involvement in numerous physiological processes. Lysosomal proteases, including cathepsins, play roles in menstruation, implantation, and placental formation, as well as in several diseases, including cancer and endometriosis. Despite its important role in key reproductive processes, the mechanism of cathepsin D (CatD) activity and its intracellular regulation have not been extensively studied in endometrial epithelial cells. In this study, we used a human endometrial epithelial cell line to investigate whether the expression and/or localization of CatD and its transporter proteins could be influenced by sex hormones. Using fluorescence microscopy and immunoblot, we observed that CatD expression shows significant variations following hormonal treatments, especially with P4, which increased the expression of immature forms of the protease. We also observed increased expression of CD-MPR under P4 and of sortilin under E2. These findings suggest that, in endometrial epithelial cells, CatD predominantly utilizes the CD-MPR pathway during the postovulatory phase of the cycle (when P4 predominates) and the sortilin-mediated pathway during the E2 phase. These studies contribute to our understanding of the mechanisms underlying the intracellular mechanism of the lysosomal protease CatD and its receptors under the influence of steroid hormones in a cell line derived from human endometrial epithelium. Unraveling the molecular mechanisms involved in E2- and P4-modulated CatD trafficking may provide new insights into endometrial function. Intracellular transport of CatD will shed further light on endometrial function and open up new avenues for developing novel approaches to improve reproduction.

A22

POLYPHOSPHATE METABOLISM IN *PSEUDOMONAS AERUGINOSA* AS A THERAPEUTIC TARGET: CONSTRUCTION OF MARKERLESS AND KNOCKOUT MUTANTS

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Polyphosphate (polyP) is a high-energy biological polymer of inorganic phosphates, ubiquitous in the microbial world, playing an essential role in the survival and pathogenesis of opportunistic pathogens such as *Pseudomonas aeruginosa*. PolyP metabolism regulated by polyphosphate kinases (Ppk1, Ppk2) and exopolyphosphatase (Ppx) is fundamental for stress tolerance, ATP synthesis, virulence factor production, and biofilm formation. Given its central role, inhibition of the enzymes involved in polyP metabolism represents a potential therapeutic strategy to combat antibiotic-resistant *Pseudomonas aeruginosa* infections. To investigate the specific functions of these genes, this study was designed to generate markerless deletion mutants in the PAO1 wild-type strain. The methodology employed a double homologous recombination process using the sacB-containing suicide vector pEX18ApGW and the helper plasmid pTNS2. The procedure began with cloning the upstream and downstream flanking regions of each target gene, along with a gentamicin resistance (Gm^{R}) cassette inserted via KpnI, BamHI, and PstI restriction sites, into pEX18ApGW. Successful ligation was confirmed by restriction digestion. The recombinant constructs were introduced into PAO1 cells by electroporation (pulsed at ~2.5 kV), followed by recovery in SOC medium. Primary mutant selection was performed by sequential plating on gentamicin, followed by stringent counter-selection on gentamicin and 5% sucrose to isolate double-crossover recombinants (Gm^{R}, Suc^{R}). These were verified by colony PCR. Subsequently, the pFLP2 plasmid was introduced via a second electroporation into the primary mutants to remove the Gm^{R} cassette through Flp recombinase-mediated recombination. Final confirmation of the markerless mutants (*Δppk1, Δppk2, Δppx*) was based on their gentamicin-sensitive and carbenicillin-sensitive (Gm^{s}, Cb^{s}) phenotypes and a final colony PCR that yielded an intermediate-sized amplicon (approximately 500 bp smaller than the wild-type fragment). In conclusion, the results confirmed the successful, high-fidelity construction and cryopreservation of two validated clones for each single-gene markerless deletion mutant. This collection provides a valuable tool for future functional assays aimed at phenotypically characterizing the impact of disrupted polyP metabolism on key bacterial traits, thereby supporting the evaluation of this pathway as a potential anti-virulence target.

A23

BACTERIAL INFECTIONS IN MUCO-OBSTRUCTIVE LUNG DISEASES: AN ONGOING CHALLENGE

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Muco-obstructive pulmonary diseases are characterized by thick mucus accumulation, leading to chronic inflammation, tissue damage, and impaired lung function. This altered environment creates hypoxic niches that favour bacterial colonization and biofilm formation, with *Pseudomonas aeruginosa* (*P. aeruginosa*) being a prevalent and persistent opportunistic pathogen. Its remarkable adaptability, metabolic flexibility, and ability to form biofilms make it a leading cause of chronic lung infections in patients with muco-obstructive diseases. In recent years, numerous carbonic anhydrases in bacteria (CA-b) have been detected, cloned, and characterized in various pathogenic bacteria. CA-b enzymes belong to a superfamily of metalloenzymes, of which three classes have been identified in bacterial genomes: α-, β-, and γ-CA-b. These enzymes catalyze the hydration of CO_2, a reaction central to bacterial metabolism, as it connects to multiple metabolic and biochemical pathways, including carboxylation reactions and pH homeostasis. *P. aeruginosa* encodes three CA-b enzymes (psCA1, psCA2, and psCA3), each with distinct regulation and function, suggesting they mediate specific physiological responses, although this adaptive mechanism remains poorly understood. Based on these observations, we postulate that hypoxia induced by mucus accumulation enhances bacterial colonization, with CA-b enzymes playing an important role in both the colonization of this environment and the persistence of infection, thereby contributing to the development of chronic pulmonary disease. To address this, we constructed *P. aeruginosa* PAO1 mutant strains lacking each of the CA-b enzymes through allelic replacement, in order to assess the individual contribution of each CA-b to bacterial pathogenicity under hypoxic conditions. Our results confirmed the successful construction of all three markerless single-gene deletion mutants. These mutants are now ready for functional analyses to assess the phenotypic consequences of disrupted CA-b metabolism on essential bacterial processes, including biofilm development and virulence. These studies will facilitate the evaluation of this pathway as a potential target for novel anti-virulence therapies, with the goal of delaying the progression of chronic infections and improving patients' quality of life and clinical outcomes.

A24

STUDY OF THE INTERACTION OF SMALL LIGANDS WITH THE 14-3-3 PROTEIN BY DIRECT TITRATION

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The 14-3-3 protein family, composed of seven paralogs in mammals, regulates critical cellular processes such as adipogenesis, cell cycle, and apoptosis. These proteins perform their function by binding to phosphorylated serine and threonine residues in target proteins through a conserved binding groove, making them attractive targets for drug development. Previous research by our group demonstrated a significant increase in the expression of the 14-3-3γ paralog during adipogenesis, highlighting its relevance in this process. With the aim of identifying binding sites susceptible to pharmacological intervention, we performed a virtual screening of 20 million compounds from the ZINC database on a 14-3-3 monomer, using molecular docking with AutoDock VINA. This analysis identified 50 compounds from the β-carboline family with high affinity for a specific region located on the opposite side of the main binding groove. The objective of this work was to experimentally validate the protein-ligand interaction by direct titration. To this end, the 14-3-3γ protein was expressed in *Escherichia coli* and purified by affinity chromatography (IMAC) and size exclusion chromatography (SEC). Among the ligands identified, those whose UV absorption peak was different from that of the protein (280 nm) were selected, allowing a spectrophotometric approach without the use of markers. The selected ligands were diluted to 2 mM in TRIS-NaCl buffer pH 7.5 with 20% DMSO. Triplicate titrations were performed for each of three protein concentrations (0.5, 1.0, and 1.8 µM) using the selected ligands. When comparing the absorption spectra of the protein-ligand complexes to those of the ligand alone, Perlolyrine was observed to show significant changes in absorbance at 380 nm. This change suggests the formation of a complex with an apparent stoichiometry of two ligand molecules per protein (dimeric form) ($n_{max} = 2$). Additionally, the compound was tested in 3T3-L1 cells induced to adipogenesis. At a final concentration of 4 µM, an increase in adipogenic differentiation was observed, as determined by Oil Red O staining measured at 345 nm. In conclusion, these results suggest the interaction and formation of the 14-3-3γ-Perlolyrine complex, supporting the usefulness of direct titration spectrophotometric assays as a complementary tool for verifying interactions predicted by molecular docking. Combining this approach with other biophysical and structural techniques will allow for more accurate characterization of binding sites in 14-3-3 proteins and advance the development of pharmacological modulators.

A25

DECODING NON-MUSCLE MYOSINS IN BREAST CANCER: BIOMARKERS AND THERAPEUTIC OPPORTUNITIES

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Breast cancer is the leading cause of cancer-related death among women in Argentina. Its high incidence, coupled with drug resistance, the adverse effects of chemotherapy, recurrence, and metastasis, highlights the need for new therapeutic strategies and biomarkers with prognostic and/or predictive value. Non-muscle myosins perform key functions in tumor progression—including cytoskeleton organization, vesicular trafficking, adhesion, and cell migration—exhibiting dual roles, acting as both tumor suppressors and promoters depending on the context. For instance: MYH9 stabilizes the tumor suppressor protein p53, MYO1B and MYO5A promote migration and invasion, MYO1C and MYO5B act as suppressors. This evidence indicates that myosins could be critical signaling modulators and potential cancer biomarkers, although their prognostic/predictive value in breast cancer still lacks exhaustive characterization. We postulate that non-muscle myosins exhibit a distinctive gene expression pattern in each molecular subtype of breast cancer with potential prognostic and/or predictive value. While certain expression patterns are associated with a good prognosis, others are related to adverse clinicopathological characteristics and a worse prognosis in breast cancer patients. The general objective of this project is to evaluate the role of myosins in breast cancer and their potential prognostic/predictive value through in silico studies (TCGA cohort) and in vitro assays in cell lines. Our preliminary results on the differential expression of non-muscle myosins in breast cancer, obtained through in silico analysis of The Cancer Genome Atlas (TCGA) cohort (1097 patients with invasive mammary adenocarcinoma, without previous treatments, and who underwent surgical resection), performed using the EdgeR method, revealed a significant differential expression of genes coding for non-muscle myosins. In total, 15 subexpressed myosin heavy chain genes were identified, with notable decreases of between 5 and 7-fold on a logarithmic scale, among which MYH2, MYH7, MYH6, MYH13, MYH1, MYH8, and MYH11 stand out. On the other hand, overexpressed genes were observed compared to normal tissue, including MYO3B, MYO19, MYH16, MYO1G, and MYO3A. These findings suggest that the dysregulation of various non-muscle myosins could be closely associated with breast cancer progression, positioning them as potential biomarkers with prognostic value and possible therapeutic targets to be explored in subsequent studies. The clinical heterogeneity of breast cancer and drug resistance underscore the need for novel therapeutic strategies. This study seeks to establish the prognostic and predictive value of specific myosins, identifying potential biomarkers and molecular targets that could open up opportunities for more effective therapies.

A26

PRESENCE OF PERITUBULAR MACROPHAGES IN THE SEMINIFEROUS TUBULES OF THE TESTICULAR TISSUE OF RABBITS FED A HIGH-FAT DIET AND SUPPLEMENTED WITH EXTRA VIRGIN OLIVE OIL

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In the wall of the seminiferous tubules of rodent's testis, the peritubular myoid cells form a monolayer. This provides peristaltic action and structural support. In recent research, a second major subpopulation of testicular macrophages, known as peritubular macrophages (PTMs), it has been observed that resides along with the more familiar interstitial testicular macrophages. This particular subset of testicular mononuclear phagocytes has been described as cells capable of releasing colony stimulating factors and enzymes involved in the biosynthesis of retinoic acid for the differentiation of spermatogonia A. However, to date, no studies have been published that describe the presence of these macrophages in rabbit testicles. Furthermore, there is an absence of evidence to suggest that these cells exhibit variation in response to high-fat diets, given that such diets are recognized as pro-inflammatory states. The objective of this study was to investigate the impact of a high fat diet (HFD) and the supplementation of extra virgin olive oil (EVOO) to an HFD on the presence and quantity of PTMs in rabbit testis. Male New Zealand White rabbits were fed a commercial rabbit pellet (normocholesterolemic rabbits: NCR), a high-fat diet (hypercholesterolemic rabbits: HCR) comprising 14% bovine fat, and a diet supplemented with extra virgin olive oil (7% bovine fat + 7% EVOO). Immune cells were detected using an anti-Iba1 antibody with confocal microscopy on histological sections. The findings of this study indicate the presence of a discrepancy in PTM levels in response to diets comprising saturated and unsaturated fats. However, further research is required to ascertain the underlying mechanisms.

A27

CRYSTAL STRUCTURE OF THE BRCT3 DOMAIN OF HUMAN TOPBP1

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TOPBP1 is a conserved scaffold with nine BRCT domains that integrates replication-stress signalling, checkpoint activation and DNA repair. Through modular BRCT-mediated interactions, TOPBP1 couples 9-1-1 clamp engagement at stalled forks with ATR pathway activation, coordinates origin firing and fork protection, and assembles repair and chromatin factors during S phase and after DNA damage. Ligand-validated specificities exist for several BRCT pairs (e.g., BRCT1/2 recognising components of the 9-1-1 pathway and BRCT4/5 recognising phosphopeptides from checkpoint and repair adaptors), yet BRCT3 remains poorly defined: its ligand preferences are unclear, structural data have been limited to lower-resolution EM/NMR models, and its contribution to the interaction network has not been resolved. Here, we report the first crystallographic structure

of human TOPBP1-BRCT3 at a resolution of 2.2 Å. Domain boundaries were selected using AI structural predictions (RoseTTAFold and AlphaFold2), the gene was cloned from cDNA into a pET28b-derived vector, and the protein was produced in *E. coli* with an N-terminal His$_6$-StrepII-TEV tag (151 aa). Crystals grew in PACT A3 (0.1 M SPG, pH 6, 25% w/v PEG 1500) and data were collected at BL13-XALOC (ALBA). Phases were obtained by molecular replacement using an AlphaFold3 model. The current model reveals a canonical BRCT fold with a well-ordered hydrophobic core and surface features suitable for phospho-dependent or adaptor-mediated recognition, but without bound ligands in the crystal. This structure closes a key gap in the TOPBP1 BRCT atlas and provides a stable reference for mapping conserved versus variable surface patches unique to BRCT3, as well as comparing pocket architecture and electrostatics with ligand-competent BRCTs across TOPBP1. Together, these results establish a structural foundation for testing mechanistic models of how BRCT3 contributes to checkpoint control, fork stability, and genome maintenance, complementing existing structural knowledge of other TOPBP1 BRCT modules.

A28

GABA$_B$R AND CHOP: FRIENDS OR ENEMIES?

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GABA signalling involves ionotropic receptors (GABA$_A$R and GABA$_C$R), mediating fast responses, and metabotropic receptors (GABA$_B$R), which mediate slower actions via G-protein coupling. The heterodimeric GABA$_B$R, composed of the GABA$_{B1}$ and GABA$_{B2}$ subunits,forms multiprotein complexes by interacting with GABAAR and other partners, such as APP, KCC2, and the transcription factors CHOP and CREB. Previous studies from our laboratory have shown that the GABA$_{B2}$ subunit declines with aging in the cerebellar cortex, potentially compromising synaptic complex function. In this context, CHOP (C/EBP Homologous Protein) is a stress-induced transcription factor with proapoptotic activity. CHOP has been proposed to act as an intermediate in GABA$_B$R heterodimerization and plasma membrane localization. While its interaction with GABA$_B$R has not been fully characterized, evidence suggests a possible protein-protein interaction under cellular stress, for example, during ischemia. It remains unclear whether such interaction occurs under physiological conditions in regions including the hippocampus and cerebellum, or how it changes with aging. We hypothesized that stress-induced CHOP overexpression during aging may promote an interaction with GABA$_B$R, impair B1/B2 heterodimer formation, lead to intracellular retention of receptors, and reduce their surface availability, thereby contributing to the decline in GABA$_B$R-mediated inhibitory signalling. Our main goal was to characterize the relationship between CHOP and GABA$_B$R in the cerebellum and to understand how this interaction operates during aging and its potential impact on inhibitory signalling. For this work, cerebellar specimens were collected from young and old male Wistar rats. Immunohistochemistry was applied to study the expression and distribution of GABA$_B$R subunits and CHOP, allowing us to assess potential colocalization and age-related changes in Purkinje cells. As expected, we observed decreased GABA$_{B2}$ levels, increased CHOP expression, and colocalization within Purkinje cell somata in the cerebellum of older rats. These results suggest that CHOP could modulate the organization and function of GABA$_B$R under the influence of aging in the rat cerebellum.

VEGETAL BIOCHEMISTRY, PHYSIOLOGY, PATHOLOGY AND PRODUCTION

A029

VEGETATIVE AND ANATOMICAL MORPHOMETRIC CHARACTERISTICS IN *VICIA SATIVA* (LEGUMINOSAE) CULTIVATED IN THREE CONTRASTING SOILS

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Crop productivity depends, among other factors, on soil quality. In the experimental field of the Facultad de Agonomía y Veterinaria de la UNRC, the growth and development of different forage species, including *Vicia sativa*, are compared in different soils: conventional tillage, direct sowing, and pristine soil. The objective of this work was to compare morphometric and anatomical characteristics of *V. sativa* roots in three contrasting soils in two consecutive crop years: 2024 and 2025 with different sowing dates (July and May, respectively). The variables analyzed were: Green weight (g), Plant height (cm), Leaflet length and width (cm), Branching, Main root diameter (µ), Vascular cylinder diameter (µ), Number of cortex cell layers, Root vessel member diameter (µ), and Number of root vessel members/surface. The design of the experiment was completely randomized with three replicates. The evaluation was performed on plants collected 75 days after sowing. For observation and measurement of root anatomical characteristics, cross-sections were made using the conventional technique to obtain histological specimens. They were observed with a Zeiss microscope and photographed with Motic Images Plus 3.0. The data obtained were analyzed using ANOVA and Fisher's LSD test. Significant differences between the evaluated in 2024 traits were found in Green weight, Plant height and Root vessel diameter, with those grown in pristine soil reaching the highest values: 3.79 g Green weight ($p=0.01$), 29.83 cm Plant height ($p=0.01$) and 2.74µ in Root vessel diameter ($p=0.03$). In 2025, there was a greater development in plants from pristine soil but significant differences are added in Leaflet width and Branching. The values were: 8.57 g ($p = 0.01$) for Green weight, 38.09 cm ($p = 0.0004$) for Plant height, 0.77 cm in Leaflet width, 6.64 in Branching and 3.36 µ ($p = 0.01$) in the Diameter of root vessel members. These data express firstly the better conditions of the pristine soil for the development of *V. sativa* in both cultivation years and secondly the earlier sowing (autumn) correlates with a notable increase in fresh organic matter in 2025, therefore, the combination of both factors in the cultivation of *V. sativa* would favor higher production.

A30

MIXED PASTURES OF *Adesmia bicolor* AND *Festuca arundinacea*: NITRATE EVALUATION UNDER IRRIGATED AND RAINFED CONDITIONS

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Nitrogen (N) is a macronutrient that constitutes chlorophyll and is present in most organic compounds found in plants. Among inorganic nitrogen, nitrate (NO^-) is the main form absorbed by plants in aerated soils. The use of a legume species associated with cut grasses results in benefits, saving on nitrogen fertilization, reducing production costs, and decreasing environmental pollution. The objective of this study was to evaluate the effect of irrigation, cutting intensity, and species proportion on soil nitrate availability in tall fescue (*Festuca arundinacea*) grown in association with adesmia (*Adesmia bicolor*). The experiment was carried out at the Experimental Teaching and Experimentation Field of the National University of Río Cuarto, Argentina, on a Typic Haplustoll soil. Twenty-four plots with different species ratios were subjected to combinations of irrigation regimes and cutting intensities. Soil nitrate concentrations ($N\text{-}NO_3^-$) were monitored over three years and analyzed using ANOVA and Fisher's LSD test. Results showed that irrigation reduced surface nitrate levels, likely due to leaching, while rainfed plots accumulated higher concentrations. Cutting intensity did not cause significant differences, although a tendency toward lower nitrate values under more intense cutting was observed. The 1:1 ratio of adesmia and tall fescue showed the highest nitrate accumulation, indicating a synergistic effect on nitrogen fixation and utilization. Soil mechanical resistance was also measured, revealing significant compaction between 20 and 35 cm depth, which may restrict root growth and resource use efficiency. These findings highlight that mixed pastures with balanced species proportions and proper water management can enhance nitrogen availability and contribute to more sustainable agricultural systems in the Pampas region.

A31

SCREENING OF ADVANCED SORGHUM (*Sorghum bicolor* (L.) Moench) LINES FOR THEIR ABILITY TO GERMINATE UNDER SIMULATED WATER STRESS CONDITIONS

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Water availability deficit is one of the main causes of yield loss in crops. Water plays a fundamental role in every stage of plant growth. Developing drought-tolerant varieties capable of maintaining performance under water stress conditions is a primary objective in plant breeding. Reducing in vitro osmotic potential with polyethylene glycol (PEG) during germination is a technique used to simulate water stress. This study aimed to evaluate the germination capacity of advanced sorghum lines under different PEG concentrations. A total of 24 genotypes, 22 advanced lines obtained at FAV-UNRC, and 2 control cultivars, were tested under three water conditions (PEG 6000: 0, 14, and 18%). Seeds were placed in a chamber at 25 °C in trays containing germination substrate and the corresponding PEG solution. Fifty seeds per tray and three replicates per genotype were used. The variables analyzed 10 days after sowing were: germination capacity (%), leaf biomass (g), root biomass (g), and total biomass (g). Based on these variables, the seedlings vigor index, the leaf/root biomass ratio, and the proportion of root biomass (%) were calculated. Data were analyzed using linear mixed models, and, in addition, for the condition of greater water stress (PEG 18 %), principal component analysis (PCA) was performed. The results showed that sorghum genotypes exhibit variable tolerance levels to water deficit during germination. As the PEG concentration increased, the means of the genotypes showed a decreasing trend for all variables, with the most significant impact at 18 % PEG, except for the proportion of root biomass, which increased with water deficit. The PCA showed a correlation between variables and revealed that the variables leaf biomass, total biomass, vigor index, and proportion of root biomass contributed most to the first principal component. Seven advanced lines show superior performance for the variables analyzed. These genotypes will be evaluated in multi-environment trials to verify their performance and assess their use in the development of cultivars suitable for regions with water limitations.

A32

WATER STRESS TOLERANCE IN SORGHUM GENOTYPES: AN APPROACH USING DROUGHT INDICES

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Sorghum (*Sorghum bicolor* (L.) Moench) is a species whose grain is used for human and animal consumption, as well as in industry. The crop is notable for its ability to thrive and produce acceptable amounts of grain, even under conditions of reduced water availability. Water deficit is one of the main factors limiting the development and productivity of many agricultural species. Indices of water stress tolerance are useful tools for evaluating and comparing the ability of crops to withstand and recover from periods of water deficit. The objective of this study was to identify advanced grain sorghum lines tolerant to water stress conditions in the early stages of cultivation. The plant material consisted of 24 genotypes (22 advanced lines and 2 control cultivars) of sorghum that were exposed to three simulated water limitation conditions with polyethylene glycol (PEG 6000: 0, 14, and 18 %) during the germination phase. Three trays with 50 seeds per genotype and treatment were placed under controlled chamber conditions (25 °C), containing the germination substrate and the corresponding solution. Ten days after germination, the total biomass of seedlings was determined, and this value was used to estimate the relative biomass index for the 14 and 18 % PEG treatments. This index was obtained as the ratio of the biomass of seedlings in the trays with 14 and 18 % PEG to the average biomass of the control samples (0 % PEG). Nine different stress tolerance indices were determined. Among them, the yield index was correlated with total biomass at 14 and 18 % PEG using a 3D graph. Significant positive correlations between the indices and biomass at 14 and 18 % PEG indicate the ability of the indices to identify genotypes with tolerance to water stress conditions. The 3D graph allowed the selection of nine genotypes with the highest biomass under both water limitation conditions. These superior genotypes will undergo additional testing in multi-environment trials to confirm their performance and use them in the development of cultivars with proven tolerance to limited water supply conditions. Overall, the drought stress indices proved highly effective for classifying and characterizing the performance of the genotypes.

A33

EMERGENCE RATE OF MAIZE (*Zea mays*) UNDER DIFFERENT IRRIGATION AND PLANTING DEPTH CONDITIONS

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The aim of this work was to evaluate the effect of water availability and sowing depth on the early development of maize (Zea mays L.) seedlings. The study compared the growth from sowing till V2 in height of maize seedlings sown at two depths (3 cm and 6 cm) and under two irrigation regimes (with initial irrigation (I1) and irrigation at 7 days (I7), irrigated to field capacity). The substrate used was a homogenized layer from 0 to 20cm of sandy-loam soil. Measurements were taken at two specific times, day seven and day nine after sowing from the soil up to the tip of the largest leaf. The results of the study show that irrigation has a positive and significant impact on the growth of maize seedlings, regardless of planting depth. Seedlings that received irrigation showed greater average growth compared to seedlings that were not irrigated till I7, both at 3 cm and 6 cm depth. Specifically, seedlings sown at 3 cm depth and with irrigation showed the highest average growth on both measurement days (14,39cm in day 7 and 23,22cm in day 9 for 3cm depth. 13,29cm in day 7 and 22,20 in day 9 for 6cm depth). This suggests that a shallower planting depth, combined with adequate water availability, promotes faster seedling development. In contrast, seedlings sown at 6 cm depth showed lower average growth, especially those that did not receive initial irrigation. This finding indicates that a greater planting depth can hinder seedling growth, particularly in conditions of water scarcity. In addition to average growth, the variability in growth within each group was analyzed, measured by the standard deviation. The variability tended to be greater on day 9 measurements, suggesting that the differences in growth between seedlings become more pronounced over time. Seedlings without initial irrigation and sown at 6 cm showed the highest standard deviation on day 9, indicating greater dispersion in growth within this group. The data are normally distributed and homoscedastic. The statistical analysis (ANOVA) revealed that there are significant differences ($p>0.05$) in growth between days 7 and 9 for all combinations of depth and irrigation. With a mean height in day 7 of 14,39 cm I1 and 7,23cm I7 at 3cm dept, 13,29cm I1 and 5,43cm I7 at 6cm dept. Day 9 23,22cm I1 and 22,20cm I7 at 3cm dept, 14,53cm I1 and 13,91cm I7 at 6cm dept. This confirms that time has a significant effect on seedling growth, and that this effect is consistent across all conditions evaluated. In terms of growth rate, it was found that this was slightly higher for seedlings with irrigation, especially at 6 cm depth. Although total growth was lower without irrigation, the growth rate was relatively high, suggesting that although they grow less, they do so at a constant rate. In conclusion, the importance of irrigation as a crucial factor for the growth of maize seedlings is highlighted. While planting depth also influences growth, the effect of irrigation is more pronounced.

A34

RESPONSE TO LATE TRANSPLANTATION OF TOPINAMBUR SEEDLINGS *Helianthus tuberosus L*

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The Jerusalem artichoke, *Helianthus tuberosus L.*, is used as a commercial product in different areas such as horticulture, in industry for obtaining inulin with great nutritional benefits, or even as fodder. In the latter case, its tubers, which are the best-known organs of this species, or the aerial part, are consumed. Topinambur tubers are sown in spring and after approximately 15 weeks the plants begin to form their reserve organs. In autumn, senescence begins and nutrients are translocated to the reserve organs. For some time now, trials have been conducted to characterize the crop and its productive response in the semi-arid region, although there is little information on this species in San Luis. The objective of this study was to evaluate the effect of transplanting on white Jerusalem artichoke seedlings with different vigor levels. They were characterized based on their height and vigor as Category 1 (C1): vigorous plants (50-60 cm), Category 2 (C2): moderately vigorous plants (40 cm), and Category 3 (C3): low-vigor plants (25-35 cm). The design was completely randomized, from the selection of C1-C2-C3 seedlings within a plantation on ridges under controlled irrigation in the experimental field of Agricultural Sciences of the FICA-UNSL in Villa Mercedes, San Luis. Planting was carried out on December 5, 2024, in ridges with a distance of 0.70 m between them and a separation of 0.5 m between plants. For each category, 10 seedlings were selected to constitute the replicates (N=30). Three flood irrigations were carried out, and the water supply from rainfall was 400 mm from planting to end of cycle. The results in height development measured in cm for January were for C1: 64.45 ±15.15; C2: 56.00 ±8.11; and C3: 52.83 ±12.86. For February, C1: 117.73 ±26.34; C2: 115.00 ±12.11 and C3: 92.5 ±23.66. For March, the mean heights accompanied by standard deviation were C1: 163.09 ±33.00; C2: 169.5 ±17.49; and C3: 146.67 ±22.58. At the end of the cycle (April), the results were for C1: 172.18 ±32.87; C2: 181.4 ±16.92; and C3: 155.17 ±21.31. Analysis of the data using ANOVA and subsequent Tukey's test ($p<0.05$) showed that for January and February there were differences between categories, with C3 statistically lower than the others. For March and April, there were no significant differences ($p>0.05$), and all plants developed with very good vigor. These data provide information that the initial transplant height did not influence the final crop height under these management conditions, making it necessary to evaluate the other characteristics.

A35

TRITICALE YAVÚ-UNRC: HOW DOES SOWING DENSITY AFFECT REPRODUCTIVE TRAITS?

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Seed availability in forage cultivars is a limiting factor which conditions its use in agricultural establishments. Hybrid cereal crops, such as triticale (x*Triticosecale* Wittmack), are affected by multiple biotic, abiotic and management factors that influence the quantity and quality of the seed produced. The aim of this experiment was to evaluate the effect of sowing density on reproductive traits in triticale. A trial was implemented with 3 densities: 88 kg/ha (equivalent to 210 seeds/m^2), 176 kg/ha (421 seeds/m^2) and 468 kg/ha (1118 seeds/m^2). Ten traits were evaluated in a completely randomized design with 3 replications. The data obtained were analyzed using ANOVA, DGC mean difference test and Pearson correlations. Differences between densities were significant in 8 traits. The number of grains/spikelet (40.3 ± 12.4) and the individual grain weight (39.5 ± 6.7 mg) were not significantly affected. The number of tillers was significantly higher in the high-density treatment (352.4 ± 108.9 tillers/m^2), as was the number of spikes (304.8 ± 82.0 tillers/m^2). The increase in the number of tillers and spikes caused a significant decrease in spike length, the number of spikelets/spike, and the number of grains/spike. The 88 kg/ha density showed the highest values, with significant differences, for the percentage of fertile tillers (99.2%), grain weight/spike (1.9 ± 0.5 g), and yield (458.0 ± 113.3 g/m^2). Yield was significantly correlated with spike and grain traits (r values between 0.42 and 0.84). The results demonstrate that Yavú-UNRC triticale possesses a high capacity to compensate for the decrease or excess of vegetative and reproductive structures by increasing grain weight per spike and the higher percentage of fertile tillers and thereby maintaining an adequate grain yield under each situation.

A36

EXPOSURE TO DIFFERENT CONCENTRATIONS OF ZINC AND CADMIUM INDUCES STRUCTURAL CHANGES IN SOYBEAN ROOTS AND LEAVES

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Heavy metals represent a global concern due to their non-biodegradable nature and accumulation in living organisms, posing ecological and health risks. This issue is mainly driven by the extensive use of fertilizers and wastewater for irrigation. Although numerous studies have explored plant responses to individual metal stressors, the effects of combined metal exposure remain poorly understood.

In this study, we examined how the interaction between cadmium (Cd), a phytotoxic element, and excess zinc (Zn), an essential micronutrient, alters the morpho-anatomy of soybean (*Glycine max* (L.) Merr) roots and leaves. Plants were grown hydroponically in Hoagland nutrient solution for 10 days, followed by no supplementation (C, control) or exposure to 40 µM $CdCl_2$ (Cd), 0.6 or 4.8 mM $ZnCl_2$ (Zn[0.6] and Zn[4.8]), and combined exposure to Cd+Zn[0.6] and Cd+Zn[4.8] for 6 days. Root results showed significant reductions in total diameter and area in Cd, Zn[4.8], and combined metal treatments ($p<0.0001$) compared to C. Root length and dry weight significantly decreased ($p<0.05$, $p<0.01$, and $p<0.001$) in all treatments compared to C. The percentage of water content (PWC) decreased in all treatments, reaching significance in Zn[0.6] and Cd+Zn combinations ($p<0.05$ and $p<0.005$). In leaves, significant reductions were observed in mesophyll thickness ($p<0.0001$) and central vein thickness ($p<0.0001$) across all treatments relative to C. Stem length and leaf area also decreased significantly ($p<0.05$; $p<0.0001$). Leaf dry weight was significantly reduced in Cd, Zn[4.8], and both Cd+Zn combinations ($p<0.0001$; $p<0.005$; $p<0.01$) compared to C. PWC decreased in all treatments, with greater significance in Cd, Zn[4.8], and Cd+Zn[4.8] ($p<0.001$ and $p<0.0001$). These findings indicate that the Cd/Zn duo alters structure and function in both organs, particularly at higher Zn concentrations, likely as a response to combined toxicity. Anatomical changes, such as the reduction of total root area and alteration of mesophyll thickness, support this conclusion. While low Zn doses may enhance Cd tolerance in soybean, high Zn concentrations induce alterations in both root and leaf structure.

A37

LIGHT EFFECT ON *ALOYSIA GRATISSIMA IN VITRO* ORGANOGENESIS

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Aloysia gratissima is a native medicinal aromatic plant valued for its digestive, antispasmodic, and sedative properties. It also plays an important ecological role in the mountain ecosystems of the San Luis province and provides various ecosystem benefits. Given the growing industrial demand and the need for sustainable production, in vitro micropropagation techniques were evaluated as an alternative for large-scale multiplication. The objective of this study was to optimize the micropropagation protocol for A. gratissima by evaluating the effect of different light spectra on organogenesis. Nodal segments of mother plants were used, subjected to two surface disinfection treatments that varied in exposure time to 70% ethanol and 30% sodium hypochlorite. The explants were grown in Murashige and Skoog (MS) medium supplemented with 20 $g\ L^{-1}$ of sucrose and solidified with 0.7% agar, under four light treatments that combined white, red, far-red, UV, and blue spectra. The cultures were maintained at 24 ± 1 °C and a 16-h photoperiod. The treatment with the longest exposure time (3 minutes in the disinfectant agents) was more effective in disinfection, significantly reducing contamination. Light treatments influenced the development of shoots and leaves. The applied light treatments showed an influence on the in vitro development of S. integrifolia. The TI treatment (UV 0.40%; red 0.98%; blue 0.01%; green 0.21%; far-red 1.23%) promoted a complete response (formation of leaves, roots, and callogenesis). In contrast, treatment TII (UV 0.03%; red 34.05%; blue 32.30%; green 25.16%; far-red 1.23%) showed low incidence of callus formation and poor root development. Treatments TIII and TIV, which had a higher proportion of red light (35.47% and 40.26%, respectively), showed minimal callus and root formation. Specific plant responses to light spectrum can sometimes be predictable based on published research; however, the overall plant reaction is difficult to predict due to the complicated interplay of many different internal responses, brought about by the action of different photoreceptors, which influence primary (production of amino acids, nucleotides, sugars, and lipids) and secondary (terpenes, phenols, and alkaloids) metabolism. The effect of the different spectra analyzed allows achieving morphogenesis in A. gratissima without the addition of growth regulators, constituting a biotechnological tool for future germplasm propagation and conservation programs.

A38

PRODUCTION DYNAMIC OF *Thynopirum ponticum* PASTURE IN THE CENTER OF SAN LUIS AND ITS RELATION WITH SURFACE AND SUBSURFACE WATER AVAILABILITY

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Among the winter perennial species adapted to semi-arid regions, on areas with water fluctuations and salinity, *Thynopirum ponticum* (agropiro alargado) is a forage resource of special interest. To understand the factors regulating its production in these environments, the objective was to determinate the dynamics of its aboveground production during one cycle and compare it with the potential water availability (surface and subsurface) during the same period. The study was conducted in the lowest topographically sector of the FICA experimental field (Villa Mercedes, San Luis), in the "El Morro" watershed. This area features a variable water table (from 3 m to the surface) and signs of salinity. During one growth cycle, the productivity of six plots of 1 m^2 with fixed defoliation frequencies every 30 days was characterized, recording aerial cover (%), height (cm), forage accumulation ($kgDM.ha^{-1}$), and phenological status. Potential water availability was described by recording daily/monthly rainfall and the variation in the water table depth recorded with a phreatometer. The information was integrated through visual comparison of forage accumulation curves and water variation. The pasture maintained excellent aerial cover -75% in winter, to over 90% the rest of the year-. Distal height and monthly accumulation were significantly different ($p<0.01$) across dates according to the season, with greater lengths in spring. The distribution of forage production was markedly seasonal: very low monthly accumulation (< 100 $kgDM.ha^{-1}$) in winter and 70% concentration in spring. The total cumulative production for the cycle was 1840 $kgDM.ha^{-1}$ ± 370 $kgDM.ha^{-1}$. The total annual precipitation was 471 mm, distributed over 55 days with precipitation. Of the total recorded, only 19 mm occurred during the winter period, representing 4% of the total. Approximately ~240 days elapsed (mid-March to mid-November) with scarce rainfall (<20 mm) and, consequently, low atmospheric water supply. Spring, meanwhile, accounted for 41.6% of the annual rainfall. The rainfall records followed the pattern described in updated literature for the area. The depth of the water table remained relatively stable, between 279 and 300 cm. Although a slight rise was observed toward May, unrelated to precipitation, the water table continued to decline with the onset of spring rains, reflecting no significant atmospheric recharge. *Thinopyrum ponticum* exhibited marked spring growth, which coincided with the occurrence of major precipitation, suggesting a strong dependence on surface water. Under the conditions of this study, no significant contribution from the water table to aerial productivity was observed. The possibility of controlled harvesting in the fall would be associated with limiting factors other than water availability. It is suggested that water availability should be analyzed at the watershed level, not locally, for a complete understanding of the dynamics.

A39

PHENOLOGICAL AND STRUCTURAL RESPONSE OF *Digitaria eriantha* TO CHANGES IN SOIL WATER AND NITROGEN AVAILABILITY

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The use of implanted perennial pastures increases the productivity of livestock systems. In the semi-arid region of San Luis, water deficit and soil nitrogen content are relevant factors affecting the growth of plant species. *Digitaria eriantha* Steud is a summer-cycle perennial used in the region as a forage resource. It also forms voluminous clumps up to 100 cm tall, considering its flowering stems. During December, it rapidly accumulates biomass, coinciding with reproductive phenological stages, and at the same time, displays a highly variable number of flowering stems for different scenarios. The study was carried out at the Faculty of Agricultural Engineering and Sciences (UNSL), using 30-liter pots for the plants. Two study factors were analyzed: irrigation and applied nitrogen level. Two irrigation levels were established: frequent irrigation (FRI) and occasional irrigation (OIR). For the second factor, a control level (0 kg N/ha) and a nitrogen subsidy were proposed, seeking potential pasture productivity (equivalent to 200 kg N/ha). A completely randomized split-plot factorial experimental design was used with 5 replications, two study factors, and two levels for each factor. Phenology, stem number, and radiation interception were recorded once a week during the trial period. At the end of the cycle, a cut was made to determine aboveground biomass accumulation (ABA). The onset and duration of phenological stages in thermal time (ºC.d) for the different treatments, as well as the efficiency of use of intercepted photosynthetically active radiation (EURFAi), were calculated. Significant effects on crop phenology were found, mainly associated with the levels of nitrogen applied to the soil. Elongation began at the same time for all treatments, while inflorescence emergence was earlier for those that received fertilization ($p<0.05$), and the flowering-anthesis stage lasted longer in these treatments ($p<0.05$). A high variation was found for the number of floral stems per plant. Likewise, a significant difference was determined in favor of the fertilized treatments, which generated a greater number of stems and a greater accumulation of aerial biomass ($p<0.05$). No significant effects were detected for the irrigation factor. Furthermore, the fertilized treatments were statistically superior in their use of radiation (EURFAi). There was a difference of 0.34 g DM per MJ of PAR captured by the plant, in favor of N200. These results show that high nitrogen inputs to the soil stimulated the production of the lignified fraction of the plant, advanced phenological stages, increased production, and improved radiation use.

BIOTECHNOLOGY AND GENETICS

A40

GREEN SYNTHESIS OF SILVER NANOPARTICLES USING GRAPE STEM EXTRACT AND EVALUATION OF THEIR ANTIFUNGAL ACTIVITY

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The study of biological systems in nanoparticle synthesis is essential for the development of environmentally friendly production methods. The use of microorganisms and plant extracts in the biosynthesis of silver nanoparticles (AgNPs) is currently proposed. Plant extracts containing polyphenols can reduce Ag+ ions in aqueous solution to AgNPs, acting as reducing and stabilizing agents. These nanoparticles can be used as antimicrobial agents and to control phytopathogens, among other applications. In this work, AgNPs were biosynthesized from a grape stem extract as a source of polyphenols and an $AgNO_3$ solution. The extract was obtained from 10 g of grape stem and 40 mL of water-ethanol (70:30, v/v), at room temperature, for 48 hours in the dark; the total polyphenol content was 1.59 mg gallic acid/mL (Folin-Ciocalteu method). To 10 mL of 10 mM $AgNO_3$ solution was added 0.25 mL of grape stem extract, the temperature was adjusted to 40°C and pH=10, with stirring. The formation of AgNPs was verified by the appearance of an absorption maximum at 409 nm, corresponding to the surface plasmon resonance. Transmission electron microscopy revealed spherical nanoparticles with an average diameter of 11.7 ± 3.75 nm. A preliminary antifungal assay demonstrated that the synthesized AgNPs inhibit the growth of *Aspergillus niger* in a microplate test containing 500 µL of PDA medium, 30 µL of spore suspension of the microorganism ($6.5x10^4$ spores/mL) and 2.5, 5, 10, 20 µL of AgNPs. The grape stem is a solid residue generated by the wine industry that is discarded or scattered in vineyards. This residue has potential application on an industrial scale in the green synthesis of AgNPs using the methodology developed in this work.

HUMAN CLINICS AND ODONTOLOGY

A41

PULMONARY FUNGAL INFECTIONS: THREE DIFFERENT CLINICAL PRESENTATIONS

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Pulmonary fungal infections are uncommon but severe diseases with high morbidity and mortality, predominantly affecting immunocompromised patients. *Aspergillus* species are the main etiological agents of invasive fungal infections (IFI), presenting with variable clinical and radiological features that frequently mimic bacterial infections.

We describe three cases of pulmonary IFI diagnosed within the past year, each caused by different sections of the genus *Aspergillus*. All patients were male and immunosuppressed. Case 1 had severe COPD on oral corticosteroids, while Cases 2 and 3 were oncology patients with stage IV solid tumors under chemotherapy. Fever was present in all cases; dyspnea occurred only in Case 1. Radiological findings included nodular lesions, cavitations, alveolar consolidation, and necrotic abscess formation. Microbiological studies revealed *Aspergillus* section *terrei* (Case 1), section *fumigati* (Case 2), and section *flavi* (Case 3). Serum and mini-BAL galactomannan assays were positive in Cases 1 and 3. Antifungal therapy was initiated; however, Cases 1 and 3 died due to pulmonary coinfection and probable nosocomial bacterial infection, respectively. Case 2 remains under antifungal treatment and follow-up. Pulmonary fungal infections act as opportunistic diseases, with increasing incidence in immunocompromised populations. Clinical and radiological overlap with bacterial infections often delays diagnosis. Antigen detection and fungal cell wall biomarkers enable earlier initiation of antifungal therapy, reducing mortality and improving outcomes. Pulmonary fungal infections (PFI) are rare but life-threatening conditions, particularly in immunocompromised patients. The genus *Aspergillus* is the leading cause of invasive fungal infections (IFI), which are associated with high morbidity and mortality rates. Clinical manifestations are often nonspecific, while radiological findings can mimic bacterial pneumonia, delaying appropriate diagnosis and treatment. This case series aims to contribute to the understanding of PFI by presenting three different clinical scenarios with distinct *Aspergillus* species as etiological agents.

A42

CHAGAS DISEASE: PREVALENCE OF *Trypanosoma cruzi* INFECTION IN PATIENTS FROM QUINES HOSPITAL, SAN LUIS (2024–2025)

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The World Health Organization estimates that Chagas disease affects over 7 million people globally, the majority of whom reside in Latin America. In Argentina, it is estimated that around 2 million individuals are infected; however, these figures are highly uncertain due to significant underreporting and underdiagnosis, particularly in socially vulnerable areas. Chagas disease is a parasitic zoonosis that poses a public health threat and progresses through two clinical phases: acute and chronic. The acute phase typically presents with mild, non-specific symptoms such as fever, fatigue, hepatosplenomegaly, and skin nodules. The chronic phase may persist for years and is mainly characterized by asymptomatic (indeterminate) forms or symptomatic cardiac, digestive, or mixed manifestations. Certain clinical outcomes, particularly chronic Chagasic cardiomyopathy, appear to be associated with patient age and disease duration. An observational, retrospective, and descriptive study was conducted using 478 serological samples processed at Quines Hospital, located in the northwest region of San Luis Province, between January 2024 and August 2025. Serological diagnosis was performed using enzyme immunoassay (EIA) and indirect hemagglutination (HAI). In cases of discordant results, a third confirmatory test (indirect immunofluorescence, IFI) was applied. Among the analyzed samples, 37 tested positives by at least two diagnostic methods, resulting in an overall prevalence of 7.74%. Most positive cases (78.38%, N=29 out of 185 samples analyzed) were detected in 2025, largely due to a screening campaign targeting individuals receiving disability pensions who attended the hospital in February–March. Analysis of HAI titers showed that 45.9% of positive patients presented with high titers (>256), indicating a robust immune response suggestive of chronic persistent infection or higher exposure intensity. Notably, the presence of elevated titers in most patients coincides with a predominance of cases among older adults (83.8% over 40 years of age), likely infected decades ago, before the effective control of vectorial transmission (San Luis has been free of vectorial transmission since 2014). Another key finding is that, although women comprised the majority of the sample (70.27%), men exhibited nearly twice the positivity rate (56.75%, N=21 in women and 43.24%, N=16 in men). This disparity may be related to reduced access to routine medical screenings among men, who may be less likely to seek medical care due to asymptomatic presentation. The higher proportion of women tested is attributed to the inclusion of prenatal screening, consistent with vertical transmission prevention programs. Based on these findings, Chagas disease persists with a significant prevalence among older adults and males, underscoring the need to strengthen screening strategies in vulnerable populations.

A43

PREVALENCE OF TOXOPLASMOSIS IN PREGNANT WOMEN IN THE NORTHERN REGION OF SAN LUIS PROVINCE, 2023–2025

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Toxoplasmosis is a parasitic disease caused by the protozoan *Toxoplasma gondii*. Primary infection in immunocompetent individuals is usually asymptomatic; however, in recently infected pregnant women, it represents a major concern, as vertical transmission may cause severe fetal damage, particularly when it occurs during the first trimester of gestation. In this context, serological screening and continuous monitoring throughout pregnancy are essential to determine prior immunity or susceptibility to infection. Early identification of seronegative women enables the implementation of preventive measures, while timely diagnosis of acute cases allows for antiparasitic treatment that significantly reduces both vertical transmission and congenital sequelae. This study analysed data from the clinical laboratory of a public hospital in the city of Quines, San Luis, Argentina, during the period from January 2023 to August 2025. A total of 408 serum samples from 368 pregnant women undergoing prenatal care across all trimesters were processed. Among the 304 women with complete data, most were young adults. The majority (66%) of the patients were in the 20–29 age range (97 patients aged 20–24 and 104 aged 25–29), while adolescents under 20 represented the smallest group (27 cases, 9%). Pregnant women aged 30–34 accounted for 57 cases (19%), and those aged 35 or older made up only 19 cases. The sequential diagnostic algorithm recommended by the Argentine Consensus on Congenital Toxoplasmosis was applied, using ELISA and ELFA serological assays to detect anti-Toxoplasma antibodies. All women were tested for IgG at their first prenatal visit. IgG antibodies were detected in 29 women (7.07%); among them, 18 (62.07%) had no previous serological records, which prompted additional IgM testing to exclude recent or active infection. No IgM-positive cases were identified, and therefore, IgG avidity testing was not required. In contrast, 346 women (94.02%) remained seronegative, underscoring the high proportion of susceptible pregnant women and highlighting the critical need for preventive public health strategies. In conclusion, this study emphasizes the importance of sustaining and strengthening serological screening and preventive education during pregnancy. The diagnostic algorithm proved effective in optimizing laboratory resources without compromising diagnostic accuracy, particularly when supported by reliable clinical records. The absence of acute infections during the study period is encouraging and suggests that, with appropriate preventive measures, both pregnant women and their unborn children can be effectively protected against toxoplasmosis.

A44

RELATIONSHIP BETWEEN AGE, STRESS, AND MEMORY PERFORMANCE IN OLDER ADULTS

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Age-related cognitive decline can be influenced by psychosocial factors such as stress, as well as by immunological and metabolic changes. Understanding these interactions is important for the early detection of cognitive impairment. Objective: To examine the associations among age, perceived stress (PS), memory, and clinical biomarkers (cortisol, glucose, leukocytes, albumin, and others) in a sample of older adults. Method: A descriptive-correlational study was conducted with 29 older adults (mean age = 68.7 years, SD = 6.3). Immediate recall tasks were administered in both forward and backward orders. Perceived stress levels were recorded, and plasma cortisol, blood glucose, albumin, globulin, albumin/globulin ratio, total leukocytes, erythrocytes, and neutrophils were measured. Descriptive analyses, one-sample t-tests, and Pearson correlations ($p < 0.05$) were performed. Data normality was assessed using the Shapiro–Wilk test. Results: Strong negative correlations were observed between age and performance on forward ($r = -0.76$, $p < 0.001$) and backwards ($r = -0.70$, $p < 0.01$) memory tasks. Perceived stress was also inversely associated with both memory measures ($r = -0.56$, $p < 0.05$). No significant correlations were found between cortisol levels and memory performance. The albumin-to-globulin ratio showed a mean value of 1.58 (SD = 0.28). Conclusions: These findings suggest that both age and perceived stress negatively affect immediate memory performance in older adults, whereas cortisol does not show significant associations. The results underscore the need for multidimensional approaches to assessing cognitive ageing.

A45
COMPARATIVE ANALYSIS OF FRACTURES IN THE ARTICULAR CAVITY OF THE HUMAN CRANIAL BASE RELATED TO THE TEMPOROMANDIBULAR JOINT

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The temporomandibular joint (TMJ) represents a complex functional unit that links osseous, muscular, ligamentous, and neurovascular structures. Its location at the base of the skull and its proximity to otological regions make it a highly clinically sensitive area. In particular, the articular cavity of the temporal bone presents relevant anatomical fissures: tympanosquamous, petrotympanic, and petro-occipital. These fissures allow the passage of structures such as the chorda tympani nerve, the anterior tympanic artery, and ligaments that connect the articular disc with the middle ear. The study aimed to compare the length of these fissures between the right and left cavities and establish their frequency of occurrence in dry human skulls. 100 human bone specimens from the osteolibraries of the Faculties of Medical Sciences and Dentistry of the National University of La Plata were analysed. Whole skulls and separate bases with preserved midcranial regions were included. Latero-medial measurements of the fissures were made using a vernier calliper, and direct observations were made with a 3x LED magnifying glass. The presence of each fissure was recorded in 50 skulls. Tympanosquamous fissure was evident in 100% of cases. Petrotympanic and petrosquamous fissures were visualized in 44% of the cavities, both right and left. In terms of length, 64% of the skulls were smaller on the right side, 29% were larger, and 7% had bilateral symmetry. The results show significant anatomical variability in the joint cavity of the TMJ. The presence of neurovascular structures in these fissures reinforces their clinical importance in the diagnosis and treatment of cranio-mandibular pathologies. It is proposed to incorporate these findings into multidisciplinary therapeutic approaches that consider the relationship between joint anatomy and otological symptoms.

A46
HOSPITAL WASTE MANAGEMENT AT THE DR. RAMÓN CARRILLO CENTRAL HOSPITAL, SAN LUIS

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This study addresses the comprehensive management of hospital waste at the Dr. Ramón Carrillo Central Hospital in the province of San Luis, Argentina, with the aim of understanding, describing, and evaluating the current state of waste management in its different areas. Inadequate management of this waste poses a significant risk to public health and the environment, making its study a key tool for strengthening environmental health and institutional sustainability policies. A descriptive study with a qualitative and quantitative approach was conducted in the form of a case study. The survey was conducted between August and December 2024 through direct observation, review of documentation provided by the hospital's infrastructure and planning department, and the use of visit forms in all areas (inpatient wards, operating rooms, laboratory, pharmacy, maintenance, among others). Data was collected on volumes generated, types of waste, and segregation practices, comparing them with current national, provincial, and municipal legislation. The results show that the hospital has a formal waste management system, with classification at source, safe internal transport, use of color codes (red for pathological waste, transparent for solid urban waste), and recording by means of removal manifests. Compliance with legal requirements for treatment and final disposal by authorized companies was verified, ensuring traceability and environmental control. A high proportion of bio pathogenic waste (35%) was observed, exceeding the WHO reference (15%), suggesting deficiencies in segregation at source and the need to strengthen training for operational staff. There is no hospital wastewater treatment system, which represents an opportunity for improvement in comprehensive environmental management. It is concluded that the Dr. Ramón Carrillo Central Hospital has an organizational structure and regulatory compliance in the province, requiring the implementation of on-site treatment technologies and the optimization of segregation processes. This study provides a situational diagnosis that can serve as a reference for other health establishments in San Luis and the country, promoting responsible management of hospital waste.

A47
PHYTOCHEMICALS FROM *Tessaria absinthioides* DECOCTION SELECTIVELY TARGET LUMINAL BREAST CANCER CELLS THROUGH S-PHASE ARREST

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Tessaria absinthioides (Hook. & Arn.) DC., known as "pájaro bobo", is a native plant from northern and central Argentina, traditionally used in folk medicine as a hypocholesterolemic, hypoglycemic, anti-inflammatory and digestive agent. We have demonstrated the cytotoxicity of its aqueous decoction (DETa) against different cancer cell lines, as well as its antioxidant and anti-atherogenic properties, and its antitumoral activity in colorectal cancer and melanoma. More recently, we analyzed systematically its chemical composition by chromatography and quantified twenty-two compounds, with tessaric acid, rosmarinic acid, naringin, caftaric acid, quercetin-3-glucoside and chlorogenic acid being the most abundant in the four harvests studied. In this study, we evaluated the cytotoxicity of DETa against luminal breast cancer cells, focusing on proliferation, viability, and cell cycle progression. DETa was prepared by boiling 50 g of dry powdered leaves in 1 L of distilled water for 10 min. Breast adenocarcinoma MCF7 cell line was used along with non-tumorigenic MCF10A breast cells as a control, and both were treated for a duration equivalent to one and two cell doubling times (DT). DETa cytotoxicity was assessed in both cell lines using the MTT assay in a dose-response manner. Effects on cell proliferation and viability were further determined on MCF7 cells by trypan blue exclusion. Finally, the impact of DETa on MCF7 cell cycle

progression was evaluated by propidium iodide staining and flow cytometry. DETa showed higher cytotoxicity against MCF7 cells with IC_{50} values of 1375 ± 473 and 1273 ± 219 μg/mL at 1DT and 2DT, compared with 3119 ± 533 and 2159 ± 83 μg/mL for MCF10A cells. At 1DT, MCF7 proliferation was reduced at concentrations ≥ 440 μg/mL (69.9-19.5% vs control) while viability decreased only at the highest dose (3520 μg/mL, 42.5%). At 2 DT, proliferation inhibition was similar, but viability was more markedly reduced, starting at 880 μg/mL (71.9-29.1%). Finally, cell cycle analysis revealed that DETa induced cell accumulation in S-phase at 440, 880 and 1760 μg/mL (48.5, 61.9%, and 48.85% respectively) compared with untreated cells (37.7%). Our findings show that DETa selectively targets luminal breast cancer cells by reducing proliferation and viability, with S-phase arrest as the key mechanism of action. This effect may be related to phytochemicals such as rosmarinic acid, quercetin-3-glucoside and chlorogenic acid, some of the most abundant in DETa and previously reported to induce S-phase arrest in cancer cells. These results highlight the potential of *T. absinthioides* aqueous decoction as a promising candidate for oncology applications.

A48

PREVALENCE OF MUSCULOSKELETAL DISORDERS AND RISK FACTORS AMONG DENTISTS IN THE CITY OF SAN LUIS

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Dental professionals have a high incidence of musculoskeletal disorders (MSDs) mainly related to ergonomic factors, which cause mild symptoms to work disability. Objective: To determine the prevalence of musculoskeletal disorders and risk factors in dental professionals from 25 to 65 years old in the city of San Luis, Argentina, during September 2024. Methodology: Quantitative, observational, descriptive, cross-sectional study. The population selected by intentional sampling was 68 professionals who were in service in the city of San Luis, Argentina, during September 2024. A digital questionnaire was used to assess sociodemographic aspects, risk factors, and MSDs in different body regions. Results: 94.1% of the population presented MSDs; 80.9% were female, and the average age was 41.7 years. Prevalent were those with more than 20 years of seniority at work (35.3%), a daily work schedule of between 5 and 8 hours (52.9%), with 6 to 10 patients (48.5%). The most frequently used working postures were sitting (48.5%) and sitting and standing (44.1%). 48.5% did not take active breaks, and 80.9% were physically active. 95.3% presented MSDs in more than one body region, and the most affected regions were the neck (85.9%), cervical area (70.3%), lumbar region (53.1%), and shoulders (51.6%). The main symptom was pain (46.3%), followed by discomfort (33.7%). In the last 12 months, the most prevalent pathologies were neck pain (61.9%), low back pain (31.7%), and back pain and carpal tunnel syndrome (15.9%), with treatments opting for either physical therapy (35.3%), pharmacological therapy (27.8%), or both (16.3%). The age range of 25 to 35 years presented the highest percentages of MSDs in most body areas, except for the back and hips, which occurred in those over 50 years of age. Having a job seniority of more than 20 years was related to more MSDs in all body regions except the lower limbs, being statistically significant for hip MSDs. Working between 5 and 8 hours a day was associated with more MSDs in all regions except the hip, with a statistically significant relationship between the hip and neck MSDs. Sitting posture and absence of active breaks were associated with higher MSDs. Conclusion: There is a high prevalence of MSDs among dental professionals in the city of San Luis. Ergonomic postures for patient care, seniority, and the number of working hours without taking active breaks are important risk factors.

A49

CORRELATION BETWEEN IODINE NUTRITIONAL STATUS AND THYROID-RELATED PARAMETERS IN WOMEN OF REPRODUCTIVE AGE

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The western side of Argentina, along the Andes, is a region naturally iodine deficient. Its main consequence for human health is the development of hypothyroidism due to dietary iodine deficiency. This is particularly important in women seeking pregnancy, since the insufficient intake of this element alters thyroid metabolism in association with poor reproductive outcomes. The nutritional status in a population is determined by urine iodine concentration (UIC). Low iodine intake alters thyroid metabolism and is inversely correlated with thyroid-stimulating hormone (TSH) and thyroglobulin (TG) concentrations. In turn, antithyroglobulin antibodies (ATG) are inversely correlated with iodine intake; their levels increase in both iodine deficiency and excess. Because of the risk associated with inadequate iodine intake, it is important to monitor iodine intake and iodine nutrition in the population. Previous studies in our laboratory demonstrate that 12% of women of reproductive age in Mendoza have iodine deficiency; however, the relationship between iodine deficiency and thyroid parameters has not been investigated in our population. Therefore, the objective of this study was to determine iodine nutritional status in women of reproductive age in Mendoza using UIC and its correlation with thyroid disease markers, including TSH, TG, and ATG. This study was carried out on a cohort of 117 women aged 18-45 years who, at the time of the study, were not under thyroid hormone treatment and attended the Instituto de Medicina Reproductiva in Mendoza province. Iodine deficiency was identified in 34.5% of patients (UIC < 100 μg/L). Thyroid dysfunction (TSH > 4UI/mL) and thyroid autoimmunity (TAG≥115 IU/mL) were present in 4.68% and 7.5% women, respectively. The correlation between UIC and thyroid parameters showed that TSH was inversely correlated with iodine status (r = -0.2089, 95% CI = -0.3768 to -0.0276, p = 0.024). The determination of UIC was directly correlated with the UIC/creatinine ratio (r=0.5032, 95% CI =0.3367 to 0.6392, p<0.0001). Conversely, UIC was not significantly correlated with TG (r=-0.04262, 95% CI=0.2782 to 0.1978, p=0.7300); as well as with ATG (r=-0.07435, 95% CI =-0.309 to 0.168, p=0.5498). Our study demonstrated that, in our population, women of reproductive age are prone to iodine deficiency, which influences thyroid stimulation that might affect the prevalence of hypothyroidism in our region. Nevertheless, the small sample size in this study did not allow for drawing conclusions about the relationship between iodine nutritional status, thyroid TG synthesis, and thyroid autoimmunity. This indicates that further studies covering a larger population should focus on the consequences of iodine deficiency on thyroid metabolism in our region.

A50

DETECTION OF CHRONIC ASYMPTOMATIC CASES OF *TRYPANOSOMA CRUZI* INFECTION AND CARDIOVASCULAR ASSESSMENT IN UNIVERSITY STUDENTS: MENDOZA, ARGENTINA 2023-2025

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Chagas-Mazza disease (CD) is a triatomine-borne parasitic disease endemic in Latin America. It is estimated that between 6 and 8 million people are infected, and 65 million are at risk of contracting the parasitic disease. Of the total infected people, it is estimated that 9 out of 10 are unaware of their condition, which impedes timely access to treatment. In Mendoza, the estimated prevalence of infection in pregnant people ranges between 2 and 40%. The objective of this study was to describe the seroprevalence and cardiovascular assessment of chronic asymptomatic cases of *Trypanosoma cruzi* infection in university students from the Faculty of Medical Sciences of the National University of Cuyo, Mendoza, Argentina, during the period 2023-2025. Participants were invited to participate through informative talks about the disease, its diagnosis, and project objectives. Participants signed an informed consent form. Blood samples were collected through venous puncture in tubes without additives for serological analysis (indirect hemagglutination and indirect enzyme immunoassay). Those with a positive diagnosis underwent cardiovascular evaluation and antiparasitic treatment, followed by medical follow-up. Of the samples analized, 0.69% were reactive out of a total of 576. A total of six patients with positive serology underwent electrocardiography and Doppler echocardiography. Of these, four were female. The mean age was 25.3 ± 13.3 years. No additional cardiovascular history was reported. Electrocardiograms revealed no significant abnormalities in any of the patients. Echocardiographic assessment of cardiac chambers showed a mean left ventricular end-diastolic diameter of 4.39 ± 0.40 cm and an end-systolic diameter of 2.73 ± 0.48 cm. The mean left ventricular ejection fraction was 65.5 ± 5%. No atrial dilation or significant increase in left ventricular mass was observed. No other significant findings were observed, and no abnormalities compatible with Chagas cardiomyopathy were identified in the studies. The findings of this study highlight a relatively elevated seroprevalence of chronic asymptomatic *Trypanosoma cruzi* infection among first-year healthcare students at FCM–UNCUYO. Despite the low absolute percentage, the presence of reactive cases in a young adult population—composed of individuals from diverse regions of Mendoza province—underscores the silent persistence of Chagas disease in non-endemic urban settings. This reinforces the need for proactive screening strategies and health education campaigns targeting asymptomatic carriers, especially in populations with heterogeneous geographic backgrounds and potential exposure histories.

A51

MORPHOMETRIC CHARACTERIZATION OF *Fasciola hepatica* EGGS OF CATTLE SAMPLES FROM USPALLATA, MENDOZA

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Fasciola hepatica is a foodborne trematode that causes a globally distributed zoonotic disease. Its transmission requires snail vectors belonging to the Lymnaeidae family. The study of this parasitic disease in cattle is particularly relevant, as it not only poses a zoonotic risk but also generates significant economic losses in the livestock industry. The disease reduces both the quality and quantity of meat, impairs growth, decreases calving rates, and results in liver condemnation at slaughter. Uspallata is a mountainous region of Argentina situated at an elevation of more than 1,900 meters above sea level, where extensive livestock farming is practiced. Morphometric analysis plays a key role in diagnosis and enables comparisons with other hosts and biotic regions. The aim of this study was to characterize the morphometry of *F. hepatica* eggs recovered from the feces of cattle from Uspallata, Mendoza, Argentina. Eggs were recovered from cattle feces using the modified sedimentation method of Lumbreras and filtration through a 140µm sieve. Measurements were performed using a calibrated eyepiece, and photographs were analized with the Fiji software of ImageJ®. A total of 169 eggs were measured, yielding the following results: mean length 134.75 µm (±11.46; min 106.36 – max 170.91 µm), mean width 69.42 µm (±6.64; min 53.64 – max 90.91 µm), and roundness index 0.52 ± 0.06. As compared to previous reports (both from South America and from other continents), the mean length we found was slightly larger; the other parameters were similar. These findings are particularly relevant, as egg morphology can vary depending on geographic location, climate, seasonality, and host species. This study contributes valuable data for parasitological diagnostics in high-altitude livestock regions and supports broader epidemiological assessments of fasciolosis under diverse environmental and host-related conditions.

A52

PREVALENCE OF THE *PALB2* PATHOGENIC VARIANT Y551* IN HEREDITARY BREAST AND OVARIAN CANCER PATIENTS FROM MENDOZA, ARGENTINA

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PALB2 (Partner and Localizer of BRCA2) has been recognized as one of the most relevant high-risk predisposing genes for breast cancer (BC) after *BRCA1/2*. PALB2 plays a key role in the homologous recombination repair pathway in response to DNA double-strand breaks. A high frequency of the Y551* variant in BC patients from Argentina has been previously reported, suggesting a possible founder effect. In this study, we describe the molecular and clinical characteristics of *PALB2* pathogenic variants identified in nineteen hereditary breast and ovarian cancer (HBOC) families from Mendoza. All participants received appropriate genetic counselling and fulfilled the criteria for HBOC testing. We detected five different *PALB2* pathogenic variants. The Tyr551* variant was present in 74% (14/19) of cases, the V989* variant in two cases (10.5%), and the R414*, T1042Nfs11, and H762Afs8 variants each in one case. All were unrelated index cases: 17/19 patients (90%) had BC, one (5%) had ovarian cancer, and one was unaffected at the time of testing but had a positive family history. The mean age at BC diagnosis was 45 years (range 35–57), and two patients (12%) had bilateral disease. Among BC cases, 70% (12/17) presented invasive ductal carcinoma, three had *in situ* ductal carcinoma, one had ductolobular carcinoma, and one had mucinous carcinoma. Molecular subtypes included 70% (12/17) luminal, 24% (4/17) triple-negative, and 6% (1/17) triple-positive tumors. Patients were of Western European ancestry, comprising 55% of individuals of Spanish descent, 28% of Italian descent and 17% of both descents. This study contributes to the characterization of the genetic landscape of hereditary breast and ovarian cancer in Mendoza and supports the relevance of considering population-specific *PALB2* variant profiling in Argentina.

A53

TRENDS IN THE PREVALENCE OF GESTATIONAL DIABETES IN A PRIMARY HEALTH CARE CENTER

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Gestational diabetes (GD), a multifaceted metabolic disorder, is defined as any degree of glucose intolerance that manifests or is detected during pregnancy. It is the most common medical complication in pregnancy and is quite often encountered in outpatient care. DG is associated with increased risks of preeclampsia, obstetrical intervention, large-for-gestational-age neonates, shoulder dystocia, birth trauma, and neonatal hypoglycemia. There is no consensus on the most appropriate methodology for screening and diagnosing GD, so its prevalence varies depending on population characteristics and the cutoff points used. The objective of this study was to estimate the annual prevalence of GD in a Primary Care Hospital over 4 years, as well as to evaluate trends. This was a retrospective cohort study, selecting as the target population all pregnant women who attended the Laboratory Service of Hospital J.G Vivas (Juana Koslay-San Luis) between 2021 and 2024. A total of 397 women who had been ordered to perform an oral glucose tolerance test (OGTT) as part of their obstetric care were recruited. Pregnancies diagnosed with pregestational diabetes were excluded, as well as 15 patients who were unable to tolerate the testing protocol, mainly due to nausea/vomiting. Informed consent was obtained from all individual participants included in the study. The recommendations of the Latin American Diabetes Association were followed: fasting plasma glucose between 100 and 125 mg/dL, repeated twice (within the same week); or 2-hour post-stimulus plasma glucose with 75g of anhydrous glucose ≥140 mg/dL (weeks 24-28). In patients with normal OGTT at 24-28 weeks of gestation but with risk factors for GD, the OGTT was repeated at 31–33 weeks of gestation. GD was diagnosed in any of the instances in which the OGTT was altered. Plasmatic blood glucose measurement was performed using an enzymatic method (CM250 WienerLab autoanalyser). The age range was 14 to 44 years ($\bar{x}$=26.9±5.7 years), with 77.1% of pregnant women < 30 years old. The overall prevalence of GD was 15% [95% CI: 11-18%]: 10% in 2021, 12% in 2022, 19% in 2023 and 18% in 2024. GD was diagnosed in the 2nd trimester in 51 women and in the 3rd trimester in 6 women. When patients with GD were stratified by age, it was observed that the prevalence of GD was similar in older compared to younger mothers (15.5% vs 14.7%). Even though the prevalence of GD found constitutes a value that is within the range described in the literature, an upward trend in GD cases can be observed from 2021 to date. Our results can be applied to improve prenatal care programs aimed at the early diagnosis and treatment of GD. We also emphasize the recommendation of performing an OGTT between 6 and 12 weeks postpartum to reclassify women who presented GD.

A54
PROGNOSTIC SIGNIFICANCE OF ATR AND HSPB1 (HSP27) IN PEDIATRIC BRAIN TUMORS: A TRANSCRIPTOMIC ANALYSIS

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Central nervous system (CNS) tumors are the most common solid neoplasms in children and represent the leading cause of solid cancer-related mortality in this age group. Despite advancements in neurosurgery and oncology, the prognosis for most pediatric brain tumors remains poor. There is an urgent need for detailed molecular characterization of these tumors, particularly concerning the biomolecules involved in their progression. The DNA damage response is critical for maintaining genomic stability and is mediated by sensor protein kinases such as ATR. These kinases activate DNA repair pathways or trigger cell death. In addition to ATR, the heat shock protein Hsp27 (HSPB1) has emerged as a promising therapeutic target in oncology. HSPB1 is overexpressed in various tumor types and is associated with poorer prognosis and treatment resistance. However, the prognostic significance of ATR and HSPB1 in pediatric brain tumors has not yet been investigated. In this study, we conducted a transcriptomic analysis of pediatric CNS tumor cohorts to evaluate the association of ATR and HSPB1 gene expression with overall survival (OS), disease-free survival (DFS), and CNS tumor grades and subtypes. RNA-seq and clinical data were obtained from the Clinical Proteomic Tumor Analysis Consortium (CPTAC) and the Children's Brain Tumor Tissue Consortium (CBTTC). The analysis included primary solid tumor samples from 116 patients aged 0-14 years. Univariable Cox regression analysis of continuous RNA expression data revealed that higher ATR expression levels tended to be associated with an increased risk of death (HR= 3.39, P= 0.056), whereas HSPB1 expression showed no significant association with OS. However, elevated levels of ATR and HSPB1 were associated with an increased risk of recurrence or disease progression (HR= 3.34, P= 0.0132 and HR= 1.45, P= 0.0051, respectively). When patients were dichotomized by RNA expression, Kaplan–Meier survival analysis with log-rank testing demonstrated that high ATR expression tended to worse OS (P = 0.0507), while high HSPB1 expression associated with poorer OS (P = 0.022) and with an increased risk of disease recurrence or progression (P= 0.0019). In multivariable analysis adjusted for cancer type, neither ATR nor HSPB1 expression showed independent prognostic significance for DFS. However, after adjusting for tumor grade, high HSPB1 expression remained independently associated with poor DFS (P= 0.00271), whereas ATR was not independent. Our results suggest that ATR and HSPB1 are promising prognostic markers for pediatric brain tumors.

A55
SUSCEPTIBILITY PROFILE OF THE MOST FREQUENT MICROORGANISMS CAUSING UNCOMPLICATED LOWER URINARY TRACT INFECTIONS IN PATIENTS ATTENDING THE PROVINCIAL MATERNITY "DRA. TERESITA BAIGORRIA"

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Antimicrobial resistance (AMR) is a global threat to health and development. By 2050, it is estimated that there will be 1.91 million deaths directly attributable to AMR and 8.22 million deaths associated with AMR worldwide. The regions projected to have the highest AMR-related mortality rates across all age groups are South Asia, Latin America, and the Caribbean. Urgent multisectoral measures are required, as the World Health Organization has declared AMR to be one of the top ten public health threats facing humanity. The misuse and overuse of antimicrobials are the main drivers of the emergence of drug-resistant pathogens. Combined with the limited availability of new drugs, this results in many bacterial infections becoming increasingly difficult to treat. One of the strategies within an appropriate Antimicrobial Stewardship Program would be to restrict the number of antimicrobials reported to the medical team, based on their local susceptibility profile. The aim of this study is to determine the susceptibility profile of the most frequent microorganisms causing Uncomplicated Lower Urinary Tract Infections (ULUTI) and, based on the data obtained, to reach a consensus report—together with the Infectious Diseases Service—restricted to a few drugs to be used in ULUTI treatment. Between January 2023 and August 2024, 3,409 urine samples from patients attending the Provincial Maternity "Dra. Teresita Baigorria" with a diagnosis of ULUTI were analyzed. The most frequent pathogens and their susceptibility profiles were determined. The positivity rate was 12.5%, and the prevalent organisms were *Escherichia coli* 83.8%, *Klebsiella pneumoniae* 4.2%, *Enterococcus faecalis* 2.4%, and *Staphylococcus saprophyticus* 2.1%.The resistance profile in *Escherichia coli* was as follows: Ampicillin 60.2%, Ampicillin/Sulbactam 11.4%, Oral Cephalosporins 10.4%, Third-Generation Cephalosporins 9.3% (due to Extended-Spectrum Beta-Lactamase production), Ciprofloxacin 27.3%, Trimethoprim-Sulfamethoxazole 27.2%, Fosfomycin 1.4%, and Nitrofurantoin 0.6%. In *Klebsiella pneumoniae*: Oral Cephalosporins 11.1%, Third-Generation Cephalosporins 11.1% (due to ESBL production), Ciprofloxacin 11.2%, Trimethoprim-Sulfamethoxazole 11.1%, Nitrofurantoin 33.3%, and Fosfomycin 16.7%. In *Enterococcus faecalis*, resistance to Ciprofloxacin was 50%, and in *Staphylococcus saprophyticus*, Methicillin resistance was 22.2%.Based on these findings, it was decided to restrict the susceptibility report for patients with ULUTI to only three antimicrobials: Oral Cephalosporins, Trimethoprim-Sulfamethoxazole, and Nitrofurantoin, provided that the pathogens involved do not present intrinsic resistance to them.

MICROBIOLOGY AND INMUNOLOGY

A56

DEVELOPING NANOBODIES AGAINST THE PCRV PROTEIN OF *Pseudomonas aeruginosa* AS A NOVEL THERAPEUTIC STRATEGY

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Pseudomonas aeruginosa is a highly adaptable and opportunistic pathogen and one of the leading causes of hospital-acquired infections, particularly in immunocompromised patients, burn victims, and those with chronic lung disease. The global rise of drug-resistant *P. aeruginosa* is a critical public health threat, linked to an estimated ~559,000 deaths annually with mortality rates ranging from 17–62%. Standard therapies often fail due to the pathogen's intrinsic resistance mechanisms, including efflux pumps, biofilm formation, and antibiotic-degrading enzymes. Escalating antibiotic doses is not a viable solution, as it accelerates resistance, increases toxicity, and remains ineffective against highly resistant strains. To address this urgent challenge, we developed nanobodies as a promising alternative therapeutic approach. Owing to their small size, high stability, and strong target specificity, nanobodies can overcome traditional resistance mechanisms. In addition to their therapeutic potential, they can also serve as effective detection tools and exhibit bacteriostatic effects. We identified the PcrV protein as an ideal antigenic target. The PcrV protein was cloned, expressed, and purified before being used to immunize alpacas. After three immunizations, alpaca immune response was induced, and blood samples were collected to isolate white blood cells. mRNA responsible for nanobody synthesis was extracted and processed to construct an immune nanobody library. From this library, five positive clones targeting PcrV were isolated using antigen-sensitized bead technology and identified via ELISA. A lead clone was selected for further study, and subsequent Western blot and ELISAs confirmed that the nanobody specifically recognizes PcrV on both the bacterial surface and in the culture medium. Current work is focused on evaluating its effectiveness in cell culture models using PcrV-GFP expressing cells and in bacterial growth assays, with the ultimate goal of developing a powerful new tool to identify and combat drug-resistant *P. aeruginosa* infections.

A57

ANTIMICROBIAL ACTIVITY OF THYMOL IN COMBINATION WITH ANIONIC AND NONIONIC DETERGENTS AGAINST METHICILLIN-RESISTANT *Staphylococcus aureus*

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important pathogen in hospital and community acquired infections, with high morbidity and mortality. Thymol (2-isopropyl-5-methylphenol) is a phenolic monoterpene with antimicrobial activity, although its low water solubility may limit its efficacy. Anionic and nonionic detergents can improve its bioavailability and enhance its action. This study evaluates the antimicrobial activity of thymol in combination with sodium dodecyl sulfate (SDS), Triton X-100 (TX100), and Tween 20 (T20) against methicillin-resistant *S. aureus* ATCC 43300. The minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) were determined using the microdilution assay in trypticase soy broth (TSB), supplemented with 0.01% (w/v) 2,3,5-triphenyltetrazolium chloride as a visual indicator of bacterial growth. Stock solutions (20,000 µg/mL) of thymol, SDS, TX100, and T20 were prepared individually in sterile distilled water or appropriate solvents, depending on the solubility of each compound. For combination assays, 1:1 (v/v) mixtures were prepared by mixing equal volumes of thymol and each detergent stock solution. Serial twofold dilutions of individual compounds and their combinations were performed to obtain final concentrations ranging from 5000 to 2.44 µg/mL. Each well of a 96-well plate received 100 µL of TSB with the indicator, 100 µL of the compound dilution, and 5 µL of bacterial inoculum (10^6 CFU/mL). Control wells containing only TSB, bacterial inoculum, or test compounds were included. Plates were incubated at 37°C for 24 h under static conditions. MIC was defined as the lowest concentration at which no visible bacterial growth was observed (absence of red coloration). MBC was determined by subculturing from the last three wells without visible growth onto trypticase soy agar (TSA). All experiments were performed in duplicate and repeated at least twice. The fractional inhibitory concentrations (FIC) were calculated to assess potential synergistic activity. The MIC/MBC values (µg/mL) against *S. aureus* ATCC 43300 were as follows: thymol 625/1250, SDS 9.76/2500, TX100 312.5/2500, T20 >5000/>5000. Combinations: thymol-SDS, 4.88/4.88 ($FIC_{thymol\text{-}SDS}$ = 0.007, strong synergy); thymol-TX100, 312.5/625 ($FIC_{timol\text{-}TX100}$ = 0.5, additive effect); thymol-T20, >5000/>5000 (FIC >8, antagonistic effect). Anionic detergents like SDS exhibited strong synergistic effect with thymol against MRSA. In contrast, TX100 showed an additive effect, while T20 led to antagonism. The reduced efficacy of nonionic surfactants may be due to micelle formation, which encapsulates thymol and limits its bioavailability. This effect appears more pronounced with T20, likely due to its higher micellar encapsulation capacity. These findings contribute to the ongoing search for effective alternative treatments against MRSA, a major public health concern. The combination of natural antimicrobials with membrane-active agents may offer promising therapeutic strategies in the fight against multidrug-resistant bacteria.

A58

EVALUATION OF MUTAGENIC POTENTIAL OF *Zinnia peruviana* ROOT EXTRACT USING AMES TEST

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The Ames test is widely used *in vitro* to evaluate the mutagenic potential of chemical compounds, based on the use of *Salmonella typhimurium* TA100 (indicator strain) deficient for the synthesis of the amino acid histidine (His-) and subsequent quantification of the His+ revertants induced by exposure to the substance under study. The auxotrophic (His-) strains of *Salmonella typhimurium* are capable of reversing to His+ and grow in a minimal medium after exposure to a mutagen. The validity of the test is ensured by the use *S. typhimurium* TA100, phenotypically characterized by their dependence on histidine and biotin, the presence of the *rfa* marker, the *uvr*B deletion, and the pKM101 plasmid. The objective of this study was to evaluate the mutagenic potential of *Zinnia peruviana* root extract and analyze its concentration dependence. For this purpose, a minimal glucose medium was prepared, the TA100 strain (10^8 CFU/mL) was inoculated, and paper discs with Z. *peruviana* root extract at various concentrations were placed onto the plates. Sodium azide (0.1 mg/mL) and distilled water were included as positive and negative controls respectively. The plates were incubated at 37°C for 48-72 hours, and the revertant colonies were counted. The results showed that the positive control induced an average of 600 colonies, in contrast to 30 colony forming units developed in the control medium. *Z. peruviana* root extract at 2.5 mg/mL, 1.25 mg/mL, and 0.625 mg/mL had mutagenicity indices (MI) of 2.42, 2.57, and 2.23, respectively. Extreme concentrations (10 mg/mL and 0.1 mg/mL) were also tested. MI values of 2.57 were obtained in both concentrations. With these values, no concentration dependence was observed in the range of 10 mg/mL. These findings demonstrate that although some extracts reached values close to the cutoff point (MI = 2.5), none significantly exceeded it ($p > 0.05$). Therefore, under the conditions of the Ames Test, *Z. peruviana* root extract shows no evidence of mutagenic activity. These findings are very interesting since the concentrations of *Z. peruviana* root extract tested showed very good antimicrobial activity in previous studies.

A59

Yersinia enterocolitica ISOLATED FROM BLOOD AND URINE SAMPLES IN A PATIENT FROM THE CITY OF SAN LUIS

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Yersiniosis is a zoonotic disease caused by *Yersinia enterocolitica*, transmitted to humans primarily through the consumption of contaminated food and water, especially raw or undercooked pork. Another route of transmission is through transfusions of contaminated blood products from healthy donors or those with a clinical history of diarrhea, which causes post-transfusion bacteremia with a high mortality rate. Its virulence is attributed to the presence of a highly conserved virulence plasmid, called pYV (plasmid *Yersinia* virulence) and several chromosomal genes. The predominant symptoms in humans are gastrointestinal: diarrhea, nausea, vomit, fever, and abdominal pain; and extraintestinal: reactive arthritis, myocarditis, glomerulonephritis, among others. In immunosuppressed patients or those with concomitant diseases, this species can disseminate to cause a systemic infection and/or an infection in a specific organ or tissue of the host. The objective of this study was to determine the antibacterial susceptibility of *Y. enterocolitica* strain isolated from blood and urine samples of a man who presented clinical symptoms. A 79-year-old male patient presented to the Central Hospital "Dr. Ramón Carillo", with a four-day history of gastrointestinal symptoms: diarrhea, fever, and vomit. He also had a history of rheumatoid arthritis, with regular use of methotrexate but not corticosteroids. Also reported a cholecystectomy, appendectomy, prostatic hypertrophy and inguinal hernia. He had not traveled recently. He didn't smoke, use alcohol, or use drugs. Based on the analysis of blood and urine samples using Matrix-Assisted Laser Desorption/Ionization Time-of-Flight (Maldi-Tof) mass spectrometry, *Y. entorocolitica* infection was diagnosed. The antibiogram revealed resistance to amoxicillin/clavulanate and cefazolin. Empirical treatment was started with intravenous ceftriaxone for 10 days and then oral ciprofloxacin for three weeks. His clinical evolution was favorable, and he was discharged. Although the clinical evolution is consistent with the common symptoms of the infection, The relevance of this clinical case is established by the fact that *Y. enterocolitica* is not frequently isolated from blood or urine, except in very severe cases such as septicemia or bacteremia. These findings suggest the presence of the bacterial species in our region and alert health authorities to focus on investigating different types of clinical samples and possible transmission routes to prevent its dissemination and provide effective antibiotic treatment.

A60

PRELIMINARY STUDY OF THE EXTRACELLULAR ACTIVITY OF *Yersinia enterocolitica* OUTER PROTEINS ON HUMAN LEUKOCYTES

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There are numerous studies on the intracellular cytotoxic activity of *Yersinia* outer proteins (Yops) from *Yersinia enterocolitica* (Ye) in several models. However, to date, no studies have explored the extracellular properties of Yops on human immune cells. The purpose of this study was to evaluate the extracellular activating and cytotoxic effects of Yops on peripheral blood human phagocytes. Yops were extracted from a wild-type *Y. enterocolitica* strain (Ye wt) and a *yopP* mutant strain (Ye Δ*yopP*). Leukocytes were isolated from the peripheral blood of healthy human donors and incubated for 30 minutes at 37°C in a 5% CO_2 atmosphere with Yops at concentrations of 4, 10, and 20 µg/ml. Three assays were performed to assess functional effects: 1. NBT (Nitroblue Tetrazolium) assay, both microscopically and colorimetrically, to assess respiratory burst; 2. MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay to evaluate cell viability/metabolic activity; 3. DNA laddering assay to detect apoptosis. Microscopic NBT analysis revealed a significant increase in azurophilic granules in samples treated with Ye wt Yops at 4 µg/mL ($p < 0.01$), although this was not confirmed by the colorimetric NBT results. The MTT assay showed a significant increase in metabolic activity in cells treated with 4 µg/mL of Yops from both Ye wt and Ye Δ*yopP* ($p < 0.001$). Furthermore, no apoptotic DNA fragmentation was detected at any tested concentration. Our findings suggest that Yops—especially YopP—may act extracellularly on human phagocytes, enhancing activation without inducing apoptosis; further studies are needed to confirm its relevance and applications.

A61

EXTRACELLULAR EFFECT OF *YERSINIA* OUTER PROTEIN P (YOPP) ON MURINE MACROPHAGE ACTIVATION AND VIABILITY

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This study investigates the extracellular effects of wild-type Yops (Yops wt) and the YopP mutant strain (Ye *ΔyopP*) from *Yersinia enterocolitica* (Ye) on the activation and viability of murine macrophages. Thus, cultures of inflammatory murine peritoneal macrophages (Mi) were incubated for 30 minutes with Yops (1 and 4 ug/ml) at 37°C in a 5% CO_2 atmosphere. NO was measured by Griess assay, ROS by NBT, and apoptosis by Annexin V/PI flow cytometry. In order to compare Mi with resident ones (M), we teasted different concentrations of Yops (0.6ug/ml-20 ug/ml). Exposure of Mi to Yops from Ye wt and Ye *ΔyopP* at 1µg/ml and 4µg/ml induced a significant increase in NO production ($p < 0.01$), surprisingly Ye *ΔyopP* at 1 ug/ml showed less capacity of NO induction than Ye wt ($p < 0.05$). NBT assay revealed that Mi + Yops WT (4µg/ml) condition displayed a significantly higher percentage of positive cells/200 cells (17.5%) compared with control Mi (<5% of positive cells/200 cells) ($p < 0.01$). Yops from Ye wt induced apoptosis in Mi at 4 µg/ml, whereas M required 10 µg/ml ($p < 0.05$ and $p < 0.001$). Unexpectedly, YopP has not induced apoptosis on Mi at 1 µg/ml ($p < 0.05$), highlighting its differential role depending on macrophage activation. These results reveal the complex role of YopP in host-pathogen interactions and warrant further investigation into its underlying mechanisms.

A62

ASSESSMENT OF THE CYTOTOXICITY OF PROTEIN FRACTIONS FROM AQUEOUS EXTRACTS OF LARREA DIVARICATA CAV. FOR FUTURE ANTIVIRAL STUDIES

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The increasing emergence of viral diseases and resistance to antiviral drugs drives the search for new plant-derived therapeutic agents, revaluing biodiversity and ancestral medicinal practices. *Larrea divaricata* Cav. (Zygophyllaceae, "jarilla"), a native species with a long-standing medicinal tradition, contains metabolites with well-documented *in vitro* antiviral activity; however, the potential effect of proteins present in aqueous extracts remains unknown. To establish safe concentrations for future antiviral assays, our objective was to evaluate the *in vitro* cytotoxicity of proteins concentrated from an aqueous extract of *L. divaricata*. Concentrated protein fractions were partially purified by centrifugation using Millipore Amicon Ultra-15 concentrator tubes with a 10 kDa molecular weight cut-off membrane. Both the retentate and permeate fractions were collected. Cytotoxicity parameters were determined in Vero cell lines using the neutral red uptake colorimetric assay. Protein fractions larger than 10 kDa showed low cytotoxicity, with a mean cytotoxic concentration (CC_{50}) of 0.10 ± 0.008 mg/mL, while fractions smaller than 10 kDa exhibited a CC_{50} of 0.021 ± 0.00016 mg/mL, indicating higher cytotoxicity. Protein fractions from *L. divaricata* showed differential cytotoxicity, allowing the definition of safe concentrations for future antiviral evaluations. These results, together with the previously reported *in vitro* activity of other metabolites, reinforce the potential of this species as a source of natural therapeutic candidates.

A63

IMMUNE RESPONSE EVALUATION IN HEN EGGS AGAINST DIFFERENT ANTIGENIC FRACTIONS OF AN AQUEOUS EXTRACT OF *Larrea divaricata* CAV

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Larrea divaricata Cav. (jarilla) contains proteins with immunogenic potential in murine models, capable of inducing antibodies with cross-reactivity against cellular and extracellular proteins of *Pseudomonas aeruginosa* and against those involved in the opsonophagocytic process. Obtaining antibodies in mice is an invasive procedure and provides a low yield from a biotechnological point of view. An alternative model was proposed that met the "3Rs" criteria (reduction, refinement, and replacement): Hy Line Brown laying hens. From their egg yolks, it is possible to purify immunoglobulin Y (IgY). In this work, we evaluated the immunogenicity of the jarilla extract proteins and the cross-reactivity of IgY against outer membrane proteins of *P. aeruginosa* (OMP). Three 6-month-old laying hens from a hatchery were used. They were immunized with two jarilla protein fractions obtained by ultrafiltration with membranes with 10 and 30 kDa cut-offs: JP10 (>10 kDa) and JP30 (>30 kDa), respectively. An immunization protocol was carried out with increasing dose schedules (75 µg and 150 µg) in emulsion with Montanide™ ISA 71 VG adjuvant (1:1), administered intramuscularly, and boosters given every 15 days. Eggs were collected before, during, and after immunization, and anti-jarilla IgY levels were evaluated by ELISA against JP10 or OMP, as sensitizing antigens (Ag). The results showed that both fractions induce specific IgY, with IgY anti-JP30 levels being significantly higher than IgY anti-JP10 ($p \leq 0.05$) for both Ag quantities. When IgY anti-JP10 and IgY anti-JP30 were tested with OMP, high IgY levels were observed. However, there was no significant difference compared to the yolks of non-immunized hens. This would indicate, on one hand, that the presence and relative concentration of the proteins forming the antigenic preparation are important; and on the other hand, the high values of the negative controls might be due to the microbiological conditions prior to the assay. Based on the background of generating anti-jarilla IgG in mice that recognize outer membrane proteins of *P. aeruginosa*, and in order to improve the values in hens, it is proposed to test new protocols with higher Ag doses and longer immunization times. Furthermore, we propose to emphasize the characterization of the antigenic determinants responsible for this cross-reactivity. This will ensure the biotechnological potential for the design of an immunological tool to combat infections caused by *P. aeruginosa*.

A64

PHYSICOCHEMICAL CHARACTERIZATION OF AN EXOPOLYSACCHARIDE PRODUCED BY *Cryptococcus laurentii* FOR POSSIBLE FOOD APPLICATION

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Exopolysaccharides (EPS) are carbohydrate-based biopolymers composed of carbohydrates that are secreted by the microorganisms into the surrounding environment. They have important applications in the food industry, as they can potentially serve as components for biodegradable films. The aim of this study was to determine the physicochemical characteristics of an EPS produced by the yeast *Cryptococcus laurentii* BNM 0525 for potential use in food applications. For EPS production, *Cryptococcus laurentii* BNM 0525, from the Industrial Microbiology Laboratory (UNSL), was grown in Erlenmeyer flasks with culture medium (g/L): glucose: 20; $(NH_4)_2SO_4$: 1.65; KH_2PO_4: 0.86; $MgS0_4.7H_20$: 0.3; NaCl: 0.1; $CaCl_2.2H_20$: 0.01; $MnSO_4$: 0.01; yeast extract: 0.05; pH 5. It was incubated at 25 °C for 72 h at 120 rpm. EPS was recovered from the culture supernatants by adding two volumes of 96 % ethanol at 4 °C for 24 h. The resulting EPS precipitate was dried at 30 °C to obtain a dry powder. The dry EPS powder was physicochemically characterized. 1) Fourier transform infrared spectroscopy (FTIR) was used to identify functional groups, using a Nicolet PROTEGE 460 spectrometer, USA. 2) Thermogravimetric analysis (TGA) to determine the thermal stability of the EPS, using a TG 295 analyzer, USA. 3) Intrinsic viscosity and molecular weight, using a Ubbelohde capillary viscometer (IVA, Argentina). For this purpose, solutions of different concentrations of EPS in distilled water were prepared: 0.01 % to 0.5 % w/v and left to stand at 4 °C for 24 h. This test was performed in triplicate and at 25 °C. The results showed 1) FTIR: a broad band was observed at 3400 cm^{-1} corresponding to hydroxyl groups, a medium band at 2900 cm^{-1} corresponding to methylene groups and an intense and broad band near 1000 cm^{-1} related to C-O bonds also stands out. 2) TGA: thermal stability was 183.7 °C, an effect that may be related to intrachain hydrogen bonds. 3) The intrinsic viscosity values were 362 to 395 cm^3/g (Huggins, Kraemer, Schulze-Blaschke and Martin method) and the molecular weight was 650,000 to 750,000 g/mol (Mark-Houwink equation). In conclusion, FTIR showed functional groups representative of an exopolysaccharide, thermal analysis indicated that the EPS is stable up to 183 °C, presenting good thermal resistance. The intrinsic viscosity values were similar to those of other polysaccharides, such as pectins, and the molecular weight was shown to be sufficiently high. The values obtained from the physicochemical characterization indicated that the EPS is suitable for potential food-related applications such as film molding.

A65

FEASIBILITY STUDY OF A FORMULATION BASED ON *Kosakonia radicincitans* bSL2 FOR USE AS A LIQUID BIOINPUT

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Agroecology promotes the use of beneficial microorganisms in the management of sustainable agricultural and food systems. Sustainable food production is a key component of the "One Health" approach, which emphasizes the interconnection between food production, environmental protection, and the promotion of human health and well-being. The bacterium *Kosakonia radicincitans* bSL2 has characteristics that promote plant growth (PGP), traits making it suitable for application in agroecological cultivation systems. The aim of this study was to evaluate the long-term viability of a liquid formulation based on *K. radicincitans* bSL2 for use as a bioinput. The strain *K. radicincitans* bSL2, from the culture collection of the Industrial Microbiology Laboratory (UNSL), was grown in a minimal medium containing 35 g/L of dehydrated bagasse and 5 g/L dehydrated yeast (by-products of beer production) and incubated at 28 °C for 48 h. Biomass was obtained by centrifugation, washed, and resuspended in sterile distilled water to a concentration of 6×10^8 CFU/mL (R_0), and stored at 4 °C for the 12 months of the study. Viability of the formulation was quantified after 3 months (R_1) and 12 months (R_2) by plate count on solid medium. The bioinput was tested in germination assays using *Lactuca sativa L*. White Boston. Seeds were placed in duplicate in plastic germination trays containing a basic solid substrate. Each well received 1 mL applied by spraying of either (a) the *K. radicincitans* bSL2-based formulation or (b) sterile distilled water (control). The germination percentage (%) was determined after 7 days. The germination assay was repeated after 12 months of bioinput storage. The viability of the formulation after 3 months (R_1) was 4.5×10^7 CFU/mL, and after 12 months (R_2) it was 3.6×10^7 CFU/mL. The germination percentage for treatment (a) was 10% higher than for (b) ($p \leq 0.05$). After 12 months, the germination percentage for treatment (a) remained 6% higher than the control (b) ($p \leq 0.05$). The native bacterial strain *K. radicincitans* bSL2 maintained its viability for at least 12 months and preserved its stimulatory effect on seed germination. The simple water-based formulation, produced using a minimal medium derived from brewery by-products, shows potential for application in agroecological systems.

A66

EVALUATION OF SOIL CHEMICAL PARAMETERS AFTER A BIOAUGMENTATION AND BIOSTIMULATION PROCESS IN A LANDFARMING SYSTEM IN THE CITY OF SAN LUIS

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Bioremediation is an effective tool for mitigating environmental pollution through the use of native microorganisms capable of degrading or transforming toxic compounds into substances that are less harmful to the environment. At the laboratory scale, three general strategies can be applied: (a) natural attenuation, (b) landfarming, and (c) landfarming assisted by bioaugmentation. The aim of this study was to evaluate the effectiveness of bioaugmentation and biostimulation techniques applied to a landfarming system by analyzing soil chemical indicators at the laboratory scale. Three treatments were carried out: bioaugmentation with strains previously isolated from the landfarming system, biostimulation with a culture medium, and a control with water only. Samples were taken at the beginning (T0) and after 30 (T1), 60 (T2), and 90 days (T3). Sulfates, phosphates, nitrogen, and organic matter were determined as soil quality indicators using the EPA 9038, NOM-021-RECNAT-2000-AS10, Kjeldahl-Arnold-Gunning, NOM-021-RECNAT-2000, and AS-07 methods, respectively. In addition, the concentrations of glycols (ethylene glycol, propylene glycol, and diethylene glycol) were analyzed using gas chromatography in samples T0 and T3, since these compounds represent the main contaminants in the treated effluent. Statistical analysis (ANOVA) showed no significant differences among treatments in terms of soil chemical parameters. However, a lower residual glycol concentration was observed in the bioaugmentation treatment compared to biostimulation and control. This suggests that both strategies enhanced glycol degradation without significantly altering soil quality parameters. In conclusion, the microorganisms present in the landfarming soil demonstrated the ability to degrade effluent glycols without significantly affecting the soil's chemical properties, with bioaugmentation proving to be the most effective strategy. These results indicate that, in the long term and in the absence of new effluent inputs, effective site bioremediation could be achieved.

A67

AEROBIOLOGICAL EVALUATION OF INDOOR AND OUTDOOR AIR IN A UNIVERSITY LABORATORY: POLLEN AND FUNGAL SPORE DIVERSITY

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The study of aerobiological particles is highly relevant to human health and environmental quality. Aerobiological monitoring allows the evaluation of different types of pollen grains and fungal spores, which are associated with allergic respiratory diseases. The aim of this study was to evaluate biological air quality in a microbiology laboratory at the National University of San Luis. Two Hirst-Lanzoni volumetric collectors were used: one installed on the laboratory terrace and the other inside the room where samples were processed. The analysis was performed during the months of August and September. Incoming aerobiological particles were collected on a Melinex-type strip coated with liquid silicone. After 7 days, the samples were cut, placed on slides, and stained with basic glycerofuscin for subsequent visualization and quantification with an optical microscope at 400X. *Cladosporium* and *Ustilago* spores were found primarily in the indoor atmosphere at representative levels of 12.42 and 8.64 m^3 of air, respectively. Additionally, *Aspergillus* and *Penicillium* spores were found in smaller amounts. These fungi are cultivated for certain tests in the laboratory, indicating their presence in the work environment. Different types of pollen grains were found in the outdoor environment. Cupresaceae was the most abundant species in the outdoor atmosphere of San Luis during August (52 pollen grains per m^3 of air), while Moraceae was the most abundant during September (102 pollen grains per m^3 of air), both considered moderate to high amounts. Positive associations between the indoor and outdoor atmosphere were observed for *Cladosporium* spores ($r = 0.64$; $P = 0.0013$) and *Ustilago* spores ($r = 0.70$; $P = 0.0036$). These fungal species are commonly associated with ocular and nasal infections. *Ustilago* spores can infect various plants, causing significant economic losses. *Aspergillus* and *Penicillium*, meanwhile, can cause allergic reactions such as asthma, rhinitis, and conjunctivitis. Pollen grains produce certain respiratory allergic pathologies, with harmful effects on human health. This study highlights the importance of monitoring both outdoor and indoor air quality to prevent allergic diseases and promote environmental health. Future research would include implementing indoor air purification strategies to evaluate their effectiveness in reducing allergenic and pathogenic bioaerosols, as well as extending these aerobiological studies to hospitals, schools, and other workplaces.

A68

OPTIMIZATION, CHARACTERIZATION AND ANALYTICAL EVALUATION OF THE ACTIVITY OF *Origanum vulgare* (OREGANO) EXTRACTS AGAINST *Escherichia coli* O157:H7

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Food safety is a crucial issue for both consumers and food industries. Food products can suffer from undesirable microbial contamination that alters their properties. Additionally, some microorganisms can cause foodborne illnesses. Shiga toxin-producing *Escherichia coli* (STEC) is known to cause hemorrhagic colitis (HC) and hemolytic uremic syndrome (HUS). It is primarily considered an emerging pathogen transmitted through contaminated bovine food. The O157:H7 serotype is the most frequent strain that is involved in HUS. *Origanum vulgare* (oregano) is an aromatic plant used as a food seasoning and as an infusion in folk medicine for the treatment of gastrointestinal disorders and for its antimicrobial properties. The aim of this study was to optimize the extraction process of oregano leaf extracts to enhance its antimicrobial activity against STEC; followed by analysis of their chromatographic and spectrometric profiles in order to find the characteristics patterns (chemical compounds). Four different aqueous oregano extracts, infusion (EOI), decoction (EOD), agitation (EOA), and ultrasound (EOU) were prepared and tested against STEC. The lowest MIC and MBC values were obtained for EOA (20 µg/mL and 80 µg/mL, respectively). The effect of a sub-inhibitory concentration (MIC/2) on planktonic culture was also evaluated. A significant decrease in the count of treated viable cells compared to the untreated STEC cultures was observed. Different morphologies in the treated (coccoid forms and short bacilli) and untreated (long bacilli) cultures were visualized by light microscopy. In this study, the production of an aqueous extract of oregano with antimicrobial effect against STEC was optimized and chemically characterized. Our results may contribute to develop a new strategy to control HUS and to implement an effective food preservative method against strains of STEC.

A69

DETECTION OF LESS PREVALENT *BLACTX-M* GENES IN ESBL-PRODUCING ISOLATES FROM HOSPITAL CENTRAL DE MENDOZA (2019 VS 2022)

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Multidrug-resistant gram-negative bacteria, frequently isolated in nosocomial infections, represent a major global public health concern. The treatment of these infections often involves β-lactam antibiotics. However, the production of β-lactamases, enzymes capable of degrading the β-lactam ring, constitutes a common resistance mechanism that limits the effectiveness of these antimicrobials. Among these mechanisms, extended-spectrum β-lactamases (ESBLs) are particularly relevant, as they confer resistance to penicillins, third- and fourth-generation cephalosporins, and monobactams. The most extensively studied ESBL families include *blaTEM*, *blaSHV*, and *blaCTX-M*, the latter being the most widely disseminated over recent decades. In collaboration with Hospital Central de Mendoza (Argentina), a total of 156 ESBL-producing isolates were analyzed, collected consecutively over two periods: 2019–2020 and 2021–2022 (78 per period). Prevalence studies of the most common ESBL genes (*blaSHV*, *blaTEM*, *blaCTX-M-1*, and *blaCTX-M-2*) revealed high frequencies of *blaSHV*, *blaTEM*, and *blaCTX-M-1* in both periods, along with a marked increase in *blaSHV* and *blaCTX-M-2* prevalence in the second period. Additionally, an upward trend in the accumulation of multiple resistance genes per strain was observed. This study expands upon previous analyses by focusing on the detection of less common *blaCTX-M* genes in Argentina: *blaCTX-M-8*, *blaCTX-M-9*, and *blaCTX-M-25*, using conventional PCR. *blaCTX-M-8* was detected in 4 out of 78 isolates from 2019–2020 and in 2 out of 78 from 2021–2022. *blaCTX-M-9* was identified in 20 and 11 isolates in the first and second periods, respectively. *blaCTX-M-25* was detected in only one isolate from the second period. Sequencing of *blaCTX-M-9*-like amplicons revealed 99% identity with the CTX-M-27 variant, which harbors the Asp240Gly (D240G) mutation, associated with a significant increase in the minimum inhibitory concentration (MIC) of ceftazidime in *Escherichia coli*. These findings underscore the need for ongoing molecular surveillance to enable early detection of emerging variants and support the development of effective therapeutic strategies.

A70

CONSERVATION OF *Serratia* sp. BASED FORMULATIONS FOR POSSIBLE APPLICATION AS BIOFERTILIZER

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Microorganisms isolated from soil can be used as biofertilizers, a key strategy for maintaining agricultural productivity without compromising ecosystem health. The objective of this work was to study the conservation of *Serratia* sp.-based formulations with biofertilizer characteristics for application as a bioinput. The ChM90c bacterium was isolated from vine soils from a farm located in Valle de Uco, Mendoza, during the veraison period (March 2023). Biofertilizer assays (nitrogen fixation, phosphate solubilization, indoleacetic acid and siderophores production) were determined. It was molecularly characterized by DNA barcoding, based on the amplification and sequencing of the 16S rRNA gene (~1500 bp) from pure cultures, using primers 27F and 1492R. Liquid and solid formulations were prepared with a standardized suspension of the bacteria in different conservation media: A) Sterile Physiological Solution, B) Medium 1, C) Glycerol 20%, D) Lactose 10%, E)Alternative Medium, F)Vermiculite, G) Peat and H) Lyophilization. The liquids were stored at 4 and 25ºC, while the solids at 25ºC, for 90 days. Viable cell counts (Log CFU/mL) were performed at t=0, 30, and 90 days; the % reduction in viability was determined as [(Log CFU/mL t=0 - Log CFU/mL t=30 or 90)/(Log CFU/mL t=0)] x100; and the % survival rate was determined as [100 - % reduction in viability]. Statistical analysis was used using the paired t-test using a $p=0.05$ and $n=3$. The results of the BLAST and MAPSeq analysis assigned the strain to the genus *Serratia* with high identity and total coverage. The survival of liquid formulations was favored at 4°C: A (92.81% and 81.17%), B (87.33% and 78.44%), C (80.83% and 76.11%), D (87.62% and 70.24%), E (77.43% and 42.24) at 30 days and 90 days respectively, while at 25ºC the values decreased. Regarding solid formulations, a reduction of less than 40% was observed after 30 days. It was concluded that *Serratia* could be preserved over time (90 days), with liquid formulations at low temperatures showing the greatest survival, while solid formulations did not. The influence of storage time and temperature on the formulations will continue to be studied.

A71

EVALUATION OF BACTERIAL STRAINS ISOLATED FROM RHIZOSPHERIC SOIL: GROWTH ON ALTERNATIVE MEDIA AND MOLECULAR IDENTIFICATION VIA DNA BARCODING

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Plant growth-promoting bacteria (PGPB) represent a sustainable biotechnological alternative to the intensive use of agrochemicals in modern agricultural systems. For their growth and production, the use of industrial by-products as alternative substrates offers an innovative and ecological approach that also fosters a circular economy by integrating waste into productive processes. The objective of this study was to evaluate the growth of bacterial strains with biofertilizer potential in alternative culture media formulated from corn grain cutter wash water, and to perform their identification through molecular DNA barcoding of the 16S rRNA gene. Three bacterial strains (ChM90c, ChM114c, and ChM120y), isolated from rhizospheric soil and exhibiting PGPB traits, were selected from the stock collection of the Industrial Microbiology Laboratory. Growth was assessed in conventional YGM (Yeast Glucose Medium) and two alternative media formulated with corn cutter wash water: RI (Industrial Residue) and RI+YL (Industrial Residue supplemented with yeast extract). Biomass was quantified by dry weight (g/L) and statistically analyzed by ANOVA followed by post-hoc tests. The selected strains were identified through amplification and sequencing of the 16S rRNA gene. The obtained sequences were analyzed using the NCBI and SILVA databases for taxonomic assignment. Strain ChM90c exhibited comparable biomass values between YGM (1.57 ± 0.03 g/L) and RI (1.52 ± 0.29 g/L), with an increase in RI+YL (2.15 ± 0.28 g/L), although without statistically significant differences ($p = 0.2313$). Strain ChM114c achieved the highest biomass production in RI (4.50 ± 0.11 g/L), significantly surpassing YGM (0.99 ± 0.06 g/L) and RI+YL (2.23 ± 0.44 g/L) ($p < 0.001$). In contrast, ChM120y yielded lower biomass in RI (0.55 ± 0.08 g/L) compared to YGM (1.49 ± 0.14 g/L) and RI+YL (2.13 ± 0.06 g/L), with significant differences among all treatments. Molecular analysis identified strains ChM90c and ChM114c as belonging to the genus *Serratia*, which is recognized for its plant growth-promotion and biocontrol properties. Corn grain cutter wash water constitutes a viable and economical substrate for bacterial biomass production, particularly for strains of the genus *Serratia.* These results demonstrate the potential of these microorganisms for the development of sustainable biofertilizers.

A72

EVALUATION OF OXAZINES AS A POTENTIAL TREATMENT FOR GRAM NEGATIVE BACTERIA

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Antimicrobial resistance (AMR) is an important global health problem that demands urgent solutions. Infectious diseases remain one of the leading causes of death worldwide, with substantial implications for public health and the global economy. In 2017, the World Health Organization (WHO) issued a global alert identifying 12 bacteria in urgent need of new treatments. The alert was repeated in 2024, including almost the same bacteria. Two of the Gram-negative bacteria present in the alert were *Neisseria gonorrhoeae* and *Salmonella* spp. This study focused on the identification of molecules with biological activity over Gram-negative bacteria, using as model *N. gonorrhoeae, Salmonella enterica* and *Escherichia coli*. We analyzed the ability of oxazines to inhibit their growth or to act as adjuvants to existing antibiotics. Initially, synthetic organic molecules (sulfur-containing, oxygenated, sulfurized, and halogenated) were evaluated through in silico structural analysis using programs such as PubChem and ACD. Structural similarities and differences between the compounds were analyzed according to several parameters. These observations were subsequently validated through in vitro assays in bacterial cultures. Antimicrobial activity was determined using microdiffusion assays, in which disks soaked in solutions of the compounds were incubated in inoculated media, observing the formation of halos of bacterial growth inhibition. The results indicated that four molecules WpD, WpF, Wp55, and Wp56 (a monocyclic, two tricyclic and one tetracyclic member of the oxazines family) showed antimicrobial activity against *S. enterica* Heidelberg. In the second phase, the adjuvant effect of the molecules was evaluated in combination with antibiotics. Following the same protocol but adding the minimum bactericidal concentration (MBC) of the antibiotic, it was observed that ten molecules with a variety of compositions (3 bicyclic, 3 tricyclic, one tetracyclic and 3 modified bicyclic with chlorine, fluorine or ether functions), namely WpB, WpD, WpE, WpF, Wp3, Wp8, Wp55, Wp56, WpG40, and T10 exhibited adjuvant activity in *S. enterica* Heidelberg. Regarding N. *gonorrhoeae*, only the molecules H07 and H08, both bicyclic, showed adjuvant activity in strains L and F. These results highlight the potential of adjuvant-active molecules to enhance gonorrhea therapy efficacy while minimizing antibiotic use and the subsequent risk of resistance development.

A73

CR3- VS CD206-MEDIATED ENTRY OF *Bordetella pertussis* DETERMINES MACROPHAGE TRAFFICKING AND SURVIVAL OUTCOMES

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During microbial infections, macrophages (MØ) display remarkable plasticity, transitioning between classically activated (M1) and alternatively activated (M2) phenotypes according to environmental cues. Our group has previously shown that *Bordetella pertussis* modulates macrophage polarization to favor intracellular persistence. The aim of this study was to evaluate the specific contribution of complement receptor 3 (CR3; CD11b/CD18) and the mannose receptor (CD206) to the adhesion, internalization, and intracellular trafficking of *Bordetella pertussis* in human monocyte-derived M0 macrophages in a non-polarized state. We also compared these processes with M2 macrophages to identify receptor-specific differences. In M0 macrophages under non-blocking conditions, 15 ± 2 bact/cell were associated, with ~50% internalized. Blocking CR3 significantly reduced adhesion to 6 ± 2 bact/cell ($p<0.01$) and phagocytosis to 25% ($p<0.01$), while CD206 blockade decreased adhesion to 4.5 ± 2 bact/cell ($p<0.01$) and internalization to 23% ($p<0.01$). Dual blockade nearly abolished adhesion (1 ± 0.2 bact/cell, $p<0.01$) and markedly reduced uptake ($p<0.01$). In M2 macrophages, higher basal interaction was observed (28 ± 3 bact/cell adhered, 80% internalized). Blocking CR3 significantly reduced adhesion to 18 ± 2 bact/cell ($p<0.01$) and internalization to 50% ($p<0.01$), whereas CD206 blockade decreased adhesion to 15 ± 2 bact/cell ($p<0.01$) and almost eliminated uptake (2%, $p<0.01$). Combined blockade abrogated both adhesion and phagocytosis (<1%, $p<0.01$). Confocal imaging at 30 min post-infection revealed CR3 and CD206 co-localizing at phagocytic cups, confirming their cooperative role in bacterial capture. In M0, colocalization with the lysosomal marker LAMP-1 showed that CR3-mediated entry resulted in higher lysosomal targeting (~82%) than CD206-mediated entry (~58%, $p<0.01$), indicating receptor-dependent intracellular routing. Together, these results demonstrate that *B. pertussis* exploits CD206-dependent uptake to evade lysosomal degradation, whereas CR3 engagement favours trafficking to bactericidal compartments, revealing a mechanism by which the pathogen modulates macrophage handling to enhance survival.

ECOLOGY, ETOLOGY AND BIODIVERSITY

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COMPOSITION OF PHYTOPLANKTON IN SHALLOW LAKES OF DIFFERENT LOCATION AND SALINITY IN THE PAMPA (ARGENTINA)

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In La Pampa there is a significant number of water bodies with highly variable characteristics. Since the phytoplankton community composition of many of them is unknown, the objective was to characterize and compare the phytoplankton composition of shallow lakes with salinity gradients and different environmental contexts. Samples were collected and limnological parameters were determined throughout an annual cycle in the following lagoons: Chadilauquen (Cha) (35°24'S; 64°19'W), General Campos (GC) (37°28'S; 63°36'W) and Flor de Lis (FL) (37°14'S, 64°01'W), surrounded by agricultural farms; Quetré Huitrú (QH) (37°22'S; 64°34'W), an urban lake in General Acha; Utracán (Ut) (37°17´S 64°36´W), a hypersaline lake in a protected area, and La Sara 1 (LS 1) (36°49´S; 66°00´W), La Sara 2 (LS 2) (36°49´S; 66°00´W), San Eduardo Chañar (SE C) (36° 52´S; 65° 44´W), San Eduardo La Espuma (SE E) (36° 45´S; 65° 41´W), in a dune landscape with natural vegetation. Environmental parameters varied over a wide range. The minimum salinity was recorded in QH (0.24 g/l) and the maximum in Ut (212.95 g/l). Transparency ranged from 0.03 to 1 m in FL and LS 1 respectively, relative to the chlorophyll-a measured there (4.58 and 6538.9 mg.m-3). Total richness was 183 taxa, 48 from the class Cyanophyceae, 53 Chlorophyceae, 31 Bacillariophyceae, 17 Euglenophyceae, and 34 taxa from other accompanying classes, including a dinoflagellate genus that was only recorded in summer in GC. The highest algal richness was recorded in QH (93 taxa), SE E (65 taxa), and LS 2 (62 taxa). Salinity influenced specific richness since the lowest number of species was recorded in Ut (9), Cha (29), and GC (32). Clustering analysis (Gower similarity index) using environmental data and algal richness by taxonomic class revealed two large groups, the first comprising only Ut due to its low richness and high salinity. The second group included the remaining lagoons and was subdivided primarily by environmental variables (especially chlorophyll-a concentration and salinity) rather than by differences in phytoplankton composition. Phytoplankton composition was more closely associated with salinity gradient and productivity than with the type of environment (agricultural, urban, or natural), with no consistent pattern of anthropogenic impact evident. Given these results, further research is needed to obtain more conclusive findings.

A75

LIMNOLOGICAL AND BIOTA CHARACTERIZATION OF A SHALLOW LAKE

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There are numerous shallow lakes in La Pampa province. Some have been partially studied, so aspects of their chemistry, trophic status, and biota are known, but the results have been presented separately, and the information is scattered. The objective is to present environmental and biological information on a semi-permanent lagoon at the San Fernando settlement (Utracán Department, 37°7'3.022"S, 64°22'13.233"W). Limnological parameters were determined, and water, phytoplankton, zooplankton, benthos, and bird samples were taken during the winter season in June and July 2025. pH and conductivity ranged between 8.8 and 17.6 mS/cm in June and 7.9 and 19.4 mS/cm in July, respectively. Water transparency was high, so the lagoon bottom was visible on both sampling occasions. The total phycological richness was 36 taxa, represented by diatoms (16), green algae (13), and cyanobacteria (7). Of the total, only 15 taxa were recorded in July 2025. In June 2025, potentially toxic cyanobacteria of the genus Microcystis were found. Five species were recorded in the zooplankton: a rotifer, a cladoceran, and three copepods. The specific association is typical of saline lakes in central Argentina, characterized by Daphnia menucoensis and Boeckella poopoensis. Both species predominated in both months, when the former represented 7% and 32% and the latter 71% and 53% of the total density. The high-water transparency may be due to the grazing of D. menucoensis on the phytoplankton, a situation already recorded in some lagoons in the region. The diversity of the ostracofauna present in the water body was represented in June by two species, Cypridopsis vidua and Limnocythere cusminskyae, and four species in the July sample: C. vidua and L. cusminskyae, Amphicypris argentinensis, and Heterocypris similis. In the June sample, C. vidua was very abundant, with the presence of adults and juveniles; in the July sample, however, it was the least developed species. The density in June was 2,000 ind./100 g of sediment, and in July, despite an increase in richness, the density decreased to 666 ind./100 g of sediment. Changes in the diversity and richness present would be closely related to changes in pH and salinity. The avifauna was represented in June and July by the families Anatidae, Phoenicopteridae, Rallidae, Charadriidae, and Recurvirostridae, and in July, representatives of the families Podicipedidae and Scolopacidae were also observed.

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INDIGENOUS YEAST DIVERSITY IN PARAJE HILARIO (CALINGASTA, SAN JUAN) DURING TWO CLIMATICALLY CONTRASTING VINTAGES

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Indigenous yeasts present on the grape surface represent a valuable enological resource, as they participate in the onset of fermentation and contribute to the expression of *terroir* typicity. Environmental factors, such as the climatic conditions of each harvest, can significantly alter the composition and diversity of these microbial communities. Paraje Hilario (Calingasta, San Juan) was recently recognized with a Geographical Indication (INV Resolution 37/2023), which further strengthens its value as a reservoir of agricultural and microbiological biodiversity. The objective of this work was to compare the diversity of yeasts isolated from grapes harvested in two contrasting vintages: 2022 (Max. T 34°C and Min. T 19°C, Precipitation: 1 mm, Cloudiness: 10%) and 2024 (Max. T 28°C, Min. T 22°C, Precipitation: 28 mm, Cloudiness: 88%). Sampling was carried out in February; yeasts were isolated on WLN medium and identified at the genus and species levels by sequencing ITS/26S regions. Diversity was assessed based on the number of genera recovered and the Shannon and Simpson indices. Comparisons between years were performed using alpha and beta diversity analyses. In the 2022 vintage, eight genera were identified, while only three were detected in 2024. Shannon and Simpson values were higher in 2022, indicating a richer and more heterogeneous community. From an ecological perspective, the dry conditions of 2022 favored the coexistence of a greater number of species, including minority genera such as *Cryptococcus*, *Starmerella*, and *Zygoascus*, which contributed to a more balanced and equitable community. In contrast, the rainfall in 2024 promoted the dominance of competitive fermentative genera such as *Hanseniaspora* and *Saccharomyces*, reducing total diversity and displacing less abundant species. The compositional analysis revealed marked differences between the two vintages, suggesting a direct effect of climatic conditions on the epiphytic microbiota of grapes. These results demonstrate that interannual climatic variability significantly impacts the diversity of indigenous yeasts in Paraje Hilario. Moreover, they highlight the need to consider these factors in the selection of indigenous yeasts with enological potential, contributing to the strengthening of the terroir identity of the region.

A77

- CHARACTERIZATION OF PHYTOPLANKTON AND BIRDS IN THE SHALLOW PERI-URBAN LAKE BAJO GIULIANI

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The objective of the present work is to characterize the phytoplankton and birdlife present in a shallow lake with significant anthropogenic influence as a preliminary study for an interdisciplinary project. Bajo Giuliani is a lagoon system located about 10 km south of the city of Santa Rosa, La Pampa. It receives stormwater, surface runoff, and discharge from Don Tomás Lagoon, which is located within the urban area of that city. "In September 2025, a total of 9 phytoplankton samples were collected by manual surface towing, and environmental parameters were recorded in the three basins that make up the system: a large basin (SI) and two much smaller ones (SII and SIII).Transparency ranged from 0.08 to 0.20 m; pH showed little variation between the sites (8.3–8.5); total dissolved solids (gravimetric method) were 6.4 g/L in SI, 118.6 g/L in SII, and 217.55 g/L in SIII. The total phytoplankton richness across the three sampling sites was 41 species, with representatives of green algae (21), diatoms (10), cyanobacteria (8), and euglenophytes (2). SI showed the greatest overall diversity with 39 species. At the same time, richness decreased considerably in SII (5) and SIII (5), which may be associated with the large variation in total dissolved solids present in the water. The avifauna in basin SI was represented by the families Phalacrocoracidae, Ardeidae, Phoenicopteridae, Podicipedidae, Anatidae, and Rallidae. Basin SII by Podicipedidae, and SIII by Phoenicopteridae, Laridae, and Recurvirostridae. It can be observed that in SI and SII piscivorous species are present, which would indicate a more complex system than in SIII. These preliminary results provide the foundation for understanding the system's complexity and inform future interdisciplinary studies.

A78

NEW DISTRIBUTION RECORD FOR *POLYPSECADIUM GILLIESII* FOR THE PROVINCE OF SAN LUIS

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The genus *Polypsecadium* O.E Schulz is a South American genus, represented by six species in Argentina. Two endemic species, *P. arnottianum* and *P. gillesii*, inhabit San Luis, mainly in mountainous areas. Demaio and Chiappella defined these mountains as areas rich in endemic species, given their orography and isolation. In particular, *Polypsecadium gillesii* (Romanczuk) Al-Shehbaz has been cited by several authors for different departments of the province, especially in hilly areas. Boelcke, 1979, cites this species for the department of Pedernera, Burkart, 1940, for Pringles in the Cerros Largos, Cerana, 1995, for Pringles in the Inti Huasi cave, while Hunziker, 1956, cites it for the Junín department in El Rincón, at the summit of the western slope of the Sierra de los Comechingones, and Pastore F., 1913, for the Pedernera department in the Sierra del Morro. The aim was to study the Brassicaceae family in areas of natural and introduced vegetation in sierran environments in the province of San Luis. The study area was delimited in the western foothills of the Sierra de los Comechingones, between the Carrizalito and Papagayos streams, east of Provincial Route Nº 1. Sampling was carried out following transects parallel to the courses of the above- mentioned streams. The specimens collected of the species under study were photographed, identified, described, and documented in the VMA herbarium (number 4327) of the FICA-UNSL and the INTA San Luis VMSL. Two specimens were also deposited in the Herbarium of the Darwinion SI Institute under number 175172. As a result, this species is registered for the Ayacucho department in the locations Villa del Carmen, (32°56'03“S, 64°59'52” W) and Papagayos stream, (32°40'55“S, 64°57'49” W). These records expand the distribution of this species endemic to Argentina in the province of San Luis, taking into account the importance of confirming the presence of endemism in areas affected by various disturbances.

A79

BIRD ASSEMBLAGES IN AQUATIC ECOSYSTEMS OF LA PAMPA PROVINCE (ARGENTINA). RELATIONSHIP WITH LIMNOLOGICAL PARAMETERS

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The aquatic ecosystems of La Pampa differ markedly in their salinity and trophic status. The birds that inhabit them are known, but the structure of their assemblages and abundance have not been related to the physical and chemical characteristics of the water bodies where they are found. The objective was to identify the birds present in shallow lakes with different characteristics and anthropogenic influences in La Pampa province. During the summer and autumn of 2024, samples were taken and aquatic birds were censused in. Quetré Huitrú (QH), Utracán (Ut), Chadilauquén (Cha), General Campos (GC), La Sara 1 (LS1), La Sara 2 (LS2), El Cañadón (ECañ) and El Bellaco (EB) shallow lakes. All are fed by rainfall, surface runoff, and groundwater inputs. Summer water temperatures ranged between 21.8 (Cha) and 26.7 ºC (EBe) and in autumn between 7.3 (LS2) to 19ºC (ECañ). The range of average salinities covered was wide, between 0.28 ± 0.01 g/L (LS1) and 111.25 ± 22.94 g/L (Ut). The mean water transparency ranged between 0.11 ± 0.04 m (Cha) and 1 ± 0.01 m (LS1) and phytoplanktonic chlorophyll-*a* concentration between 5.87 ± 0.18 mg/m^3 (LS1) and 759.5 ± 230.5 mg/m^3 (Cha). The birdlife was represented by the families Podicipedidae, Phalacrocoracidae, Ardeidae, Threskiornithidae, Phoenicopteridae, Anatidae, Rallidae, Recurvirostridae, Charadriidae, and Scolopacidae, and the richness varied between 5 to 17 species depending on the lakes. The largest number of species were recorded in QH (17) and Cha (16), characterized by a very high trophic state (high chlorophyll-*a* concentration and low water transparency) and also by the presence of fish. The most frequent species (in 7 of the 8 lakes) were *Anas georgica* and *Himantopus melanurus,* while *Chroicocephalus cirrocephalus*, *Bartramia longicauda*, *Pluvialis dominica*, *Dendrocygna viduata*, *Plegadis chihi*, *Ardea alba*, *Phalacrocorax olivaceus*, *Podilymbus podiceps, and Podiceps occipitalis* were recorded in a single lake, different according to the species. The most numerous species was *Phoenicopterus chilensis*, represented by 1015 individuals in Ut and 1369 individuals in Cha. The higher density of this species in lakes with such different salinity, transparency, and chlorophyll-*a* may be due to the fact that the food supply provided by zooplankton in both is greater than in the rest of the lakes. In Ut, the total zooplankton density was 228.95 ind/L, dominated by *Artemia persimilis* (a species that can reach 1 cm in length), and in Cha it was 7410 ind/L, dominated by the copepod *Boeckella poopoensis*, one of the species most consumed by these flamingos in South America.

A80

EFFECTS OF GRAZING ON SCORPION ASSEMBLAGES IN AREAS SURROUNDING THE SIERRA DEL GIGANTE, SAN LUIS, ARGENTINA.

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The Sierra del Gigante is part of the Protected Areas System of San Luis Province (Provincial Law IX-0309-2004) and is of great ecological interest due to its location within an ecotone between the Dry Chaco and the *Monte de Llanuras y Mesetas*. One of the main economic activities in the area is goat and cattle ranching, based on the use of natural grasslands as a forage resource. Grazing acts as a disturbance that, by altering soil vegetation cover, impacts epigean arthropod communities. With this background, the present study evaluated scorpion diversity around the Sierra del Gigante and the effect of grazing on it. Two contrasting environments were selected: one with high grazing intensity (ZP) and another with low or no grazing pressure (ZBN). In each environment, three sites approximately 3 km apart were sampled. Each site included 12 pitfall traps arranged along three 100 m linear transects, with four traps per transect. A total of 72 traps were installed and remained active for seven days in December 2018. The collected material was processed in the laboratory and identified at least to the genus level. A total of 21 individuals were recorded. ZBN showed higher abundance and richness (3 species: *Timogenes elegans*, *Brachistosternus ferrugineus*, and *Bothriurus cf. cordubensis*) than ZP (2 species: *T. elegans* and *Brachistosternus* sp). *T. elegans* was the only species shared between both environments, while *B. ferrugineus* and *B. cordubensis* were restricted to ZBN. Alpha diversity was consistently higher in ZBN ($q_0 = 3$; $q_1 = 2.98$; $q_2 = 2.96$) than in ZP ($q_0 = 2$; $q_1 = 1.98$; $q_2 = 1.96$), with non-overlapping confidence intervals, indicating a negative effect of grazing on local scorpion diversity. Beta diversity was high ($\beta_{sor} = 0.60$), mainly due to species turnover ($\beta_{sim} = 0.50$), while the nestedness component was low ($\beta_{sne} = 0.10$). These results indicate that differences between environments are mainly explained by species replacement rather than simple taxon loss. The observed patterns suggest that increased bare soil and the loss of refuges associated with grazing differentially affect scorpion species, altering community structure.

DEVELOPMENTAL AND REPRODUCTIVE BIOLOGY

A81

AMMONIUM TETRATHIOMOLYBDATE INCREASES DNA FRAGMENTATION WITHOUT AFFECTING MMP-MEDIATED INVASIVE CAPACITY IN A MURINE MODEL OF ENDOMETRIOSIS

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Endometriosis (EDT) is a chronic, estrogen-dependent gynecological condition with a high prevalence (affecting roughly 190 million females of reproductive age worldwide) and a significant impact on the quality of life of those affected. It is characterized by the growth of endometrium-like tissue outside the uterine cavity, which exhibits resistance to cell death and a high invasive potential. The search for safer and more effective therapies remains a priority in research. Ammonium tetrathiomolybdate (TM), a copper (Cu) chelator, has been shown to reduce lesion volume and estradiol levels in mice with induced EDT and elevated levels of the metal. Therefore, this study aimed to investigate the effects of TM administration on estrogen receptors (ER)-α and ER-β expression and DNA fragmentation in endometriotic lesions and the activity of metalloproteinases (MMPs) in peritoneal fluid. Sixteen female C57BL/6 mice were divided into two experimental groups: EDT and EDT+TM. EDT was induced by autologous transplantation of uterine tissue into the intestinal mesentery. The EDT+TM group received 0.30 mg/day of TM in the drinking water for two weeks, starting on postoperative day 15. At the end of the treatment, lesions were collected for analysis of ER expression (ELISA) and histological assessment of DNA fragmentation (TUNEL). Peritoneal fluid was also collected to evaluate MMP-2 and MMP-9 activity (zymography). Data were statistically analyzed using Student's *t*-test ($P < 0.05$). Regarding the results, TM administration did not alter ER-α or ER-β expression, but it significantly increased the percentage of cells with DNA fragmentation ($P < 0.001$). Notably, MMP-2 and MMP-9 activity was not affected by the Cu chelator. In conclusion, our results suggest that TM affects endometriotic cell viability without inducing changes in ER-α and ER-β expression or in MMP-mediated invasive capacity. Since previous studies have shown that TM reduces estradiol levels, a key hormone in the progression of EDT, the estrogenic pathway could be attenuated primarily by the reduction of its ligand.

A82

AMMONIUM TETRATHIOMOLYBDATE MODULATES *Tnfr2* AND ER-β EXPRESSION, PROMOTING CELL DEATH IN ENDOMETRIOTIC LESIONS OF TNFR1-DEFICIENT MICE

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Endometriosis (EDT) is a chronic, estrogen-dependent, inflammatory gynecological disease that affects 1 in 10 females of reproductive age. It is characterized by the ectopic growth of endometrial-like tissue, resistant to cell death and hormone-responsive, within an inflammatory environment. The TNF system (TNF-α and its receptors TNFR1 and TNFR2) is known to become progressively unbalanced as the disease worsens, with an increase in TNFR2. There is currently no cure for this complex pathology, and available treatments often have adverse effects. Ammonium tetrathiomolybdate (TM) is a drug being studied in proliferative diseases, which has been shown to normalize estradiol and copper levels in EDT, reduce the volume of endometriotic lesions, and modulate the inflammatory response in mice. Further light shed on the drug's action mechanisms, this study aimed to determine whether TM alters the expression of *Tnfr2* and estrogen receptors, with potential consequences for DNA fragmentation, in endometriotic lesions of TNFR1$^{-/-}$ mice with aggravated disease. Sixteen female C57BL/6 TNFR1$^{-/-}$ mice were divided into two experimental groups: EDT and EDT+TM. EDT was induced by autologous transplantation of uterine tissue into the intestinal mesentery. The EDT+TM group received 0.30 mg/day of TM in their drinking water for two weeks, starting on postoperative day 15. At the end of treatment, lesions were collected for analysis of *Tnfr2* mRNA expression (RT-qPCR), estrogen receptors expression (ER-α and ER-β, ELISA), and histological evaluation of DNA fragmentation (TUNEL). Data were statistically analyzed using the student's *t*-test ($P < 0.05$). The results show that TM decreased *Tnfr2* and ER-β expression ($P < 0.05$) but did not affect ER-α expression compared to untreated animals. Furthermore, TM significantly increased the percentage of cells with DNA fragmentation ($P < 0.001$). In conclusion, in TNFR1$^{-/-}$ mice, TM attenuates the progression of EDT by modulating *Tnfr2* and ER-β expression, thereby impacting signaling pathways associated with proliferation and promoting cell death. This reinforces its potential as a treatment capable of acting even under conditions of imbalance in the TNF system.

A83

IMPACT OF DIETS ENRICHED WITH BEEF FAT ON THE HEIGHT AND MORPHOLOGY OF THE EPIDIDYMIUM EPITHELIUM IN C57BL6J MICE APPLIED FOR A SHORT PERIOD

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C57BL6J mice are a widely used model for the evaluation of fat-enriched diets. The objective of this work was to evaluate whether two percentages of beef fat have different effects on the epididymal epithelium of 12-week-old male C57BL6J mice. The mice were randomly divided into 3 groups and fed for 16 weeks with: balanced feed (C; n=2), feed enriched with 7,5% wt/wt beef fat (mB; n=2) and 24% wt/wt beef fat (B; n=2). The initial region, the caput, and the cauda of the epididymis were analyzed. Ten round tubules were selected from each of these regions, and the epithelial heights were measured at four different points within each tubule. Regarding the height of the epididymis epithelium, it was observed that in the initial region, the epithelial height of group C was greater than that of groups mB ($p<0.01$) and B ($p<0.05$), and it was also observed that the height of group mB was lower than that of group B ($p<0.01$). In the caput, the epithelial height of group C was greater than that of groups mB and B ($p<0.01$). No differences were observed between groups in the cauda. These preliminary results were analyzed using the Kruskal-Wallis test and Dunn's post hoc test. Regarding the morphology of the epididymis, it was observed that in the caput region, the presence of vacuoles in the apical zone of the epithelium of group mB and the presence of central and apical microvacuoles in the epithelium of group B were observed. These vacuoles were not observed in the epithelium of group C. In the initial region and cauda, no morphological differences were observed between the groups. Both the decrease in epithelial height and the morphological changes seem to indicate that diets enriched with bovine fat are affecting the initial region less and the head of the epididymis more. They would have no impact on the cauda epididymis.

A84

HUMAN SPERM ASSESSMENT USING COMPUTER VISION AND ARTIFICIAL INTELLIGENCE

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Research and innovation in health-related technologies are producing continuous improvements in human healthcare worldwide. Image-based diagnosis and prognosis are giving rise to novel applications and methods for image interpretation. Like many other areas of human activity, in the last decades, medicine has seen a constant increase in the amount of data generated during clinical routine. Infertility is a global health issue affecting millions of people of reproductive age worldwide. Available data suggest that between 48 million couples and 186 million individuals have infertility globally. Infertility may occur due to male factors, female factors, a combination of male and female factors, or may be unexplained. Semen analysis is considered the main diagnostic source of information in the evaluation of male reproductive capacity. The nature of the spermatozoa (their vitality, motility and morphology) and the composition of seminal fluid are also important for sperm function. This analysis is routinely performed using images taken with optical microscopy devices on carefully prepared samples. Particularly, morphological analysis refers to the sperm head shape and size. Nevertheless, this analysis may involve classification errors related to subjectivity, sampling variability, the operator's training and experience, or differences among multiple operators. New methods and systems are needed to standardize, automate, and accelerate the sperm classification process. In this context, we present a framework to classify sperm heads as normal, tapered, pyriform, and amorphous using shape, intensity and texture features based on machine learning techniques. The framework extracts descriptive features to characterize the sperm head condition. Subsequently, a Random Forest classifier is trained and tested to classify each sperm head into the proposed categories. The model is trained and tested using a public dataset, the Human Sperm Head Morphology (HuSHeM), where the sperm samples were manually labeled by consensus among three specialists. The classification model achieves a 91% of accuracy in the discrimination of normal, tapered, pyriform, and amorphous spermatozoa. The use of machine learning has a good predictive performance in the classification of sperm head normality or abnormality.

A85

ESTROGENIC REGULATION OF LYSOSOMAL PROTEIN TRANSPORT IN RCE-1 EPIDIDYMAL CELLS

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The mammalian epididymis is essential for sperm maturation and acquisition of motility, processes that are closely dependent on hormonal regulation. Although morphological and biochemical alterations of the organ are primarily associated with androgen depletion, the mechanisms of estrogenic regulation are not well characterized. In various species, several lysosomal proteins such as cathepsin D (CatD) and prosaposin (PSAP) are acquired by spermatozoa during their transit through the epididymis, acting as modulators of sperm maturation and male fertility. However, the mechanisms of secretion of these proteins and their hormonal regulation remain largely unexplored. Since the CatD gene contains an Estrogen Response Element, it is suggested that estrogen could regulate its expression and secretion, as observed in other cellular models; similarly, PSAP is also sensitive to estrogenic regulation. The intracellular transport of CatD and PSAP could occur through complementary pathways mediated by mannose-6-phosphate receptors (MPRs: CD-MPR and CI-MPR) and sortilin (Sort). CatD binds to MPRs but can also be transported by Sort when forming complexes with PSAP. Similarly, PSAP can interact with both MPRs and Sort, facilitating its trafficking to lysosomes or secretion into the extracellular medium. Previous studies from our laboratory showed that castration, as a model of androgen depletion, increases CD-MPR expression and epididymal secretion of CatD, highlighting the hormonal influence on this lysosomal trafficking system. To investigate estrogenic regulation, RCE-1 epididymal cell cultures were treated with 20 nM 17β-estradiol, with or without 2 µM tamoxifen (Tx, an estrogen receptor antagonist), for 24 and 48 h, including untreated controls. CatD, PSAP, CD-MPR, and Sort were evaluated by immunoblot and immunofluorescence. Estradiol exposure increased Sort expression and decreased CD-MPR, effects that were reversed by Tx. An apparent increase in PSAP and CatD was also observed, reversible by Tx. Immunofluorescence revealed high colocalization between PSAP and CatD in all treatments, suggesting a possible functional interaction. These results indicate that estradiol could modulate lysosomal protein transport and secretion in epididymal cells, underscoring its relevance in sperm maturation.

A86

SECRETIONS OF MACROPHAGES MODIFY THE PROGESTERONE RESPONSE OF LUTEAL CELLS FROM RAT POLYCYSTIC OVARY. EFFECT OF DEXAMETHASONE

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Polycystic ovary syndrome (PCOS) is characterized by varying degrees of ovulatory dysfunction, luteal phase deficiency, and infertility. Pathophysiology is multifactorial and includes immune system dysregulation, where elevated androgens trigger pro-inflammatory responses. The beneficial effect of corticosteroid treatment in patients with ovulatory dysfunction was reported, although the mechanism underlying its beneficial effects is not precisely understood. We have previously shown that secretion from spleen macrophages (SMϕ) treated with dexamethasone (DEX) can modulate *in vitro* androstenedione release from whole rat polycystic ovary (PCO). Our aim was to study the effect of splenic macrophage-conditioned medium on progesterone (P) release by PCO rat luteal cells. PCO condition was induced by injecting 60-day-old Holtzman rats with a single 2 mg estradiol valerate. After 2 months, the rats were sacrificed. The MΦ ($1x10^6$ cells) from PCO and no-PCO (control) rats were cultured for 24 h in RPMI medium in the absence or presence of 10^{-6}M DEX. Afterwards, the medium was removed, MΦ were washed twice, and finally, the cells were cultured for an additional 24h period. The respective culture media (MΦ secretions) were collected and used to stimulate luteal cells (500,000 cells/mL) from PCO and control rats for 4 hours at 37°C, 5% CO_2. In the luteal cell supernatant, the release of P was measured by electrochemiluminescence (Cobas e411), and nitric oxide (NO, as nitrites) was quantified using the Griess reaction. The mRNA expression of tumor necrosis factor-alpha (TNF-α) and 3β-hydroxysteroid dehydrogenase (3β-HSD, enzymes of P synthesis) was assessed in MΦ and luteal cells, respectively, by RT-PCR. PCO luteal cells released more P and less NO after stimulation with secretions of PCO MΦ+DEX, compared with PCO MΦ secretions ($p<0.05$). The mRNA expression of 3β-HSD in PCO luteal cells incubated with secretions from PCO MΦ+DEX was higher than that obtained with PCO MΦ secretions ($p<0.05$). In PCO MΦ, the TNF-α release and expression were higher than in control and PCO MΦ+DEX ($p<0.01$ and 0.05, respectively). These results suggest that in a high TNF-α environment, DEX can mediate immunomodulatory effects that improve P secretion from rat PCO luteal cells. Therefore, the luteal P level may be enhanced in PCOS by decreasing TNF-α content with DEX. A better understanding of the factors affecting P production in PCOS would aid in the development of more effective therapeutic strategies for the syndrome.

A87

CORTISOL AND CORTISONE MODULATE ROS, ACROSOME REACTION, AND MOTILITY IN BOAR SPERMATOZOA

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The assessment of stress markers in pigs, particularly cortisol and cortisone, represents a key tool to understand how neuroendocrine stress responses affect spermatogenesis, seminal plasma composition, and consequently, semen quality and fertilizing potential. Determination of these glucocorticoids in biological matrices such as plasma and semen doses provides a significant advantage over traditional measurements in serum, saliva, or hair, as it more directly reflects the physiological and local environment of spermatozoa, offering a more precise indicator of stress impact on reproductive function. The aim of this study was to identify stress biomarkers in porcine plasma and semen doses and to evaluate their impact on sperm physiology. Cortisol and cortisone were quantified in seminal plasma (SP), saliva (S), and semen doses (SD) from adult boars. Cortisol concentrations followed the pattern SP > SD > S, whereas cortisone concentrations showed SP > SD/S and SD ≈ S. A strong positive correlation was observed between cortisol and cortisone in SP, and a negative correlation between cortisol-SP/S and cortisone-SP/S. In functional assays, hydrocortisone (synthetic cortisol) increased reactive oxygen species (ROS) generation in capacitated spermatozoa and did not induce the acrosome reaction, but dose-dependently inhibited the progesterone-induced acrosome reaction. Under storage conditions at 17 °C, both cortisol and cortisone reduced total and progressive motility in SD. The detection and quantification of these glucocorticoids in SP and SD, together with their detrimental effects on ROS levels, acrosome reaction, and sperm motility, suggest a local modulatory role with operational implications for semen dose quality and reproductive efficiency. We propose the integration of cortisol/cortisone measurements in SP and SD as biomarkers for quality control and as an additional selection and management criterion in artificial insemination (AI) centers for swine.

BIOCHEMISTRY, PHYSIOLOGY AND NEUROCHEMISTRY

A88

RENIN-ANGIOTENSIN SYSTEM IN AN EXPERIMENTAL MODEL OF PARKINSON`S DISEASE

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The Renin-Angiotensin System (RAS) is a complex hormonal cascade with roles in both normal physiology and disease, including neurodegenerative diseases. Within the central nervous system, RAS plays a key role in processes like inflammation, oxidative stress, and neurotransmitter secretion, and its dysregulation is linked to aging and neurodegenerative conditions like Alzheimer's and Parkinson's. Specifically, the two main receptors, AT1R and AT2R, are expressed differently and regulated differently throughout the brain, influencing various neurological functions. Parkinson's disease (PD) is characterized by the loss of dopaminergic neurons in the nigrostriatal pathway, leading to a decrease in the neurotransmitter dopamine, which is crucial for motor control. This neuronal death is accompanied by inflammation, especially from activated microglia, and the formation of abnormal protein deposits called Lewy bodies that are made of aggregates of the protein α-synuclein. Previously, we evaluated the effect of the neurotoxin rotenone in rats in an experimental model of PD. Significant changes were observed on behavioral motor tests after 6 weeks of treatment and altered distribution of angiotensin II receptors were found in the midbrain of treated animals. Taking into account these findings, the aim of this work was to evaluate the precise timing when these alterations appear in the midbrain and its correlation with the motor impairments in this model. Histological and immunohistochemical (IHC) assays were performed in rotenone treated rats after 3-week and 6-week treatment. Light microscopy–IHC observations of rat midbrain evidenced a death of dopamine neurons as indicated by the decrease of immunoreactivity for tyrosine hydroxylase. Likewise, the number of AT1R and AT2R immunopositive cells were decreased in comparison with animal control. Nissl staining exhibited cells with aberrant morphology and we observed many nigral cells with α-synuclein aggregates. These findings contribute to understand the potential role of brain renin angiotensin system in neurodegenerative processes

A89

INSULIN TRIGGERS POST-TRANSCRIPTIONAL SUPPRESSION OF 14-3-3β IN A DOSE-DEPENDENT MANNER

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14-3-3 proteins play diverse roles in adipogenesis by regulating transcription factors, cell cycle progression, signal transduction pathways, protein localization, and interaction with adipogenic proteins. Their exact role may vary depending on the specific context and stage of adipocyte differentiation, highlighting their importance in the regulation of adipogenesis. Initial investigations into the adipogenic differentiation process indicated that insulin had an effect on the mRNA levels of the 14-3-3γ (YWHAG) and 14-3-3β (YWHAB) paralogs. To precisely isolate the direct effect of insulin from the complex transcriptional reprogramming of differentiation, we designed a simplified model using undifferentiated 3T3-L1 preadipocytes. This approach allowed us to interrogate post-transcriptional events in a controlled setting. Cells were maintained in DMEM supplemented with FBS 10% and treated for 6 hours with a range of insulin concentrations typical for *in vitro* differentiation models (5, 10, and 15 µg/mL). Subsequent quantitative Western blot analysis showed an evident and dichotomic response at the protein level. The 14-3-3β paralog showed dose-dependent suppression. Its protein levels decreased strongly and progressively with increasing insulin, culminating in the protein being nearly undetectable under our experimental conditions at the highest dose. In contrast, the 14-3-3γ paralog displayed stability, with its abundance remaining relatively constant across the lower insulin doses and showing only a moderate increase at the 15 µg/mL concentration. This work identifies a quick post-transcriptional regulatory mechanism whereby insulin signaling selectively depletes the 14-3-3β paralog while leaving 14-3-3γ largely unaffected. These findings significantly advance our understanding of 14-3-3 biology by revealing an unappreciated layer of paralog-specific regulation directly at the interface of metabolic hormone signaling.

A90

GENETIC AND METABOLIC RISK FACTORS OF ESSENTIAL HYPERTENSION

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Arterial hypertension (HTA) is a complex, polygenic disorder, a primary risk factor for cardiovascular disease and one of the leading causes of mortality and morbidity worldwide. Its etiology is multifactorial, resulting from the interaction of environmental, behavioral, and genetic factors. Among the latter, polymorphisms in genes of the renin-angiotensin system (RAS) and endothelial function have been widely studied for their role in blood pressure regulation and the development of cardiovascular complications. The objective of this study was to analyze the association of the insertion/deletion of angiotensin-converting enzyme (ACE I/D), angiotensinogen (AGT) M235T, the angiotensin II type 1 receptor (AT1R) A1166C and the endothelial nitric oxide synthase (eNOS) G894T polymorphisms with clinical, anthropometric and biochemical parameters in a population from San Luis. A case-control study was conducted, including 397 individuals (230 hypertensive and 167 normotensive). Written informed consent was obtained from all participants. Anthropometric, clinical, and biochemical data were recorded; in addition, genomic DNA extraction and genotyping by Polymerase Chain Reaction combined with Restriction Fragment Length Polymorphism (PCR-RFLP) were performed for each of the study participants. We analyzed traditional cardiovascular risk factors in the population. The Odds Ratio (OR) analysis revealed that the age ($p < 0.001$), the overweight ($p < 0.001$), the elevated fasting glucose (p 0.005) and elevated triglycerides ($p < 0.001$) as significant predictors of HTA. The polymorphisms studied were not associated with an increased risk of hypertension in this population, but showed significant differences in relevant metabolic parameters. Associations were identified between certain genotypes and higher body mass index (BMI), fasting glucose, triglycerides, and total cholesterol levels. Furthermore, the sex-stratified analysis showed that hypertensive women presented more marked differences compared to hypertensive men. This study highlights obesity/overweight as one of the main determinants of hypertension risk in the total population. In conclusion, the findings reinforce the importance of genetic factors in the predisposition to hypertension and associated metabolic disorders, and provide local and regional evidence that could contribute to the development of more appropriate and effective prevention and treatment strategies for populations in San Luis and the region.

VETERINARY, ANIMAL ANATOMY, HISTOLOGY AND PHYSIOLOGY

A91

FREE RANGING DOGS AND THEIR PARASITES IN THE RURAL-NATURAL ECOTONE OF MENDOZA

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As part of the project "Human-fauna intersections in dryland socio-ecological systems: free-ranging dogs as a socio-environmental issue", we aimed to evaluate the parasites infecting dogs from rural settlements (*Puestos*) situated in the foothills of the Mendoza Metropolitan Area. We worked in three *Puestos* located in western Godoy Cruz and Luján, where subsistence livestock farming is carried out. In the winter of 2024, we collected a total of 19 feces from dogs living in these *Puestos*. The feces were processed using an adaptation of the Teuscher´s technique (double sedimentation-centrifugation-flotation) with a saturated solution of sucrose (density 1300), which allows us to diagnose parasitic forms of protozoa, nematodes, and cestodes. We used a sedimentation technique to detect trematode eggs. The observed parasitic forms were measured using an ocular micrometer and photographed with a digital camera attached to an optical microscope. Parasite structures were evident in 36.8% of the samples. The evolutionary stages corresponded to at least six parasite species. Among them, we detected non-sporulated coccidia oocysts and sporulated oocysts of *Cystoisospora* (syn. *Isospora*); eggs of *Trichuris* sp., *Toxascaris leonina*, *Toxocara canis*, and unidentified cestode eggs (tapeworm-like eggs). The average measurements of the helminth eggs were: *Trichuris* sp. 62.80µm x 29.80µm (n=6), *Toxascaris leonina* 87.32µm x 70.41µm (n=23), *Toxocara canis* 90.31µm x 78.38µm (n=14) and tapeworm-like eggs 32.00µm x 28.80µm (n=11). When analyzing the parasite richness, we found that the most frequent observation were coinfections by 2 parasites species (21.1%). The maximum richness was found in 5.3% of the samples (n=1), parasitized by 4 species. Regarding parasite prevalence and intensity, the species with the highest apparent prevalence were *Toxascaris leonina* (31.6%) and *Toxocara canis* (21.1%), while the highest parasite intensity was detected with tapeworm-like eggs (123 eggs per gram of feces). Although these results are preliminary, they highlight the occurrence of domestic animal parasite species that are important for public health, as their transmission can cause disease in humans. Furthermore, all diagnosed parasitic species would have the potential to infect native mammals such as gray foxes, wild cats, guanacos, and pumas (among others) that inhabit the sampling area.

A92

MORPHOLOGICAL AND HISTOCHEMICAL CHARACTERISTICS OF VISCACHA HARDERIAN GLAND (*Lagostomus maximus*) DURING PREGNANCY

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The Harderian gland (HG) is a predominantly exocrine gland located within the ocular orbit in a wide variety of terrestrial vertebrates. The exact location of HG, its shape, size, morphological characteristics, kind of secretion, functions and regulatory pathways are species-specific. The objective of the present work was to study the morphological and histochemical characteristics of HG in non-pregnant and pregnant viscachas, a native rodent with seasonal reproduction and nocturnal habits. Females are characterized by being natural poly-ovulators (200-800 oocytes per estrous cycle). Adult female viscachas were captured in their natural habitat and divided in two groups: Non-pregnant (NP) (n=3) and Pregnant (P) (n=3). Serum estradiol and progesterone levels were quantified using the RIA. The HGs were extracted and processed for light microscopy. Estradiol (75 ± 2.89pg/ml) and progesterone (53.75 ± 2.39ng/ml) serum concentration was higher in pregnant than in non-pregnant (18 ± 3.19pog/ml, 0.72 ± 0.11ng/ml, respectively). In non-pregnant, the gland is surrounded by a thin connective capsule that compartmentalizes the parenchyma into lobules. Each one, constituted by adenomeres lined by a simple cuboidal epithelium with nucleus located basally. Two kinds of adenomeres constituted the parenchyma: large ones with wide lumen (123.22±1.57µm), lower epithelium (22.57±0.63µm) and cytoplasm intensely acidophilic and small adenomeres with reduced lumen (52.40±1.03µm), higher epithelium (35.23±0.55µm) and pale cytoplasm. In pregnant, morphological organization was similar to what described in non-pregnant. The main differences were a lower distribution of large adenomeres (Luminal Diameter (LD): 119.22±1.59µm, Epithelial Height (EH): 22.47±0.61µm) and a predominance of small ones (LD: 51.25±1.25µm, EH: 37.25±0.40µm) in relation to non-pregnant. Furthermore, an increased number of adenomeres with lumen PAS-positive (+) was observed, suggesting a greater secretory activity. According to our results, pregnancy produces changes in the HG morphological organization, probably due to sex hormones effects, with the increase in serum progesterone level during this stage. However, future studies are necessary to establish the HG functions in viscacha during the pregnancy.

A93

POSTNATAL MORPHOLOGICAL DEVELOPMENT OF THE PROSTATE AND SEMINAL VESICLES IN *Lagostomus maximus:* A COMPARISON BETWEEN PREPUBERAL AND IMPUBERAL STAGES

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Our experimental model, viscacha (*Lagostomus maximus*), is a seasonally breeding rodent that exhibits pronounced photoperiodic and androgen-dependent regulation of its reproductive activity. Seasonal changes in the reproductive physiology of the adult male are evident in its natural habitat, where gonadal activity intensifies during the summer and early autumn, followed by a marked decline during the winter period. Accessory sex glands have been previously studied, and these studies revealed that seminal vesicles (SV) of prepuberal and adult animals were radially organized into three well defined histological layers: mucosa with a pseudostratified epithelium and a thin lamina propria, a muscular layer, and an adventitia. Prostate (P) of adult animals was lined with pseudostratified columnar epithelium and displayed two distinct regions: the central and peripheral zones, differing in epithelial height and degree of folding, and in luminal diameter. The objective of this work was to examine the postnatal morphological maturation of the prostate and seminal vesicles, with emphasis on the differences observed in comparison to the impuberal and prepuberal stages. Eight males were captured in their habitat and divided in 2 groups according to their weight and microscopic observation of the testes: 4 impuberal (1-2 kg) and 4 prepuberal animals (3-4 kg). Serum testosterone levels were quantified using a total testosterone assay, and accessory sex glands were removed and processed for light microscopy. Serum testosterone levels of immature animals were below the detection limit (<0.20 ng/dl) while in pre-puberal they were 139 ± 30.77 ng/dl. Hematoxylin-Eosin, Masson's trichrome and PAS histochemical stains were performed. In the impuberal stage, SV exhibited a simple low columnar to cuboidal epithelium and a fibromuscular stroma with abundant collagen fibers and smooth muscle cells. Unlike the prepuberal and adult animals, no clear arrangement between lamina propria and muscular layer was observed. The prostate of impuberal viscachas showed few large adenomeres with a highly convoluted lumen, and there was no organization into central and peripheral zones. Epithelial folds of a pseudostratified epithelium were surrounded by a thin layer of fibromuscular stroma. The periphery of the glandular adenomeres consisted of a large amount of irregularly arranged dense connective tissue. These differences observed among the studied groups highlight that morphological changes occur gradually, and point to the regulatory role of androgen levels in organ development.

A94

EVALUATION OF ULTRASONOGRAPHIC PREDICTION OF RIBEYE AREA IN LAMBS

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The rib-eye area (REA) is a widely used parameter in meat production, providing individual valuable information regarding the carcass quality expected to exhibit post-slaughter. It allows the prediction of the animal's muscularity and is associated with the proportion of retail cuts. Moreover, as it can be measured in the live animal, REA offers pre-slaughter information that aids in evaluating the animal not only as a meat producer but also as a potential breeder. Previous studies have reported a correlation of approximately 0.70 between in vivo REA measurements and postmortem determinations. The objective of this study was to evaluate the predictive accuracy of ultra-sonographic measurements of the rib-eye area in heavy Highlander lambs. Thirteen lambs with an average pre-slaughter weight of 35.92 ± 4.41 kg were evaluated. Ultra-sonographic measurements of REA were performed on July 22, 2021, using an Aquila Pro Vet ultrasound device, four days prior to slaughter. The images were obtained by a certified technician and analyzed by specialists. Results indicated mean REA values of 9.12 ± 1.08 cm² measured by ultrasound and 13 ± 1.64 cm² determined by planimetry on carcasses. These measurements showed a statistically significant correlation ($p = 0.02$) between ultra-sonographic REA (REA us) and postmortem REA (REA_pm), with a correlation coefficient of 0.74, indicating a linear relationship between variables. Linear regression analysis demonstrated that ultra-sonographic measurements explained 55% of the variation observed postmortem ($R^2 = 0.55$) with statistical significance ($p = 0.02$). The estimated root mean square error of prediction (RMSEP) was 2.33, indicating an average difference of 2.33 cm² between predicted and measured REA values. A little part of this discrepancy may be attributed to the four-day interval between ultrasound assessment and slaughter date, and partly due to an interpretation technique error by interpreters with more experience in bovine determinations, that owns larger rib-areas. Additionally, both ultra-sonographic and carcass REA values were correlated with the subjective carcass conformation score (0.81 and 0.86, respectively) and, to a lesser extent, with cold carcass weight (0.40 and 0.50, respectively). It is concluded that the ultra-sonographic measurements obtained in this study were representative of the actual rib-eye area measured postmortem, and carcass conformation, confirming that ultrasound imaging is an effective predictive tool. However, increasing the sample size (n) and performing additional measurements, in live animal or post-slaughter, could allow the inclusion of other variables and further refinement of the prediction model.

A95

MORPHOMETRIC ASSESSMENT OF RENAL ALTERATIONS IN *Zenaida auriculata* Induced BY DICLOFENAC, AN EMERGING CONTAMINANT

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Diclofenac (DFC) is an emerging contaminant recently detected in central Argentinean rivers. The drug is known to impair renal function in birds, leading to population collapses like those reported in South Asia. However, studies in this geographic region are lacking. Therefore, it is crucial to evaluate the DFC's effects on local avifauna. This study aimed to evaluate the histopathological effects of DFC on the kidneys of the eared dove (*Zenaida auriculata*). Four groups of animals (n = 7) were exposed for 10 days to different DFC concentrations: 0.005 mg/kg (G1), 0.25 mg/kg (G2), and 2.5 mg/kg (G3), administered by gavage at the same time each day. A control group (G0) received only water. At the end of the exposure period, birds were euthanized and kidneys were collected and processed for light microscopy. Histological sections were prepared and stained with hematoxylin-eosin. These sections were then used for image analysis. We quantified renal damage by measuring the area of Bowman's space, calculated as the glomerular corpuscle area minus the glomerular tuft area. Statistical analyses were subsequently performed. Histological analysis revealed alterations in renal structure, with a significant dilation of Bowman's capsule in DFC-treated birds from G3 compared to controls ($P < 0.005$). Mild cortical hemorrhage was also observed, suggesting microvascular damage. These findings demonstrate the nephrotoxic effect of DFC in eared doves. The observed damage is likely caused by prostaglandin inhibition and subsequent ischemia, which disrupt the filtration barrier and endothelium, thus explaining both blood extravasation and glomerular capsule distension. In conclusion, these results indicate that a 2.5 mg/kg dose of DFC induces structural damage to the kidneys of this species. Supported by UNSL-PROICO 2-0820 and CONICET- PIP 163- 2023 to F.D. Cid.

A96

PRESENCE OF HORN FLIES (*Haematobia irritans*) IN RED DEER (*Cervus elaphus*)

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The red deer (*Cervus elaphus*) is a mammal that was introduced to the province of La Pampa for sport hunting. The horn fly (*Haematobia irritans*) is a small, blood-sucking dipteran that frequently parasitizes cattle and, to a lesser extent, horses. Its presence is seasonal, with peak populations typically occurring during the warmer seasons of the year, peaking in late spring and early autumnwhile populations decline dramatically with the first frosts. In cattle with a high insfestation of red deer fly, milk production or weight gain may be affected. The objective of this study was to determine whether red deer carry external parasites. In the province of La Pampa, 116 red deer were sampled between 2020 and 2025, of which 60 were hunted during the fall-winter period and 56 during the spring-summer period. The presence of *Haematobia irritans* (horn fly) was observed in two individuals. The parasitized deer were hunted in late winter and spring. The presence of Haematobia irritans in red deer raises the possibility of its geographic expansion to areas where cattle are scarce.

A97

EFFECT OF MELATONIN ADMINISTRATION ON TESTICULAR AUTOPHAGY IN *Lagostomus maximus*

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In several studies, it has been observed that the melatonin rhythm plays a key role in the regulation of gonadal morphology and physiology according to the specific reproductive season of each species. The viscacha (Lagostomus maximus) is a wild South American rodent with nocturnal habits and seasonal reproduction. The main objective of this work was to use the viscacha (Lagostomus maximus) as an experimental model to analize the administration effects of melatonin on testicular histology and the immunohistochemical expression of autophagy specific proteins: LC3B (ABCAM) y P62 (ABCAM). The adult animals were captured during the period of maximal gonadal activity in their habitat near San Luis city. The adult males were divided in two groups: 1) Experimental Group (EG) (n=3) received two daily subcutaneous injections of melatonin (Sigma, 100µg/kg body weight in aqueous solution) at 09:00 h and 17:00 h for 9 weeks, and 2) Control Group (CG) (n=3) received only the diluent. The blood samples were obtained from anesthetized animals. Serum testosterone levels were determined by a solid phase competitive chemiluminescent enzyme immunoassay. Testicular samples were surgically removed and processed for optical microscopy. Serum testosterone levels were significantly lower in EG (159±36.43) than CG (487.50±45.35). The seminiferous tubules diameter was similar in CG (523.50 ± 8.18) and EG (556.88 ± 3.00). However, it was observed germinal epithelium disorganization with loss of contiguity between the germinal and Sertoli cells, epithelial vacuolation and germ cell desquamation within seminiferous lumen in EG. These observations were contrary to what was observed in CG. LC3B expression in CG was limited to spermatids, while in EG intense expression was detected in all germinal stages, mainly in spermatids. P62 expression was negative in both studied groups. According to our results, melatonin administration produces changes in testicular morphological organization and autophagic activity to recycle damaged or unnecessary cellular components in our experimental model. The male gonad could develop cellular rearrangement mechanisms to preserve homeostasis in a particular situation of exacerbated exposure to melatonin. Further studies are needed to establish the mechanisms of action developed by this hormone.

A98

SUBLETHAL EFFECTS OF THE IMIDACLOPRID ON HEPATIC ARCHITECTURE OF EARED DOVES (*Zenaida auriculata*)

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The extensive agricultural use of neonicotinoid insecticides in Argentina has raised growing concern about their environmental persistence and unintended effects on non-target species. Among these compounds, imidacloprid (IMI) is widely applied as a seed coating in major crops, posing a potential risk to granivorous birds that feed on treated seeds. This study evaluated the chronic sublethal effects of IMI on hepatic histological biomarkers in the eared dove (*Zenaida auriculata*). Eighteen adult doves were randomly assigned to three groups and orally dosed by gavage once daily for 21 days. The control group (Co) received only water, while the low-dose (LD) and high-dose (HD) groups were exposed to 3.93 mg/kg body mass/day (1/15 LD_{50}) and 11.8 mg/kg/day (1/5 LD_{50}) of formulated IMI, respectively. After exposure, birds were euthanized, and liver samples were processed for light microscopy. Histological sections were stained using techniques for subsequent image analysis and statistical evaluation of morphometric parameters. The size of hepatocytes, central veins, and portal areas was quantified (using hematoxylin-eosin staining). Additionally, the area occupied by collagen fibers (using Masson's Trichrome) and the amount of iron deposits (using Perl's Prussian Blue) were measured. The Co group exhibited normal hepatic architecture, while the LD group showed mild alterations such as steatosis, sparse inflammatory foci, and discrete iron deposits, with no significant morphometric differences from controls. In contrast, the HD group displayed pronounced histopathological lesions, including hepatocellular atrophy, necrotic areas, leukocytic infiltration, sinusoidal dilation, and bile duct epithelial alterations. Quantitatively, significant increases were observed in the size of portal areas and central veins. Morphometric analysis revealed decreased cytoplasmic and nuclear size of hepatocytes in Zone 1 (periportal zone) and a reduction in nuclear size in hepatocytes of Zone 3 (centrilobular zone). Additionally, a greater amount of collagen deposition forming portal-portal bridges and increased iron accumulation were observed. These results demonstrate that chronic exposure to environmentally relevant doses of IMI induces dose-dependent hepatic alterations in *Zenaida auriculata*. Although low-dose exposure produced subtle, potentially reversible effects, the high dose caused structural and metabolic impairment of the liver, revealing its high sensitivity to neonicotinoid toxicity. The histological and morphometric changes identified here constitute sensitive biomarkers for assessing sublethal pesticide exposure in wild birds and reinforce the ecological risk associated with the widespread agricultural use of imidacloprid. Supported by UNSL-PROIPRO 02-3723 (V.P. Filippa), UNSL-PROICO 02-0820 (F.D. Cid), and CONICET PIP 163-2023 (F.D. Cid).

A99

IDENTIFICATION AND CHARACTERIZATION OF TICK PARASITIC BURDEN IN DOGS FROM URBAN AND PERI-URBAN AREAS OF GUAYMALLÉN, MENDOZA

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Historically used for protection and labor, dogs have strengthened their bond with humans, complicating the landscape of zoonotic diseases. Tick-borne vector diseases are expanding, driven by factors such as climate change. In Mendoza, cases of ehrlichiosis, anaplasmosis, hepatozoonosis, babesiosis, and mycoplasmosis have been diagnosed, associated with *Rhipicephalus sanguineus* and *Amblyomma tigrinum*. This study aimed to identify tick species and quantify their parasitic load and stage distribution in dogs from Guaymallén. Tick samples were collected from dogs between 2023 and 2025. Specimens were preserved in 70% alcohol until analysis. Identification was performed using taxonomic keys. Statistical tests (Chi-square, Fisher's exact test, and z-test) were applied with a 5% significance level ($\alpha = 0.05$) using R 4.3.1. A total of 38 dogs were sampled—21 (55.2%) males and 17 (44.7%) females—ranging from 2 months to 16 years old, all attending a private veterinary clinic in Guaymallén. Of the ticks collected, 93.54% were *Rhipicephalus sanguineus* and 6.45% *Amblyomma tigrinum*. The average parasitic load was 13.8 ticks per dog (min. 1; max. 72; n=542). Only one dog presented co-infection. The proportions of *R. sanguineus* were: 52% ($\mu=7$) adult females; 28.9% ($\mu=3.8$) adult males; 17.16% ($\mu=2.3$) female nymphs; 0.99% ($\mu=0.13$) male nymphs; and 0.19% ($\mu=0.02$) female larvae, with 0% male larvae. For *A. tigrinum*, the distribution was 25.7% ($\mu=0.23$) adult females and 74.3% ($\mu=38$) adult males, with no nymphs of either sex detected. Females were more prevalent across all developmental stages, particularly among nymphs (94.6%) and adults (64.5%) ($\chi^2 = 34.97$, df = 2, $p < 0.0001$). A significantly higher proportion of female nymphs compared to adults were confirmed ($p < 0.0001$). A specific comparison between adult females and males revealed a significant difference ($z = 5.82$, $p < 0.0001$), indicating a predominance of females in the adult population. The results demonstrate a higher parasitic load of *Rhipicephalus sanguineus* in dogs from Guaymallén, with female predominance across all stages, especially nymphs. The lower proportion of *Amblyomma tigrinum* and the detection of co-infection in only one individual reinforce the role of *R. sanguineus* as the primary vector in the area. Significant differences in sex distribution by developmental stage, confirmed through statistical analysis, suggest biological or ecological patterns that may influence tick population dynamics. In the context of a growing human-dog bond and the expansion of vector-borne diseases, these findings provide relevant information for veterinary public health surveillance and control strategies.

PHARMACOLOGY AND TOXICOLOGY

A100

DETERMINATION OF TRACES ANTIMONY BY SOLID SURFASE FLUORESCENCE PRIOR TO A SURFACTANT-SENSITIZED CHEMOFILTRATION STAGE

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Antimony is a metal nonessential to life and is currently considered an emerging contaminant due to its increasing presence in the environment and its toxic effects on humans, plants, and animals. Human activities such as mining, smelting, and burning of fossil fuels, along with the erosion of minerals and waste, release antimony into soil and water, posing a serious threat to ecosystems and public health. The objective of this study was to evaluate trace levels of antimony (Sb (III)) in water samples from the northern and central regions of Argentina using a novel methodology with 1,4-dihydroxy-9,10-anthraquinone (quinizarin, QZ) as the fluorophore. Sb (III) was determined by complex formation with QZ, followed by solid-phase extraction using filter paper pretreated with hexadecyltrimethylammonium bromide (HTAB). The analysis was subsequently quantified by solid-phase fluorescence ($\lambda_{em} = 575$, $\lambda_{exc} = 490$) with a detection limit of 1.22 ng L^{-1} and a quantification limit of 2.69 µg L^{-1}. The calibration curve was linear from 2.22 to 4.6×10^{3} ng L^{-1} of Sb (III) ($R^2 = 0.9983$). Samples of mains, natural and bottled (untreated) water from 10 Argentine provinces were successfully analyzed, with an average recovery close to 100%. Solid-phase extraction demonstrated efficacy in removing potential interfering ions. Reproducibility (inter-day precision) was evaluated over 5 days, performing five daily determinations, and the CV% obtained was 0.37. The results were validated using electrothermal atomic absorption spectrometry (ETAAS) with good agreement. The new methodology has a low operating cost, is easy to implement, and does not require organic solvents. The sensitivity and selectivity achieved through chemofiltration make it a suitable alternative to conventional techniques for determining traces of Sb (III).

A101

QUANTIFICATION OF CADMIUM IN *Chamaemelum nobile* BY SURFANT- MOLECULAR FLUORESCENCE ASSOCIATION

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Cadmium is a known human carcinogen and is commonly found in air, soil, and water. Due to its long biological half-life, it accumulates in plants and animals. The main sources of cadmium exposure are industrial work environments, tobacco, and food. Cadmium toxicity is associated with various clinical complications: cancer, liver and kidney dysfunction, increased risk of bone fractures, hypertension, arteriosclerosis, and severe anemia. Current evidence suggests that cadmium exposure induces genomic instability through complex and multifactorial mechanisms; there are no proven effective treatments for chronic cadmium poisoning. Due to consumer demand for more natural treatments, traditional medicine, with regard to the leaves and flowers of *Chamaemelum nobile*, can be considered in modern pharmacological contexts. Because it exhibits soothing, anti-inflammatory, and digestive properties, it is used to relieve stomach problems such as indigestion and heartburn, as well as to reduce inflammation. Furthermore, it can help with insomnia and skin irritations, and is useful for decongesting the respiratory tract. However, *Chamaemelum nobile* plants possess the ability to absorb cadmium from the soil and accumulate it at unusually high concentrations in their leaves. The objective of this study was to develop a new methodology for the quantification of Cd (II) in leaves and flowers of *Chamaemelum nobile* of known commercial brands using luminescent methods. Cadmium was determined by the intensification of the fluorescent signal of rhodamine B (RhB) on a nylon membrane filter pretreated with the anionic surfactant SDS. The method showed good sensitivity, adequate selectivity, and good tolerance to foreign ions, and was applied to the determination of traces of Cd (II) with satisfactory results, representing a novel alternative to conventional analytical methods. Working under optimal conditions, quantitative recovery of Cd (II) (≥99.9%) was achieved, with a detection limit of 0.3 ng L^{-1} and a quantification limit of 1.1 ng L^{-1}. Calibration of the new methodology showed linearity over four orders of magnitude. It was applied to the determination of Cd (II) in 10 samples of *Chamaemelum nobile* infusions marketed in Argentina with satisfactory results, representing a novel alternative to conventional methods for trace metal analysis.

A102

PHARMACOEPIDEMIOLOGICAL STUDY IN NURSING HOMES IN THE CITY OF SAN LUIS

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Evaluating medication use, particularly among older adults, is essential because they help to improve pharmacological therapy in this patient population. An association exists between age and drug consumption, attributable to the increased prevalence of chronic conditions and comorbidities among the elderly. Polypharmacy—defined as the use of five or more medications—increases the risk of drug interactions and adverse events, therefore, pharmacoepidemiologic studies are essential. Objective: To assess drug prescription in nursing homes in the city of San Luis. A descriptive, cross-sectional observational study was conducted in three nursing homes in San Luis during January 2025. The prescribed medications classified according to the Anatomical Therapeutic Chemical (ATC) Classification System were analyzed. A total of 37 patients were included, 32% male and 68% female. The age distribution was as follows: 60–69 years: 15%; 70–79 years: 30%; 80–89 years: 38%; 90–99 years: 15%; and one patient aged 102 years. Out of a total of 260 prescribed drugs, the main ATC groups were as follows**:** N: 42.7%; C: 25.7%; A: 10.3%; Other groups: 21.3%**.** Within group N: N05 (Psycholeptics): 28% and N06 (Psychoanaleptics): 28%**;** N03 (Antiepileptics): 24.3%**;** Other: 19.7%. Within group C: C09 (ACE inhibitors): 37.3%; C07 (Beta-blockers): 17.9%; C10 (Lipid-lowering agents): 16.4%**;** C08 (Calcium channel blockers): 12%**;** Other: 16.4%**.** Within group A: A02 (Antacids and antiulcer agents): 50%; A10 (Antidiabetics): 50%. Among psycholeptics, quetiapine was the most frequently prescribed drug. Under the psychoanaleptic group, memantine was the most prescribed drug. Among antiepileptics, clonazepam was the most prescribed drug. In the C09 group**,** losartan and enalapril were the main drugs prescribed; in C07, bisoprolol**;** and in C10, atorvastatin. Among antacids, omeprazole was the most prescribed, and among antidiabetic medications, insulin and metformin were predominant. Polypharmacy was observed in all individuals, with the majority receiving five or more medications daily. The most frequently prescribed medications targeted the nervous, cardiovascular, and digestive systems, reflecting the most common conditions in this age group, such as dementia, depression, hypertension, dyslipidemia, and diabetes mellitus**.** It is essential to continue conducting studies of this kind to promote the appropriate use of medications in the elderly, aiming to avoid polypharmacy whenever possible and ensure that drug use in this population improves their quality of life**.**

A103

PHARMACOEPIDEMIOLOGICAL STUDY. PRESCRIPTION OF MEDICINES AT THE SAN LUIS MENTAL HEALTH HOSPITAL

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The prescription of drugs that act on the central nervous system (CNS) is a central part of the approach to mental disorders. Advances in the conceptualization and treatment of these diseases have led to the increasing medicalization of mental health, with a significant impact on people's daily lives, making them among the most commonly prescribed drugs today. To evaluate the prescription of medications at the time of admission of patients to the San Luis Mental Health Hospital from May to August 2025. An observational, descriptive, cross-sectional, and prospective study was conducted. Prescribed drugs classified as group N according to the Anatomical Therapeutic Chemical Classification System (ATC) were analyzed, as were diagnoses recorded according to the International Classification of Diseases (ICD). A total of 165 patients were included. Of the total number of patients, 52% were women, 46% were men, and 3% identified with another gender. The predominant age group was 20 to 39 years (68%). Five therapeutic subgroups were identified: N05 (psycholeptics, n = 345; most prescribed drug: Lorazepam), N06 (psychoanaleptics, n = 96; Sertraline), N03 (antiepileptics, n = 94; Valproic acid), N02 (analgesics, n = 4; Paracetamol), and N04 (antiparkinsonian drugs; Biperiden). The most frequent diagnoses were: suicidal ideation, suicide attempt, psychoactive substance abuse, psychotic disorder, schizophrenia, depression, and psychotic decompensation. The most common diagnosis-treatment combinations included: Sertraline and Lorazepam for suicidal ideation, Diazepam and Sertraline for substance abuse, and Haloperidol and Olanzapine for psychotic disorders. The highest proportion of patients was concentrated between the ages of 20 and 40, which is an unfortunate fact that must be taken into account. Suicidal ideation was the most prevalent diagnosis. Psycholeptics were the most commonly prescribed pharmacological group, with a high use of benzodiazepines and antidepressants. These findings suggest reflection on prescribing criteria and the need for comprehensive mental health strategies.

A104

STUDY OF GASTROPROTECTIVE ACTIVITY OF THE ARGENTINE MISTLETOES: *Ligaria cuneifolia* (Ruiz & Pav.) Tiegh. AND *Tripodanthus flagellaris* (Cham. & Schlecht.) Tiegh. (Loranthaceae) IN RATS

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Ligaria cuneifolia (Ruiz & Pav.) Tiegh. ("liga roja", "liga", "muérdago criollo") is an hemiparasite species used in Argentine folk medicine as a substitute for the European mistletoe (*Viscum album* L.). *Viscum album* (Loranthaceae) decoction showed a remarkable gastroprotective activity against ethanol model of ulcerogenesis. *Tripodanthus flagellaris* (Cham. & Schlecht.) Tiegh., popularly known as "liga blanca", "liguilla", is used in folk medicine for therapeutic on circulatory system and as antihypertensive. *L. cuneifolia* is employed for the treatment of headaches, stomach and throat aches. Both species belong to the Loranthaceae family. Studies of flavonoid demonstrated that the only detected flavonol is quercetin, in both species. Others phytochemical analysis revealed quercetin-3-O-rhamnosylglucoside and proanthocyanidins in *T. flagellaris*. Besides, leucoanthocyanidins and proanthocyanidins were detected in *L. cuneifolia.* The aim of this study was to evaluate and compare the gastroprotective effect in rats, of both species. Infusions of the plant materials: *L. cuneifolia* (10%, Del Vitto LA; EM Petenatti & MR Fusco 9245, UNSL) and *T. flagellaris* (10%, Del Vitto LA & EM Petenatti 8553, UNSL), were prepared according to Argentinean Pharmacopoeia, separated by filtration and the aqueous extracts were concentrated and lyophilized to preserve it. We examined the effect on gastric damage induced by oral administration of absolute ethanol (EtOH). *L. cuneifolia* and *T. flagellaris* (125, 250 and 500 mg/kg, *p.o.*) were administered before EtOH to rats (n=6-8). By the other hand, we evaluated the role of sulfhydryl groups, prostaglandins and nitric oxide, which seem to play a mechanistic role in gastroprotection. The rats were then euthanized with CO_2, their stomachs were removed, and the damage (mm^2) was quantified. The scanned images of stomach were analized by using a program developed by National Institutes of Health. EtOH produced gastric ulcers in all the animals treated. *L. cuneifolia* (250 and 500 mg/kg) prevents the formation of gastric lesions induced by EtOH (mm^2 damage: 13.66±5.8 ($p<0.01$), 7.55±3.46 ($p<0.001$), respectively, vs. EtOH: 134.11±9.13 mm^2). The effect elicited by *L. cuneifolia* at 500 mg/kg was not attenuated by pretreatment with N-ethylmaleimide (10 mg/kg, s.c.), a blocker of sulfhydryl groups; LNNA (40 mg/kg, i.p.), a nitric oxide synthase inhibitor and indomethacin (10 mg/kg, i.p.), a prostaglandins synthesis inhibitor. This suggests that the gastroprotective mechanism of action of *L. cuneifolia* does not involve sulfhydryl groups, nitric oxide and prostaglandins, at the dose assayed. *T. flagellaris* (125, 250 and 500 mg/kg) was not prevent the formation of EtOH-induced gastric lesions. Several reports have shown that flavonoids protect against experimental ulcer. The anti-ulcerogenic effect of *L. cuneifolia* could be due, in part, to the presence of flavonoid fraction in this plant. Although, both species possess quercetin, a gastric protector, *T. flagellaris* did not show gastroprotection. These findings suggest a potential beneficial use of *Ligaria cuneifolia,* while *Tripodanthus flagellaris* does not, on gastric protection.

A105
EFFECT OF *Prosopanche americana* ON DIURETIC ACTIVITY IN WISTAR RATS

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The main advantages of using herbal medicines are the low cost, affordability and usually fewer side effects. *Prosopanche americana* (R. Br.) Baillon is a perennial hemiparasitic native plant distributed in Argentina (Córdoba, Santiago del Estero, Mendoza, La Rioja, San Luis), belonging to the family Hydnoraceae. Commonly known as "guaycurú santiagueño", "huaycurú", "huáchar", "guacharo", "flor de fierro", "flor de la tierra" o "espinazo de lagarto". The fruit is edible, and rhizome are used in folk medicine as vulnerary, homeostatic, expectorant, anti-inflammatory, cardiac disorders, antidiabetic and diuretic. Specimens were deposited in the Herbarium of the Universidad Nacional de San Luis under registration UNSL#560 (Del Vitto LA & EM Petenatti). Infusion to 10% was prepared following the methodology outlined in the VII Ed Argentine National Pharmacopoeia and then lyophilized to preserve it. This study was aimed to investigate the effect of *P. americana* rhizome lyophilized aqueous extract (PALE) on diuretic activity in rats. *P. americana* was administered, *p.o.*, in concentrations: 0 (control group), 500 mg/kg and 750 mg/kg. The proposed method used adult Wistar rats with a body weight range from 150-180 g in a randomized manner and assigned into groups (n=6-8). All experiments were conducted in accordance with ANMAT No. 9236/2023. Experimental protocols approved by the Committee for Animal Care and Laboratory Use (CICUAL) of the Faculty of Chemistry, Biochemistry and Pharmacy, Universidad Nacional de San Luis (Protocol F-386/21). Lipschitz *et al.* method was used, and control (saline solution), furosemide and hydrochlorothiazide (reference drugs) groups were established. Urinary volume was measured at 15 min intervals for 3 hours to determine urinary volumetric excretion (UVE). The urine samples showed normal chemical parameters in all the cases. Urine Na+ and K+ contents were analysed. Urinary density and pH were measured. Rats treated with 750 mg/kg infusion showed a significant diuretic effect (UVE: 81.84 ± 4.11, $p< 0.01$) respect the control (57.74 ± 1.49). Excretion followed values from 41.73% compared with control group. Urinary sodium excretion was not significant at doses 750 mg/kg, while urinary potassium excretion was significantly increased (3.44 ± 0.29 mEq/Kg, $p<0.001$) vs negative control (0.44 ± 0.04 mEq/Kg). Urinary density and pH were similar to controls. Further phytochemical investigations will be necessary for analysis of involucre metabolites. The diuretic activity value is an indicator for evaluating efficacy compared to standard diuretics. These preliminary results, in this model, are a contribution to its medicinal use as a diuretic.

A106
DIURETIC ACTIVITY OF THE AQUEOUS AND METHANOL EXTRACT OF *Jungia polita* Griseb. IN RATS

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Jungia polita Griseb. (Asteraceae–Multisieae) is popularly known as "zarzaparrilla" or "viña". This shrub species is used in Argentine folk medicine as a diuretic, anti-sclerotic, hypotensive, for skin affections; antihyperlipidemic, bradycardic, and depurative. Infusion (10%) of the aerial parts prepared, separated by filtration, and the aqueous extract was concentrated and lyophilized to preserve it. Material was macerated in methanol (80%), then it was filtered through Whatman filter paper and evaporated by using rotary evaporator. This study was designed to compare the diuretic and natriuretic activity of the *J. polita* lyophilized extract (JPLE) and methanol extract (JPME). The test was performed as described by Lipschitz *et al.* and the experiments were approved by CICUAL (Protocol F-405/22; F-466/24). Wistar rats (150–180 g) were employed. The animals, randomly assigned into groups (n = 6–8), were deprived of food for 18 h before starting the experiments and had free access to water. The test groups were administered with different doses of JPLE (250 and 500 mg/kg, orally) and JPME (125 and 250 mg/kg). The reference group received Furosemide (10 mg/kg, intra-peritoneal). The control group received only the vehicle (50 mL/kg, orally). Immediately after administration, the rats were paired and placed in metabolism cages. At the end of the experiments, the animals were euthanized by inhalation of CO_2. Urinary volumetric excretion (UVE), urine chemical parameters, urine Na^+ and urine K^+ were measured in 3-hour diuresis. All values were expressed as the mean ± SEM. Student's *t*-test was performed to evaluate the differences between the control and the experimental samples for each time point. The group treated with JPLE (500 mg/kg) showed diuretic activity between 45 min (UVE: 20.06 ± 8.04 *vs.* control: 4.84 ± 1.69; $p<0.01$) and 180 min (UVE: 82.95 ± 8.92 *vs.* control: 52.74 ± 6.03; $p<0.001$). While the group treated with JPME (250 mg/kg) showed diuretic activity between 150 min (UVE: 72.96 ± 6.13 vs. control: 51.55 ± 2.44; $p<0.05$) and 180 min (UVE: 79.63 ± 3.64 vs control: 55.41 ± 1.05; $p<0.01$). The lot treated with JPME (125 mg/kg) did not show diuretic activity at any of the observed times. The urine samples presented normal chemical parameters in all cases: urinary density and pH were similar to controls. Group treated with JPLE showed natriuretic activity: 250 mg/kg doses (urine Na^+ (mEq/L): 17.13±5.52 vs. control: 9.01± 2.65; $p<0.05$) and 500 mg/kg doses (urine Na^+ (mEq/L): 14.91±4.67 vs. control: 9.01±2.65; $p<0.05$). The urinary K^+ showed significant differences for the group treated with 500 mg/kg JPLE [urine K^+ (mEq/L): 66.79±9.25 vs. control: 50.30±10.23; $p<0.05$]. On the other hand, JPME (250 mg/kg) showed significant differences vs. control, for both Na^+ ($p<0.001$) and K^+ ($p<0.01$) values. This diuretic activity could be due, in part, to the presence of flavonoids in this plant. These results provide scientific support for the traditional use of this plant species.

A107

TOXICOLOGICAL AND REPRODUCTIVE IMPACT OF GLYPHOSATE ON THE FRESHWATER SNAIL *Pomacea canaliculata*

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Glyphosate is one of the most widely used herbicides worldwide and which can reach freshwater ecosystems and bioaccumulate in different living organisms and foods for human consumption. The species *Pomacea canaliculata* has been reported to exhibit high tolerance to glyphosate exposure. At low concentrations, this herbicide stimulates oviposition, whereas at high concentrations, both oviposition and clutch fertility decrease after 28 days of exposure, attributed to morphological alterations in the ovary. The apple snail *P. canaliculata* has been proposed as a bioindicator of environmental contamination due to its high survival rate and successful reproductive strategy. In this study, we aimed to determine the toxicity induced by acute glyphosate exposure administered as a single dose and to evaluate its impact on reproductive parameters. Adult individuals (4 months old) of both sexes were initially exposed to increasing concentrations of glyphosate to study the toxicity of the compound and to determine LD50 and no observed effect concentration on lethality ($NOECL_{48hs}$). Glyphosate exposure was performed via intramuscular injection with concentrations ranging from 55.6 to 7120 µg/g of the animal's body weight and mortality was recorded after 48 hours of exposure. Replicates of the exposed groups were performed at intermediate curve points. Subsequently, to determine effects on reproduction after acute exposure, 4 couples were exposed to the $NOECL_{48hs}$, and different parameters were monitored for 7 days pre- and 7 days post- glyphosate exposure. During both weeks, we monitoring the oviposition frequency, copulation frequency, clutch weight, and egg fertility in each pair of snails. All measurements were taken twice daily, and the experiment was replicated (N= 8 couples). As expected, *P. canaliculata* showed low sensitivity to glyphosate, tolerating high concentrations with an LD50 of 2659 µg/g and a NOECL of 1557.5 µg/g. Among the reproductive parameters evaluated, no significant differences were observed when comparing pre- and post-exposure data, but oviposition frequency appeared to be partially affected by glyphosate. Acute single-dose exposure, as could occur in accidental spills, seemingly does not significantly affect this species. Further studies are needed to verify previously described effects under laboratory conditions and to elucidate potential mechanisms, aiding the use of this species as a contamination biomarker of glyphosate in water.

A108

ACUTE ORAL TOXICITY STUDY OF AN AQUEOUS EXTRACT OF *SPIROGYRA SP*. IN A MURINE MODEL FOR ITS APPLICATION IN FUNCTIONAL FOODS

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The growing demand for sustainable foods generates an increased interest in algae due to their high nutritional value. Charophytes, which are rich in proteins, carbohydrates, and fibers, have emerged as promising ingredients for functional food development. *Spirogyra sp*., a filamentous green alga isolated from a river in San Luis (Argentina), represents a potential source for such applications; however, its safety must be verified before recommending consumption. Toxicological evaluation in animal models is crucial for identifying potential risks and establishing safe dosage ranges. Owing to the lack of toxicological data on *Spirogyra sp*., studies confirming its safety are warranted. This study aimed to assess the potential acute oral toxicity of *Spirogyra sp*. aqueous extract in mice. Balb/c mice of both sexes (20–30 g), obtained from the UNSL animal facility, were used under controlled conditions with CICUAL approval. Following a three-day acclimatization period and a 4-hour fast, acute toxicity was evaluated according to OECD Guideline 423. Animals received a single oral dose by intragastric gavage: saline solution (vehicle) for the control group and 5, 50, 300, or 2000 mg/kg of the *Spirogyra sp*. extract for the experimental groups (three males and three females per dose). Clinical signs, body weight, and food intake were monitored for 14 days. At the end of the observation period, animals were euthanized for macroscopic examination of vital organs. Data was analyzed using GraphPad Prism (one-way ANOVA followed by Bonferroni's multiple comparison test), with statistical significance set at $p < 0.05$. A single oral administration of the aqueous *Spirogyra sp*. extract (5–2000 mg/kg) produced no mortality or observable signs of toxicity during the 14-day observation period. Body weight gain, food intake, and relative organ weights (liver, kidneys, spleen, heart, lungs, and gonads) showed no statistically significant differences compared with the control group ($p > 0.05$). No macroscopic alterations were observed in any organ, and normal behavioral patterns were maintained throughout the study. These results demonstrate the absence of acute oral toxicity even at the highest dose tested, indicating a wide safety margin for the extract. The findings provide preliminary yet consistent evidence supporting further toxicological evaluation and potential application of *Spirogyra sp*. as a safe ingredient in the formulation of functional foods

A109

CAN SPIRULINA COUNTERACT CADMIUM TOXICITY? SEARCHING FOR SAFER ALTERNATIVES: SPIRULINA AS A NUTRACEUTICAL AGENT AGAINST CADMIUM INTOXICATION

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It is dramatic that the global decline of amphibians is due to their ecosystem's destruction caused by urbanization, climate change, and extensive aquatic pollution. These animals are highly susceptible during their developmental stages, which makes them an excellent research model to assess the environment influence on growth, while also serving as highly sensitive bioindicators of environmental health. Remarkably, they can establish survival strategies in response to unfavorable or advantageous environments by modifying their metamorphosis to either leave or remain in the water, taking advantage of their aquatic larval stage and terrestrial adulthood. Over the years, our laboratory has extensively studied cadmium (Cd) intoxication. Cd exerts its action mainly through the induction of oxidative stress, among other mechanisms. In search of protective strategies, we explore Spirulina, a high nutritional value microalga as a potential nutraceutical agent. Amphibians are a sensitive bioindicator model, given their complex ontogeny and high susceptibility to environmental contaminants. In this study, we investigated the effects of Spirulina supplementation on Cd-induced toxicity in *Rhinella arenarum* tadpoles. Larvae (Gosner 1-18) were collected from a controlled university pond, and larvae were exposed to acute and chronic toxicity assays (Gosner 25-30). In the first case, we fed one group with spinach and another one with Spirulina. After a week, we determined the LD_{50} (Lethal Dose 50%). In chronic assays we exposed the tadpoles for 15-30 days to sublethal Cd concentrations (0.25 and 0.5 mg/L) or to diets enriched with Spirulina (5–100%). Growth parameters (weight and total length) and developmental progression profile were assessed. These preliminary results showed that Cd exposure accelerated larval growth and metamorphosis in a dose-dependent manner while Spirulina supplementation reduced growth and delay development. Interestingly, Spirulina-fed tadpoles showed increased resistance to acute Cd toxicity and exacerbated Cd effects on growing and development also in a dose's dependent manner. These results suggest that while Cd accelerates metamorphosis as an adaptive survival strategy, Spirulina may act as a protective agent, accelerating development under toxic conditions and enhancing survival. Although preliminary, our findings suggest that Spirulina could represent a safe, accessible, and cost-effective nutritional strategy to mitigate cadmium toxicity. Given that Cd exerts its effects through oxidative stress—mechanisms conserved across species—Spirulina supplementation may offer translational benefits for human populations chronically exposed to this heavy metal. These results support further investigation into Spirulina as a potential protective agent in environmental and clinical toxicology.

NUTRITION AND HEALTH

A110

NEW LUMINESCENT METHODOLOGY FOR THE DETERMINATION OF Co(II) IN FOODS CONSUMED IN VEGETARIAN AND VEGAN DIETS

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Cobalt is an essential trace element for human and animal metabolism, including red blood cell production and the synthesis of DNA and fatty acids. Cobalt deficiency can cause megaloblastic anemia and affect the development of the nervous system and immune response. High intakes can cause polycythemia, hypothyroidism, and thyroid and heart failure. The determination of cobalt traces is of interest in clinical, biochemical, and toxicological analysis, especially in restrictive diets. For these reasons, the development of analytical methodologies with high sensitivity and precision for its quantification is necessary. The objective of this work was to develop a new methodology for the quantification of Co(II) in food samples using solid-phase fluorescence. The metal was determined by complex formation with 8-hydroxyquinoline (8-HQ), followed by solid-phase extraction with a nylon membrane in the presence of the anionic surfactant sodium dodecyl sulfate (SDS). Cobalt was subsequently quantified by solid-phase fluorescence ($\lambda_{em} = 460$, $\lambda_{exc} = 390$) with a detection limit of 4.3 10^{-2} ng L^{-1} and a quantification limit of 0.14 ng L^{-1}. The calibration curve was linear from 0.14 to 4.6 x 10^{3} ng L^{-1} of Co (II) ($R^2 = 0.9992$). Cobalt is found in foods of animal origin, as well as in dairy products, brewer's yeast, and certain nuts and green leafy vegetables. In this case, only those consumed in vegan and vegetarian diets will be selected. The samples were successfully analyzed, with an average recovery close to 100%. Reproducibility (inter-day precision) was evaluated over 5 days, performing five daily determinations, and the coefficient variance CV% obtained was 0.243. The solid-phase extraction method was used for the selective retention/preconcentration of Co (II), which is an effective tool for the sensitive determination of the analyzed samples. The good tolerance to high concentrations of regular foreign constituents demonstrates the high selectivity and versatility of the new methodology. Precision and accuracy were tested and validated by ETAAS with good agreement.

A111

DETERMINATION OF ZINC BY SOLID SURFASE FLUORESCENCE IN NATURAL ADAPTOGEN SAMPLES

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Zinc is an essential element for living organisms which plays an important role in the metabolism of proteins and nucleic acids, participating in the activity of approximately 100 enzymes and collaborating in the proper functioning of the immune system. Deficiency of Zn (II) is associated with growth retardation, impaired immune response, premature birth, weight loss and anorexia. On the other hand, adaptogens are a unique group of herbal ingredients used to improve the health of the adrenal system, which is responsible for managing the body's hormonal response to stress. Dietary supplements are often combined in clinical practice to achieve synergistic effects and consequently greater health benefits. The objective of this study was to develop a new method for monitoring zinc (II) in natural adaptogens and to demonstrate a potential magnifying effect on health benefits. The determination of zinc is proposed from the exaltation of the fluorescent metal complex o-phenanthroline (o-phen) and the dye eosin (eo), using filter paper as a solid supported (without pretreatment) by solid-phase fluorescence at λ_{em} = 440 nm (emission), using $\lambda_{ex}t$ = 370 nm (excitation). Under optimal experimental conditions, selective and quantitative retention of the metal was achieved, with a detection limit of 0.12 ng L^{-1} and a linearity range from 0.43 to 7.55 x10^5 ng L^{-1}.The methodology showed high sensitivity, good selectivity and adequate tolerance to possible interferents. It was applied to the determination of Zn (II) in a natural adaptogens samples with satisfactory results, representing a novel alternative to conventional methods for analysis of trace metals.

A112

PHYSIOLOGICAL REGULATION OF ACADEMIC STRESS: THE ROLE OF MINDFULNESS IN EXAM ANXIETY

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Mindfulness has established itself as an effective strategy for modulating the stress response by promoting an attitude of conscious, non-judgmental acceptance of the present moment, which fosters adaptive physiological and emotional self-regulation. This study aimed to analyse the correlation between exam anxiety (EA) and mindfulness (M) abilities in university students to provide evidence of the role of M in regulating academic stress. A quantitative, cross-sectional, descriptive, and correlational design was employed. The sample consisted of 81 students (85.1% women; 14.9% men; $\bar{x}$=25.06 years). The University Exam Anxiety Questionnaire (CAFEU), which assesses physiological, cognitive, and behavioural dimensions, and the Five Facet Mindfulness 4Questionnaire (FFMQ), which assesses five facets of M, were administered. Data collection was performed using electronic forms. Most common symptoms were gastric discomfort (70%) and insomnia (54%), which indicate a high prevalence of physiological stress activation, as well as negative anticipatory thoughts (65%). Seventy-four percent (74%) of participants reported moderate anxiety levels, 15% high levels, and 11% low levels. The highest-scoring dimensions of EA were physiological ($\bar{x}$=41.09) and cognitive ($\bar{x}$=34.14), followed by behavioural ($\bar{x}$ =17.33). The three EA dimensions were positively correlated with one another (r=.709, p<.001). Regarding M, the highest-scoring facets were Describing ($\bar{x}$=25.9), Observing ($\bar{x}$=25.35), and Acting with Awareness ($\bar{x}$=24.14). Correlations showed that the Acting with Awareness and Non-judging of Inner Experience facets were inversely related to anxiety levels across all three dimensions (p<.001), while Observing was positively associated with EA. Women presented higher levels of physiological and cognitive anxiety, and students who performed regular physical activity showed higher scores in Describing and Non-reactivity to Inner Experience. These AP dimensions can be considered adaptive coping mechanisms and protective factors that modulate the physiological response to stress. This supports the implementation of M training programs as a preventative health and wellness-promoting strategy.

A113

VALORIZATION OF NADES EXTRACTS FROM MALBEC GRAPE POMACE: ANTIPROLIFERATIVE EFFECTS ON PROSTATE CANCER CELLS

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Viticulture is the main agro-industrial activity in Mendoza, Argentina, producing large amounts of grape pomace waste rich in polyphenols with antioxidant and potential antitumor properties. This study evaluated the biological effects of Malbec grape pomace extracts (from organic and conventional crops) obtained with natural deep eutectic solvents (NADES, citric acid:glycerol:water, 1:3:9) on prostate cancer (PCa) cell lines with different aggressiveness and hormonal dependence (LNCaP, PC3, DU145), compared with aqueous extracts. Phenolic compounds were characterized by HPLC-UV. Cell proliferation (MTT), viability (Trypan Blue), and migration (wound healing) were assessed. NADES extracts contained higher levels of anthocyanins and total phenolic compounds (particularly gallic acid, quercetin, quercetin-glucoside, and myricetin) than aqueous extracts. NADES extracts exhibited stronger antiproliferative and cytotoxic effects across all PCa cell lines ($p < 0.05$). The NADES-extract from organic crops was more potent than conventional in DU145 and PC3 (IC50: 3.197 vs. 4.859 mg/mL and 3.649 vs. 7.339 mg/mL, respectively), while differences in LNCaP were not significant. Aqueous extracts displayed a similar trend, extracts from organic crops being more effective than conventional ones in DU145 and PC3, whereas the extract from conventional crops was more active in LNCaP. None of the extracts significantly affected cell migration. In conclusion, grape pomace extracts exerted antiproliferative and cytotoxic effects in PCa cells. While agronomic management (organic vs. conventional) produced modest differences, the extraction method was decisive, with NADES-derived extracts consistently outperforming aqueous ones. These results highlight the value of green extraction technologies to enhance bioactive metabolite recovery, and they support grape pomace as a sustainable source for functional food development and cancer prevention research.

A114

PROTECTIVE EFFECT OF GLUTAMINE AGAINST CADMIUM-INDUCED TOXICITY ON SERUM PARAMETERS AND INTESTINAL MORPHOLOGY

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Cadmium (Cd) is a toxic heavy metal that accumulates in several organs, causing severe health effects in humans and animals. However, its impact on intestinal structure and metabolism remains poorly understood. This study aimed to evaluate whether dietary glutamine could mitigate the adverse effects of Cd exposure. Adult male Wistar rats (180–200 g) were divided into four groups: (1) control (standard diet + drinking water); (2) control diet + Cd (50 ppm) in drinking water; (3) diet supplemented with glutamine micronized 3%g/l; and (4) diet with glutamine micronized 3% g/l + Cd (50 ppm) in drinking water. Feeding was ad libitum for 30 days. Before sacrifice, animals were fasted, and duodenal samples were collected and fixed for histological analysis. The samples were stained with haematoxylin–eosin and morphometry were performed with ImageJ software. Serum triglycerides (TG), total cholesterol (TC), HDL-C, and glucose were determined using Wiener kits. Cd exposure caused significant disruption of intestinal mucosal architecture. The simple columnar epithelium with microvilli exhibited cytoplasmic vacuolization in enterocytes, some resembling goblet cells, suggesting increased secretory activity or vacuolar degeneration associated with Cd treatment. Mononuclear inflammatory cell infiltration indicated a local inflammatory response. Disruption of the apical villus pole and loss of structural continuity were also observed, compromising absorptive function. In animals receiving glutamine along with Cd exposure, these histological alterations were markedly reduced, showing significant improvement in morphometric analyses. Cd exposure led to decreased serum TG and glucose levels, whereas glutamine supplementation prevented glucose reduction. HDL-C values remained unchanged across groups. Serum changes are consistent with intestinal morphological damage and may also suggest liver damage due to altered lipid profile. In conclusion, Cd exposure induces degenerative and inflammatory intestinal damage and alters serum parameters. Glutamine supplementation exerts a protective effect, improving both morphological and biochemical outcomes. Future studies should address whether these metabolic disturbances are primarily of intestinal or hepatic origin and confirm the observed trend toward increased total cholesterol in Cd + glutamine-treated animals. In conclusion findings could have implications for dietary recommendations in populations exposed to environmental pollutants.

A115

EFFECTS OF INTERMITTENT FASTING AS A NON-PHARMACOLOGICAL STRATEGY IN A D-GALACTOSE-INDUCED AGING MODEL

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Intermittent fasting (IF) is a non-pharmacological strategy capable of modulating energy metabolism, reducing oxidative stress, and promoting cellular longevity. The D-galactose-induced aging model reproduces oxidative, metabolic, and functional alterations similar to those observed during physiological aging. Several molecular pathways, including AMPK, SIRT1, NAMPT, mTOR, and NRF2, are involved in the regulation of energy homeostasis and antioxidant responses, and may be modulated by IF. Here, we investigated the effect of IF on enzyme activity and gene expressions in the heart in a D-galactose-induced aging model in rats. Wistar rats were randomly divided into three groups receiving daily: 1) physiological saline solution (CTL) via intraperitoneal injection (IP), 2) D-galactose 150 mg/kg (GAL) via IP and, 3) D-galactose 150 mg/kg via IP + IF protocol (GAL+IF) for eight weeks. The IF protocol consisted of alternating 24-hour feeding and 24-hour fasting cycles during D-galactose treatment. In heart tissue samples, gene expressions of *ampk1*, *mtor*, *sirt1*, *nampt*, and *nrf2* were assessed by RT-PCR, and catalase enzymatic activity was determined spectrophotometrically. The GAL+IF group showed a trend towards higher expression of *nampt* and *ampk1* and decreased *nrf2* compared with the other groups, while no significant differences were observed in *mtor* and *sirt1* expression or in cardiac catalase activity among groups. Previous results from the same model revealed notable metabolic improvements in the GAL+IF group, including reductions in body and liver weight, lower glucose and triglyceride levels, and higher HDL-c, as well as differential modulation of gene expression and enzymatic activity in liver and hippocampus. Intermittent fasting may exert modulatory effects on metabolic and antioxidant pathways in the heart. Although the changes observed were not statistically significant, the results, together with previous findings, suggest an organ-specific response to fasting. Overall, these data support the potential of intermittent fasting as a non-pharmacological protective strategy against D-galactose-induced aging and highlight the need for further studies integrating molecular and functional analyses across different tissues.

A116

EVALUATION OF A HIGH-FAT DIET ON METABOLIC ALTERATIONS AND ITS POSSIBLE RELATIONSHIP WITH COGNITIVE PERFORMANCE

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Previously, we established a nutritional model of adult obesity and characterized it anthropometrically, nutritionally, and metabolically. Some studies associate obesity and insulin resistance with cognitive impairments. Here, we analysed the effects of a high-fat diet from oleo-margarine on biomarkers of insulin resistance and spatial memory. To this end, two-month-old male Wistar rats were fed a high-fat margarine purified diet (HFM, n=12) for 14 weeks, while another group was fed a normocaloric (NC) purified diet (AIN-93M, NC group, n=12). All animals were maintained under 12h-light:12h-dark conditions and 22-24°C, with water and food ad libitum. Among the metabolic parameters we determined: body weight (BW), BMI, glucose (G) and insulin (Ins) levels, and the HOMA-IR index. For spatial learning studies, a modified version of the Barnes maze test was used. Our results showed that BW, BMI, G and Ins levels, and the HOMA-IR index increased significantly in the HFM group (all $p<0.01$). When we evaluated cognitive functions, we observed that in tests (T)1 and 2, which evaluate long-term, recent, and remote spatial memory, respectively, the HFM group: (a) made a greater number of errors ($p<0.05$); (b) exhibited a longer latency to the goal box during T2 ($p<0.05$); (c) explored the target sector less frequently in T1 and 2 ($p<0.05$ and $p<0.01$, respectively); (d) explored less frequently during T1 ($p<0.05$); (e) travelled a shorter distance during T1 and 2 ($p<0.05$ and $p<0.01$), compared to NC. In conclusion, it is possible that the effect of the high-fat diet, and the insulin resistance associated with obesity, may be able to induce alterations in the spatial memory of the animals.

A117

SOCIODEMOGRAPHIC, ANTHROPOMETRIC AND LIFESTYLE CHARACTERISTICS AND ZINC CONSUMPTION AMONG UNIVERSITY STAFF

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Zinc deficiencies are very common worldwide, especially in the most disadvantaged and developing populations, and can have negative effects on health. This study evaluated the consumption patterns of zinc-containing foods among university teaching and non-teaching staff and older adults to estimate the risk of zinc deficiency. The population was previously characterized according to demographic, socioeconomic, anthropometric, and lifestyle variables. The study's methodological design was descriptive and cross-sectional, with simple random sampling during the years 2018 and 2021. A validated and pilot-tested survey was used to determine reliability. From a sample of n = 679, n=394 belongs to teaching staff and n=285 to non-teaching staff. Most of them (79.3%), were adults, compared to 20.7%, of older adults. Concerning to sex, 62 % were female, versus 38% of male. 70.5% of adults and 90.8% of older adults reported some pathology, where the most prevalent in both groups were: high blood pressure, high cholesterol, hypertriglyceridemia and thyroid disorders. Regarding medication use: 55.4% of adults and 63.1% of older adults reported using them. In relation to nutritional status, more than half of adults (139) (56.3%) were overweight and only 1.5% were underweight; in contrast, among older adults, 25.5% were overweight and 18.4% were underweight. Referring to physical activity, 77.7% of adults and 81.6% of older adults practiced mostly 3-4 days a week. 22.3% of adults currently smoke; this percentage increases to 50.4% among older adults. On the other hand, 91.1% of adults and 95.8% of older adults reported psychological stress. Regarding zinc consumption, a higher percentage of zinc deficiency was observed in the older adult group (61%) compared to adults (24%). This deficiency was observed mostly in men, both in adult and older adult groups. Considering the importance of zinc in the human body and the impact of its deficiency on health, especially in old age, interdisciplinary actions, supported by scientific evidence, are required to propose, implement, and evaluate different public health policies and programs to prevent and reduce zinc deficiency in the population and thus contribute to promoting healthy aging.

A118

ANTI-INFLAMMATORY DIETARY PATTERN EFFECT COMBINED WITH 16/8 INTERMITTENT FASTING ON ANTHROPOMETRIC AND CLINICAL PARAMETERS IN OVERWEIGHT ADULTS

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Nutritional interventions based on anti-inflammatory dietary patterns and intermittent fasting (IF) strategies are positioned as integral tools in the prevention and management of chronic metabolic diseases. The objective of this study was to evaluate the impact of a time-restricted eating (16/8) protocol, combined with a low-carbohydrate diet rich in healthy fats and high biological value proteins, on anthropometric and clinical parameters in overweight or obese adults. Sixty adults (30 women and 30 men) participated over a period of six consecutive months, under personalized functional nutritional follow-up. The dietary pattern was based on natural foods, minimizing ultra-processed foods, refined sugars, and industrial vegetable oils, prioritizing anti-inflammatory sources such as fish, olive oil, avocado, nuts, and low-glycemic index vegetables. Significant reductions ($p<0.05$) were observed in body weight, fat percentage, and abdominal circumference, along with improvements in blood glucose, triglycerides, cholesterol, and LDL cholesterol levels. Average pre- and post-treatment values were: blood glucose 130 mg/dl to 95 mg/dl, triglycerides 170 mg/dl to 98 mg/dl, total cholesterol 240 mg/dl to 195 mg/dl, and LDL cholesterol 110 mg/dl to 90 mg/dl. Adherence to the protocol was high (82%), with good tolerance to the schedule and a subjective perception of greater energy and satiety. The results suggest that combining intermittent fasting with an anti-inflammatory diet may promote metabolic homeostasis and contribute to a reduction in cardiometabolic risk, representing a sustainable and accessible therapeutic strategy in the current clinical context.