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Creating with-science: Technological advances and their challenges in biology

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A01

APPLICATION OF *DE NOVO* TRANSCRIPTOMICS TO THE STUDY OF THE PEANUT–FUNGAL PATHOGEN INTERACTION: BIOINFORMATICS CHALLENGES AND SOLUTIONS

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Argentina is the world's leading exporter of peanut (*Arachis hypogaea*), with more than 70% of national production concentrated in the province of Córdoba. Peanut smut, caused by *Thecaphora frezii*, has become the most relevant disease affecting this crop in recent years. Current management strategies, including crop rotation and fungicide application, remain insufficient. There is a need to generate new molecular knowledge to support the design of innovative control strategies. The absence of fully annotated genomes for cultivated peanut varieties and *T. frezii* limits understanding of plant–pathogen interactions at the molecular level. *De novo* transcriptomics provides a robust alternative to characterize the expressed gene repertoire without relying on reference genomes. Here, we present a bioinformatic pipeline integrating *de novo* assembly, transcript quantification, differential expression analysis with DESeq2, and functional enrichment using topGO. The workflow was applied to RNA-seq data from *T. frezii* and three peanut varieties exhibiting contrasting responses to infection. This strategy generated high-quality reference transcriptome assemblies and enabled the identification of differentially expressed genes during early infection stages. Functional enrichment analyses revealed key biological processes associated with pathogenicity and host defense. These results provide a framework for the selection of RNA interference target genes and the construction of functional networks. Moreover, this approach can be applied to the study of other fungi affecting peanut crops and, more broadly, to diverse plant–pathogen interactions.

A02

EFFECT OF COVER CROPS ON THE ABUNDANCE AND RICHNESS OF SOIL MACROFAUNA IN LAS ROSAS (SANTA FE)

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The objective of this study was to evaluate the changes in soil macrofauna communities in crop sequences that included different cover crops (CC). The experiment was conducted in Las Rosas (Santa Fe, Argentina), on a typical Argiudoll soil. The treatments analyzed were four plots with different CC and soybean as the cash crop, as well as a control plot with fallow. The CC considered were: oat (*Avena sativa*), vetch (*Vicia sativa* and *Vicia villosa*), and a mix of vetch, oat, and radish (*Raphanus sativus*). Sampling was carried out in May 2025 and consisted of extracting five soil monoliths of 25 cm on each side and 20 cm deep, from each plot. Samples were manually inspected in laboratory to collect the macrofauna organisms present, which were then placed in a 70% alcohol solution. Abundance (number of organisms) was determined by manual counting, while richness (number of taxa) was defined through taxonomic identification of the collected specimens down to the family level. Results were statistically analyzed using Generalized Linear Models and Fisher's LSD test for the comparison of means ($\alpha=0.05$). No significant differences were found between treatments for any of the variables evaluated ($p>0.05$), but the observed trends were similar. The highest average abundance corresponded to *V. villosa*-soybean (15.6 ± 2.5 organisms) and the CC mix-soybean (14.6 ± 2.4 organisms), while the lowest abundance was observed in oat-soybean (10.8 ± 1.9 organisms). Similarly, the first two treatments also had the highest richness (4 ± 0.87 taxa in *V. villosa*-soybean and 3.4 ± 0.8 taxa in the CC mix-soybean), while the lowest was detected in fallow-soybean (2.8 ± 0.8 taxa). The results are consistent with the idea that the quantity and quality of organic materials provided by CC directly influences the presence of soil macrofauna organisms, especially vetch that provides residues that are easily utilized by these organisms, resulting in an increase in their abundance and diversity. Likewise, variations in soil organism's communities also respond to changes in the soil environment, primarily due to the effects of CC roots on soil structure and porosity. In conclusion, the inclusion of CC in crop sequences favorably modified the community parameters of soil macrofauna, with variations observed in relation to the species included. However, it is necessary to continue evaluating the site in order to define trends associated with different crop sequences that also take into account interannual variability in soil conditions.

A03

ASSESSMENT OF VEGETATIVE VARIABLES OF THREE *Vitis vinifera* L. VARIETIES IN A VINEYARD IN SOLDINI, PROVINCE OF SANTA FE, ARGENTINA

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Although the Cuyo region has historically led the winemaking sector in Argentina, in recent years wine grape growing has resurged in the province of Santa Fe as well as in other provinces. Even though the activity is incipient, there are established enterprises in the Province of Santa Fe, such as *Don Esteban* vineyard in Soldini, where this research was carried out. The objective was to assess vegetative variables of wine grapes under the soil and climate conditions of the region with the aim of providing technical information to support the development of viticulture in Santa Fe. Vines were planted in November 2018, in a bilateral Royat training system with a trellis, in a 1.0 m × 3 m within and between row layout, with rows-oriented N-S. The varieties studied were Tempranillo, Malbec and Ancellotta, all of them ungrafted. The variables assessed were vegetative development (calculated from pruning weight), vigor (average weight of canes), stem diameter, and Ravaz Index (vine balance calculated as the ratio between reproductive and vegetative production of the vine), following a completely randomized design with 12 replicates per variety. Data were analyzed with InfoStat statistical software, and analysis of variance and comparisons of means between treatments were performed with the Tukey's test with significance value set at 0.05. No significant differences in vegetative development were found between the Tempranillo and Malbec varieties, but they both differed significantly from Ancellotta vines, which had the lowest pruning wood weight (135.33 g). Vigor did not vary significantly among the three varieties, although Tempranillo had the highest average value (27.33 g per cane) followed by Malbec and Ancellotta (26 and 17 g respectively). While vigor values for Tempranillo and Malbec are within the 20-40 g range considered optimum for balanced vines with moderate vigor, Ancellotta needs to increase cane vigor. Stem diameter differed significantly between varieties, with Tempranillo showing the highest value (4.23 cm), nearly twice that of Ancellotta (2.44 cm). The Ravaz Index results were 7.43 for Malbec, a near-threshold value of 9.69 for Tempranillo, and 11 for Ancellotta. Values above 10 mean that the vines are producing more fruit than the plant can support, with the risk of failure to produce fruit and even plant death due to low cane vigor. Also, a high Ravaz Index value can negatively affect grape quality. In conclusion, the best results for the variables evaluated under the soil and climate conditions of the region were obtained for the Tempranillo and Malbec wine grape varieties.

A04

IMPACT OF AGROECOLOGICAL AND CONVENTIONAL MANAGEMENT ON THE SANITARY QUALITY OF SEEDS IN EXTENSIVE CROPS

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All seed production is conditioned by multiple quality factors, including sanitary quality. This factor has a high impact on germination power, the presence of mycotoxins and the presence of inoculum in stubble. Biological control using microorganisms such as *Trichoderma* spp or *Bacillus* spp. would act in defence of the plant through competition. Agroecological models emerged as a new practice for the sustainability of agricultural systems, in contrast to conventional models. The objective was to evaluate the frequency of pathogens present in soybean, corn, and wheat seeds/grains from two contrasting models: agroecological vs. conventional, and the effect of *Trichoderma* (Tch) as a biological agent on sanitary quality. The trial was conducted in the SIPA (Integrated Agroecological Production System) production module of the Faculty of Agricultural Sciences, where plots A, B and C are surrounded by a biodiversity border and managed agroecologically. Plots D and 22 are production plots managed conventionally. The following were determined in the seed samples: germination power (GP); incidence (I%) and frequency - Fr (number of pathogen colonies out of total seeds) of pathogens (Pg). The seeds were incubated in dextrose potato agar with alternating 8/16-hour light/dark cycles (ISTA rules). A total of 200 seeds from each crop were analysed and identified using a magnifying glass and microscope. To evaluate the effect of Tch, blotter tests were performed with treated seeds (Tch inoculum). The blotters were incubated in an oven for 7 days, except for wheat, which was previously subjected to 24 hours of cold treatment. There were differences between batches with respect to Fr (Duncan's test –ANOVA). Fr in soybeans was: *Rhizoctonia*, *Nigrospora*, *Fusarium graminearum*, *F. verticillioides*, *Cercospora*, *Aspergillus flavus*, and *Alternaria* in batches B and C. In maize, Fr was: *F. verticillioides*, *F. graminearum*, *Aspergillus flavus*, *Penicillium*, *Stenocarpella* and *Alternaria*, where both batches (22 and A) had a similar incidence of Pg. In wheat, Fr was *Alternaria* as the pathogen with the highest incidence in batches C and D. With regard to PG, in soybeans, there were significant differences between plots B and C and plot D, with intermediate values (~50%) (F: 10.68, p: 0.0001). In maize, there were differences, with plot 22 presenting a high PG (~85%), while plot A had values of ~55% (F: 15.48, p: 0.0003). In wheat, both plots showed a PG close to 0%, indicating a total loss of viability (F: 1, p: 0.324).

In the biological control trial, the seeds had a low presence of fungal Pg; PG was higher in treated seeds (Tch), with significant root development in maize. The presence of fungal pathogens in seeds was evident in an agroecological system compared to a conventional one. The results show that seed quality is influenced by species, cultural/chemical or genetic management, and the presence of stubble or alternative hosts. Biological control played a significant role in the management of fungal pathogens and as a root growth stimulator.

A05

EFFECT OF ORGANIC SOIL AMENDMENTS ON ALMOND TREES ESTABLISHMENT

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The incorporation of organic amendments in intensive production systems is a strategy to improve soil quality and enhance production sustainability. Compost derived from deep-litter pig farming systems represents a potential nutrient source, while humic substances act as organic soil amendments that improve soil properties, nutrient use efficiency, and water availability. However, information on the effects of these amendments on fruit crops is scarce at the national level. The objective of this study was to evaluate the incorporation of deep-litter pig compost (DLP) and humic substances (HUMIPLEX® 50G) on almond tree establishment. The experiment was conducted on almond trees (*Prunus amygdalus* (L.) Batsch), cultivar Nonpareil, grafted onto Nemared rootstock, planted in August 2024 in Zavalla, Santa Fe, Argentina. Treatments consisted of: control (T1); DLP at 10 t ha⁻¹ (T2); DLP at 15 t ha⁻¹ (T3); and HUMIPLEX® 50G at 40–50 kg ha⁻¹ (T4). Amendments were applied to the planting holes at planting. The experimental design was a randomized complete block with three replicates of three plants per treatment. Plant height, stem circumference of rootstock and scion, and canopy diameter were measured at planting and six months after planting. Data were analyzed using ANOVA and Tukey's test ($p \leq 0.05$). Six months after planting, T4 showed significantly higher rootstock circumference, plant height, and canopy diameter compared with the control. Compost treatments did not differ significantly from either the control or HUMIPLEX® 50G. Compost application reduced the need for synthetic fertilizers, while humic substances promoted superior early plant establishment.

A06

EVALUATION OF THE NUTRITIONAL PROFILE AND AGRONOMIC TRAITS OF DIFFERENT LENTIL (*Lens culinaris* Medik.) VARIETIES

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Lentil (*Lens culinaris* Medik.) is a crop of great importance worldwide, particularly in developing countries, due to its high content of proteins, carbohydrates, vitamins, and minerals such as iron and zinc. In recent years, the global demand for pulses has increased and this trend is expected to continue. Therefore, it is necessary to improve production levels through comprehensive approaches that consider diversity, yield, and quality, to generate alternatives that satisfy population nutritional needs, improve agricultural productivity, and promote sustainable development. In Argentina, lentil is mainly cultivated/grown in the northern Pampas region and is a good alternative to wheat crops, due to its ability to fix atmospheric nitrogen in the soil within crop rotation systems, contributing to more sustainable agriculture. The objective of this study was to compare the nutritional profile and agronomic performance of eight pre-commercial varieties from the INTA FCA UNR breeding program (A6, A12, A16, A25, A32, A55, BT1, 12R) and two commercial varieties (Silvina, Turca). During 2024/25 growing season, these ten varieties were sown at EEA Oliveros in a randomized complete block design with three repetitions. Days to flowering and harvest yield were evaluated. Samples from each repetition were ground, homogenized to a particle size of 250 microns, and analyzed in duplicate under laboratory conditions. The following parameters were determined: protein content (% dry basis), dry matter (%), and soluble proteins, using the corresponding standardized IRAM methods. Analysis of variance (ANOVA) and mean comparison using Fisher's LDS test were performed with InfoStat Software. All variables analyzed, except soluble protein, showed significant differences ($p < 0.05$) between varieties. The mean protein content was $25.93 \pm 1.22\%$ (db), Turca, Silvina, and 12R showed the highest protein content (27.40, 27.22, and 27.18% db, respectively), while variety A16 showed the lowest value (23.94% db). Regarding agronomic traits, A6 and A55 were the varieties that reached the earliest flowering (97 days), while Turca was the latest (117 days). In addition, the pre-commercial lines A32 and A25 showed the highest yields (893.57 ± 52.93 and 866.29 ± 236.38 , respectively), despite having intermediate protein contents (25.02 ± 0.61 and 25.58 ± 0.14 , respectively). These results are interesting for the breeding program. Materials like A32 and A25 were identified as potential commercial varieties in the future. Furthermore, this information could be used for parent selection, so that their crosses may be used as a starting point for the development of lentil varieties with high yield potential and elevated protein content.

A07

IN VITRO BEHAVIOR OF DIFFERENT EXPLANTS OF *Cannabis sativa*

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Within plant tissue culture techniques, several aspects influence the response of the evaluated species, including the culture medium used, the combination of plant growth regulators, and the explants used to initiate the cultures. The objective of this work is to present the in vitro response of different *Cannabis sativa* explants. The explants evaluated were: 1- seeds, 2- nodal segments, 3- leaves, and 4- female inflorescences (cymes). The media evaluated depended on the type of explant, but all consisted of Murashige and Skoog salt base and Gamborg vitamins. The energy source used was sucrose at 30 g L⁻¹, and the pH was adjusted to 5.8. The cultures were solidified with 7 g L⁻¹ agar. The growth regulators used were 6-benzylaminopurine (BAP) and naphthaleneacetic acid (NAA). A medium containing metatopolin, specific to cannabis, was also evaluated. For explant disinfection, different immersion times (between 5 and 10 minutes) were used in sodium hypochlorite (2 to 3% active chlorine) with Tween 20, followed by a triple wash with sterile distilled water. Growth conditions were 27 ± 2°C with a 16-hour photoperiod. 1- Seeds germinated between 3 and 7 days, depending on the variety. The time from germination to transplanting to soil was one month. Vigorous mother plants and seedlings were obtained from these explants. 2- Nodal segments regenerated vigorous shoots 20 days after *in vitro* sowing. 3- 4- Callus formation was observed on leaves and flower cymes. High-performance liquid chromatography (HPLC) was performed on these calluses to determine THC (tetrahydrocannabinol) and CBD (cannabidiol). These compounds were found in calluses from flower cymes but not in those from leaves. The species responds favorably to in vitro culture, and it is feasible to regenerate complete plants from seeds and nodal segments. Callus production should be more efficient in cannabinoid production; future work will evaluate other explants such as anthers and meristems.

A08

**ANTIOXIDANT CAPACITY OF GREEN ASPARAGUS (*Asparagus officinalis* L.)
GENOTYPES UNDER POSTHARVEST TREATMENTS**

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Asparagus is a semiperennial horticultural crop with high nutraceutical value, mainly due to antioxidant compounds present in its spears. Preserving these compounds and their properties during postharvest is crucial to maintaining spears quality. The aim of this study was to compare the antioxidant capacity of green asparagus genotypes and its relationship with different postharvest treatments. Plant material included three experimental hybrids (E1, E2 and E3) from the UNR breeding program, and the commercial cultivar 'Atticus'. The four genotypes were grown at the Horticultural Section of the Facultad de Ciencias Agrarias (FCA-UNR) in a randomized complete block design with three replications of ten plants each, arranged in rows 140 cm apart and with 20 cm between plants. In spring 2024, 20 cm long spears were harvested and were subjected to four postharvest treatments: T1 (harvest without hydrocooling), T2 (harvest with hydrocooling), T3 (storage for 10 days at 4 °C without hydrocooling), and T4 (storage for 10 days at 4 °C with hydrocooling). For each genotype and treatment, at least five spears per replication were used. Methanolic extracts were obtained from 0.2 g of dried plant tissue (spears) from each sample/replication. The antioxidant capacity of the extracts was determined using the 2,2-diphenyl-1-picrylhydrazyl (DPPH) method, with a solution 0.1 mM in 70% methanol, incubated in darkness for 30 min at room temperature, and the absorbance was read at 517nm using a Perkin Elmer Lambda Bio+ spectrophotometer. Antioxidant capacity was expressed as the percentage of radical inhibition (%I) and calculated using the equation: %I=[(Abs. Control – Abs. Sample) / Abs. Control] x 100, where 'Abs. Control' is the absorbance of DPPH + Methanol (1:1) solution, and 'Abs. Sample' was the absorbance of each sample with DPPH. Three replicates were performed for each sample/replication. Statistical analysis (ANOVA, Fisher's LSD, $\alpha = 0.05$) revealed significant differences among genotypes ($p = 0.0056$), with the highest values for E3 and E2 (85.8% and 81.3%, respectively). No significant differences were detected among treatments or for genotype × treatment interaction (0.0546 and 0.6879, respectively). Genotype differences were detected only under T3 conditions ($p = 0.0131$), where the genotypes E3 and Atticus exhibited the highest antioxidant activity (87.3% and 85.4%, respectively). These results suggest that antioxidant capacity in green asparagus is mainly genotype-dependent, and storage at 4 °C without hydrocooling is an adequate postharvest treatment to preserve antioxidant properties.

A09

ARTHROPOD ASSEMBLAGES IN DIFFERENT ENVIRONMENTS OF THE SAN JORGE NATURAL RESERVE, FUNES (SANTA FE)

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The so-called "San Jorge Reserve" (Funes, Santa Fe), located upstream from the Ludueña stream retarding dam within its floodplain, comprises approximately 500 ha with a high diversity of environments, ranging from floodable grasslands to shrublands. Despite its ecological relevance, the arthropod fauna of the area remains an incipient field of research requiring more exhaustive characterization. Generating knowledge about this group is fundamental for evaluating habitat heterogeneity, ecosystem-level biodiversity, and the ecological integrity of the reserve, thus providing key information for the design and implementation of effective management and conservation strategies. The objective of this study was to characterize the arthropod communities present during the spring-summer period across different environments of the San Jorge Reserve. Two sampling campaigns were conducted (11/24 and 12/24) in a 5000 m² sector covering 140 m of the Ludueña stream bank (32°57'S; 60°47'W). Four environments were selected: two low-lying areas (a clayey beach with halophytic vegetation dominated by *Cyperus brevifolius* and a cordgrass field dominated by *Sporobolus spartinae*) and two elevated areas (a natural levee with herbaceous vegetation and another with native woody vegetation). In each environment, 5 pitfall traps were placed 10 m apart. Each 11 cm diameter trap contained 200 cm³ of preservative solution (5% acetic acid + 2.5% formalin) and captured arthropods for 7 consecutive days. Richness, abundance, and diversity were calculated for each environment, and differences were evaluated using ANOVA. Samples were ordered using Detrended Correspondence Analysis (DCA), specific composition was analyzed through MRPP (Multi-Response Permutation Procedures), and an Indicator Species Analysis was performed. A total of 5049 individuals from 163 different species/morphospecies were captured, grouped into 4 classes, 20 orders, and 84 families. Overall, 65% of the material was identified to species level, 10% to genus, and the remaining 25% as distinct morphospecies. Eight trophic groups were detected. The most species-rich groups were predators (53%), herbivores and detritivores (39% and 35%), and ants and parasitoids (13% and 10%). Regarding abundance, 89% corresponded to ants (42%), detritivores (26%), and predators (21%). Species composition did not differ between sampling dates ($T = 1.478$; $P = 0.085$) or relief types ($T = 1.841$; $P = 0.056$), but significant differences were found between treatments ($T = -9.420$; $P < 0.001$). Data ordering differentiated the clayey beach from the woody levee along Axis 1, which may represent soil moisture. Although the cordgrass field is a low-lying area, it was dry during the sampling period, and its samples overlapped with those of the herbaceous levee. The highest arthropod abundance and richness were detected on the beach and were lowest in the cordgrass field; the other environments showed intermediate values. Evenness and the evaluated diversity indices did not differ among environments. The Indicator Species Analysis detected 29 species with high fidelity to the four studied environments. The habitat heterogeneity characterizing the San Jorge Reserve provides the necessary conditions to sustain high arthropod diversity, enhancing its value as a conservation enclave in an environment subject to strong anthropogenic pressures.

A10

FIRST INVENTORY OF THE INVERTEBRATE FAUNA OF THE SAN JORGE NATURAL RESERVE, FUNES (SANTA FE)

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The "San Jorge Reserve" comprises an area of approximately 500 ha within the Ludueña stream floodplain, upstream from the retarding dam in the Municipality of Funes. The relief is slightly concave, featuring internal lagoons and several drainage channels towards the main stream bed. Low-lying areas consist of floodable grasslands with halophytic vegetation, while higher areas host isolated tree and shrub species, including both native and invasive exotics. Topographic and floristic characteristics define distinct environments that harbor high faunal diversity. Knowledge of the local arthropod fauna is a key tool for understanding habitat heterogeneity, evaluating biodiversity across multiple scales, and monitoring the environmental health of ecosystems. The objective of this work was to compile the first checklist of arthropods present in different environments of the San Jorge Reserve. Two sampling campaigns were conducted in November and December 2024 within a 5000 m² sector covering 140 m of the Ludueña stream bank (32°57'S; 60°47'W). Four environments were selected: two low-lying areas (a clayey beach with halophytic vegetation and a cordgrass field) and two elevated areas (natural levees, one with herbaceous vegetation and another with native woody vegetation). In each environment, 5 pitfall traps were placed 10 m apart. Each 11 cm diameter trap contained 200 cm³ of preservative solution (5% acetic acid + 2.5% formalin) and collected arthropods for 7 consecutive days. These were supplemented by direct observation records obtained during trap placement and by searching under dry logs or leaf litter. The material, preserved in 70% ethanol, was identified to species level or assigned to distinct morphospecies. A list of 213 species/morphospecies is presented, grouped into 7 classes, 24 orders, and 101 families. Overall, 73% of the specimens were identified to species level, 8% to genus, and the remaining 19% as distinct morphospecies. The class Insecta accounted for 85% of the richness (S), followed by Arachnida (11%). Five orders concentrated 72% of S: Coleoptera (27%), Lepidoptera (14%), Hymenoptera (13%), Diptera (9%), and Araneae (9%). The families with the highest richness were Carabidae (7%), Formicidae (6%), Nymphalidae (4%), Lycosidae (3%), Curculionidae (3%), and Tenebrionidae (2%); the remaining 91 families showed very low S. The most diverse trophic groups were

herbivores and predators (35% and 31%), followed by detritivores (16%), ants (6%), and parasitoids (5%). Thirteen ant species from 5 functional groups were detected; among them, tropical climate specialists, generalist Myrmicinae, and subordinate Camponotini were the most species-rich groups (69%). Among the 15 Carabidae species detected, mesophilic species predominated in elevated environments and the cordgrass field, while hygrophilic and riparian species prevailed on the beach, notably including a "bombardier beetle" (*Pheropsophus aequinoctialis*) which is very rare in the region. The high arthropod richness found positions the reserve as a strategic site for biodiversity conservation, rendered even more significant by its location within a landscape under heavy anthropogenic pressure.

A11

OPTIMIZATION OF A GENETIC TRANSFORMATION PROTOCOL IN *Eragrostis curvula*: VALIDATION USING THE RUBY REPORTER GENE

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Eragrostis curvula is a warm-season forage species widely cultivated in arid and semi-arid regions due to its high tolerance to drought and low soil fertility. However, its predominantly apomictic reproduction restricts conventional breeding, making genetic transformation a key strategy for genetic improvement. Despite its relevance, transformation efficiency in this species remains low, limiting its application in functional genomics and trait development. Here, we established and optimized an *Agrobacterium tumefaciens*-mediated transformation protocol for *E. curvula* cv. Tanganyika INTA using strain EHA105 harboring the pUBI::RUBY construct. The *ruby* reporter gene enables rapid, non-destructive visualization of transgene expression through betalain accumulation. Somatic embryos derived from the shoot apical meristem were infected and subjected to a combined strategy including mechanical sectioning to enhance bacterial access, heat treatment (43 °C for 4 min), and vacuum infiltration (720 mmHg for 4 min). Regenerated plantlets obtained from treated explants showed visible red pigmentation under stereomicroscopic observation, confirming ruby expression, whereas untreated controls exhibited no detectable signal. Based on the number of infected explants and expressing plantlets, preliminary transformation efficiency was estimated at approximately 6%, pending molecular confirmation by PCR. The integration of wounding, heat shock, and vacuum infiltration significantly improved transgene expression compared with non-treated explants. This optimized protocol provides a reproducible platform for genetic transformation in *E. curvula* and establishes *ruby* as an effective visual reporter system. These advances represent a critical step toward functional gene analysis and future genome editing applications in this agriculturally important apomictic species.

A12

ANALYSIS OF *IN VITRO* REGENERATION FROM THE SHOOT APICAL MERISTEM OF MATURE EMBRYOS OF *Eragrostis curvula* UNDER DIFFERENT CULTURE MEDIUM COMPOSITIONS

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Plant biotechnology is a fundamental tool for genetic improvement and functional study of genes in Poaceae species. In species such as *Eragrostis curvula* -a C4 grass of high forage value, and a model species for the study of drought tolerance and apomictic reproduction-, *in vitro* regeneration represents a critical bottleneck for transformation and genetic editing. The efficiency of this process depends greatly on the type of explant and the culture medium's composition. Although immature inflorescences have been the most efficient explants, their availability is limited to the species flowering period. Thus, mature embryos are a strategic source of material that is available all year round, even if their regenerative capacity requires further optimization. The objective of this study was to analyze the effect of the culture medium composition on the inductive capacity of shoot apical meristem (SAM) of mature embryos of *E. curvula* cv. Tanganyika INTA. Specifically, the induction of embryogenic structures and/or multiple shoots in response to the different media was studied, paying special attention to the combination of plant growth regulators and nutritional supplements. At the same time, the effect of a subculture to fresh medium three weeks into the process was compared to keeping the explants on the initial induction medium for six weeks. Four culture media were tested based on Murashige and Skoog (MS), with modifications in their concentrations of macronutrients, vitamins, amino acids, hydrolyzed casein and gelling agents (Phytigel™ at 0.3% or 0.5%). All media had 3% of maltose and different combinations of growth regulators 6-benzylaminopurine (BAP) and 2,4-dichlorophenoxyacetic acid (2,4-D). Medium 1, 3 and 4 had BAP (8.9 µM) and 2,4-D (2.2 µM), Medium 2 had the inverted concentration of both phytohormones. The cultures were maintained under a light intensity of 55.2 µmol m⁻² s⁻¹, a photoperiod of 16/8 hours and a temperature of 25 ± 2 °C. For each medium, four replicates of 40 explants were used. Half of the replicates (two per medium) were subcultured after three weeks of culture. Logistic regression analysis revealed that culture medium had a highly

significant effect on morphogenic induction ($\chi^2 = 69.8$; $df = 3$; $p < 0.001$). Medium 3 was the most efficient, followed by Media 1, 4 and 2. The "subculture" factor on its own was not statistically significant ($p=0.086$), but it did show a significant interaction with the culture medium ($\chi^2 = 16.1$; $df = 3$; $p = 0.001$). The lack of subculture significantly increased the induction rate in Media 1 (OR = 7.7), 4 (OR = 5.2) and 2 (OR = 12.7). In contrast, induction in medium 3 was high and stable regardless of subculture. This study contributes to the establishment of efficient regeneration protocols for *E. curvula*, which is essential for genetic transformation and biotechnology-assisted breeding.

A13

PRELIMINARY FLORISTIC SURVEY IN FUNES (SANTA FE) TROUGH CITIZEN SCIENCE: EVALUATING iNATURALIST AS A COMPLEMENT TO TRADITIONAL MONITORING AND CONSERVATION METHODS

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Citizen science, driven by platforms such as iNaturalist, has established itself as a powerful tool for collecting up-to-date biodiversity data. This study evaluates the effectiveness of this platform as a complement to rather than a replacement for traditional floristic surveys, while simultaneously fostering collaboration and mutual learning. In Argentina, the "ArgentiNat" site operates as the national node of the iNaturalist network. The primary objective of this research was to explore the potential of iNaturalist to generate a preliminary inventory of the flora of Funes (Santa Fe), with a specific focus on native species. Given the absence of prior site-specific inventories, the evaluation was based on the analysis of the percentage and characteristics of observations reaching "Research Grade" (RG). This platform criterion establishes a quality and reliability threshold to observations containing dates, coordinates, photographs, and at least two concurring identifications by the community. The inventory composition was contrasted with expected botanical family patterns for the Pampean ecoregion, alongside the mapping and analysis of temporal and taxonomic biases. Georeferenced data from urban areas and the San Jorge Reserve were collected through individual observations and collaborative citizen science events, such as the Fundación Vida Silvestre Safaris and the City Nature Challenge. From a total of 1,247 observations analyzed (2017–2025), 654 records of native flora were identified, forming the core dataset. Among these, 80.89% achieved RG status. A total of 160 vascular plant species belonging to 48 families were recorded by 37 observers and 107 identifiers. The complete list is available for consultation in the "Flora Argentina en Funes" Collection Project on the iNaturalist platform. The families with the highest species richness align with expectations for Pampean ecosystems: Asteraceae (27 taxa), Solanaceae (17), Poaceae (11), and Malvaceae (11), suggesting that iNaturalist data accurately reflect ecological patterns. Notable findings relevant to conservation include the presence of *Sporobolus spartinus*, highlighting the value of urban reserves and green spaces in Funes as biological corridors and floral reservoirs. This study demonstrates that iNaturalist is an efficient and complementary tool for expanding floristic knowledge and establishing baseline data in urban conservation planning. Although limitations persist regarding unequal observation distribution and taxonomic precision in certain groups, the established protocol provides sufficiently robust data to detect general patterns and key species. Community participation not only generates valuable data but also fosters a connection with nature that is essential for conservation amidst rapid urbanization. We recommend promoting training activities and periodic monitoring to strengthen record quality for urban conservation plans, as well as designing specific field days to target underrepresented groups, such as the Poaceae family.

A14

SELECTION OF AGRONOMICALLY SUPERIOR VARIETIES IN LENTIL (*Lens culinaris* MEDIK)

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Lentil crop faces significant production challenges. Its expansion has been limited by factors such as the scarcity of varieties adapted to local conditions and their susceptibility to various diseases and adverse conditions. Therefore, the development of new varieties is imperative. Our lentil breeding program seeks to overcome these limitations by introducing new varieties that exhibit higher yields, disease resistance, tolerance to adverse environmental conditions, and improvements in nutritional quality. The objective of this work was to identify lentil varieties with superior agronomic characteristics for their subsequent use as parents in breeding programs. To this end, 25 lentil varieties from the active seed bank of Plant Gene Resources of Canada, recently introduced into our germplasm collection, were characterized morphologically and productively. The varieties were sown in June 2024 at the "J. F. Villarino" Experimental Field of the Faculty of Agricultural Sciences (UNR), in 3 m long plots with 60 plants, in a completely randomized block design with 2 replications. Qualitative traits were evaluated and the frequency of each was determined in the analyzed genotypes. The following quantitative traits were analyzed: Plant

height (PH), Days to 50% flowering (DF), Number of flowers per peduncle (NFP), Number of pods per plant (NPP), Seed size (mm) (S), Weight of 100 seeds (g) (W), and Yield/plant (g) (Y). Analysis of Variance, comparison of average values using Tukey's test, and a Principal Component Analysis (PCA) were performed to select superior varieties using the Info-Stat program. The frequency distribution indicated the presence of variability for the qualitative traits studied. Only 38% of the genotypes exhibited anthocyanin pigmentation in the stem; the majority showed upright growth habit (59%), intermediate branching intensity (62%), oval leaflet shape (69%), white flowers with violet veins, brown seed color (72%) with a smooth pattern (83%), and yellow cotyledon color (93%). The Shapiro-Wilk normality test showed a normal distribution for all quantitative traits. The analysis of variance showed significant differences between genotypes ($p < 0.01$), demonstrating the existence of phenotypic variability for all evaluated traits. The PCA showed that the first two components (PC) explain 58% of the total variability observed between genotypes. The variables that contributed most to PC1 were NPP, NFP, DF, and Y. The CP2 group was primarily composed of the variables PH, S, and W. The group comprising the genotypes CN51, CN46, CN39, and CN64 stood out for its earliness and presenting the highest values for Y and its components (NPP and NFP), positioning them as promising varieties for inclusion in future breeding programs aimed at increasing productivity and shortening the crop cycle. This group also shares the common characteristic of possessing genes for resistance to different races of anthracnose, making them ideal for use as parents in crosses to obtain new improved varieties.

A15

OBTAINING TRANSGRESSIVE SEGREGANTS FOR PRODUCTIVE AND QUALITY TRAITS IN THE LENTIL (*Lens culinaris* Medik) CROP

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In the lentil crop, it has been shown that hybridizations between *macrosperma* (A) and *microsperma* (R) subspecies can generate transgressive segregants (TS) for seed yield; however, this has not yet been studied for quality traits. The objective of this work was to obtain TS considering productive, nutritional, and antinutritional traits from crosses between A x R subspecies. Three A x R crosses were performed, and 37 recombinant inbred lines (RILs) were obtained: 6 from cross C₁ (16A x 30R), 15 from C₂ (42A x 42R), and 16 from C₃ (57A x 8R). Lines were planted in the field in 2024 in a completely randomized block design with two replications. We evaluated: days to 50% flowering (DF), height/plant (cm) (H), number of seeds/pod (NSP), number of pods/plant (NP), number of seeds/plant (NS), 100-seed weight (g) (W), yield/plant (g) (Y), legumin-vicilin ratio (Leg/vic), tannin content (T), phenols (P), and phytic acid (PA). Analysis of variance (ANOVA) was performed. Variables that did not show a normal distribution were evaluated using the Kruskal-Wallis's test (KW). Transgressive segregants were identified as RILs whose mean values exceeded those of the parent with the highest mean value by at least two standard deviations, with the standard deviation calculated based on the offspring. For C₁ cross, the parents and the derived inbred lines only showed significant differences for T and Leg/vic traits. C₂ cross showed significant differences for T, P, PA, and Y traits. The parent 42R had the lowest Y (0.69 g), and 42A had an intermediate Y (0.92 g), while lines C₂ (12), C₂ (52), C₂ (43), and C₂ (34) stood out for exceeding 3 g/plant, with the latter having the highest Y (5.21 g/plant). Regarding P and T content, the parental lines 42A and 42R presented contents between 4.45–5.70 and 27–29 mg/g, respectively, while lines such as C₂ (42), C₂ (26), C₂ (34), C₂ (55), and C₂ (82) showed much lower values (between 0.003–0.13 and 1.50–8.50 mg/g), these results are desirable since P and T are considered antinutritional compounds. C₃ cross showed significant differences in W and PA. Lines C₃ (13) and C₃ (26) presented the highest W values (4.75 and 8.79 g, respectively), exceeding the mean value of the parents (8R = 2.7 g and 57A = 4.1 g). For PA, all lines presented higher values than the parents (1.20 and 0.31 vs. 4.56–18.48 g/mg). The presence of transgressive segregants was detected in the F₆ generation derived from the different crosses evaluated, demonstrating the generation of new variability in the population that could be exploited in breeding programs. Furthermore, the variability detected in T and Leg/vic highlights the importance of considering these traits to simultaneously improve yield and quality.

A16

QUALITY OF SOYBEAN SEEDS TREATED WITH OZONE AS A CONSERVATION METHOD

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Proper seed conservation for future sowing is a fundamental strategy for obtaining crops that can express their full productive potential. In this regard, the use of hermetic seed storage containers promoting an atmosphere with low oxygen levels has proven to be a useful tool for maintaining physiological quality (PQ) over time by minimizing the metabolic activity of both the seeds and associated living organisms. Nevertheless, the presence of pathogens in seeds often conditions the success of appropriate field germination. In this context, ozone (O₃) is a potent oxidant commonly used in environments requiring aseptic conditions. Concurrently, its oxidative power could also affect the biological components of the seeds, potentially altering their PQ. The present study postulated that treating soybean seeds (*Glycine max. L. Merr.*) with appropriate levels of O₃ could reduce the presence of pathogens without affecting their PQ, thus preserving a high-quality product until its use in the subsequent planting season. Seeds of the varieties DM 46E25 SE and DM 60K60 SCE were exposed in a hermetic chamber to an atmosphere of 10 ppm of O₃ for 10 and 20 minutes (T10 and T20). Untreated seeds from both varieties were used as controls (Tc). PQ was measured through Germination Power (GP) and Accelerated Aging (AA) tests, conducted immediately after O₃ treatments and after one month of storage. Pathogenic load was evaluated by incubating seeds on potato dextrose agar in Petri dishes at 25 °C for seven days following the O₃ treatments. Two replicates of 50 seeds were evaluated for GP and AA, and 10 replicates of 10 seeds per treatment/cultivar were used for phytosanitary analysis; corresponding controls were included in all cases. Data were analyzed using ANOVA and Fisher's test ($\alpha = 0.05$). Average GP and AA values were high (~100% and >90%, respectively), and no significant differences were found between T10, T20, and Tc for any of the varieties or analysis periods. The percentage incidence of *Cercospora*, *Aspergillus*, *Penicillium*, and the *Diaporthe/Phomopsis* complex varied between varieties; meanwhile, the presence of *Drechslera sp.*, *Nigrospora sp.*, *Fusarium sp.*, *Epicoccum sp.*, and bacterial colonies was not significant. Additionally, in both varieties, O₃ treatment (T10 and T20) significantly decreased the presence of *Penicillium* relative to the respective control (Tc). These results indicate that O₃ treatment on soybean seeds offers potential benefits by reducing the pathogenic load without affecting PQ. However, the findings suggest the need for further studies involving more varieties with different initial physiological and sanitary qualities, as well as alternative O₃ exposure treatments and post-treatment seed storage durations.

A17

EFFECT OF TWO ENVIRONMENTS ON THE MULTIPLICATION OF ARBUSCULAR MYCORRHIZAL INOCULUM

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It is estimated that more than 70% of plant species have a symbiotic relationship with arbuscular mycorrhizal fungi (AMF), which contribute to nutritional efficiency, water balance, and protection from biotic and abiotic stress. All AMF are biotrophs, so the simplest way to multiply them and use them as a microbial inoculant is through trap cultures. In this system, a host plant (trap) that can be massively colonized by numerous AMF species present in an inoculum source (soil, colonized roots, etc.) is used for the propagation of these microorganisms. The objective of this study was to analyse the effect of two different environments on the production of AMF inoculum in trap culture. The species employed as the host was sorghum (*Sorghum bicolor* (L.) Moench). Pristine soil from an uncultivated area in the "J. F. Villarino" Experimental Field of the Faculty of Agricultural Sciences (UNR) was used as the initial inoculum. Sorghum seeds were sown in 5-litre pots containing a mixture of three equal parts of perlite, peat and pristine soil, without any prior treatment, at a density of 80 seeds per pot. Five pots were kept for a minimum of four months in two environments: 1) inside a greenhouse with temperature and humidity control located in the Horticulture Section of the FCA, UNR 2) outdoors (without control) located on a table in the same Section. Substrate moisture was maintained close to field capacity in both environments through manual irrigation. However, in the outdoor environment, the water supply had to be more reactive to climatic conditions due to fluctuations in temperature, relative humidity, and rainfall. In order to evaluate the most suitable propagation environment, the spore density per gram of final inoculum was estimated in each environment. To estimate the success of mycorrhization, the intensity and frequency of colonization were measured by root staining. The colonization intensity in the external environment was $6.0 \pm 0.0\%$, with a colonization frequency of $71.5 \pm 10.6\%$ and an average spore density of 90.0 ± 33.9 per gram of soil. In the internal environment, the colonization intensity was $7.5 \pm 0.7\%$, the colonization frequency was $86.0 \pm 8.5\%$, and the density was 142.0 ± 17.0 spores per gram of soil. The results obtained demonstrate a tendency towards higher spore density, higher colonization frequency, and a slight increase in colonization intensity in the internal environment compared to the external environment. In conclusion, controlled greenhouse conditions offer a more stable and favorable environment for the development and propagation of AMF in trap cultures.

A18

IN VITRO EVALUATION OF FUNGAL AND BACTERIAL INTERACTIONS: POSSIBLE EFFECTS AND BIO-ECOLOGICAL ROLES

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The diversity of fungal and bacterial communities inhabiting soil results from different mechanisms of genetic variability and reproductive strategies. These microorganisms are biodegraders of cellulose and lignin and contribute to soil formation and aggregation. Due to their adaptive capacity, they establish mutualistic and/or competitive interactions with other communities; therefore, understanding their biological role in the ecosphere is valuable. Fungal genera (*Fusarium*, *Aspergillus*, *Rhizopus*, *Mucor*, *Gliocladium*, *Trichoderma*) and bacterial genera (*Bacillus*, *Streptomyces*), isolated from roots, seeds, and soil, were grown on potato dextrose agar (PDA) at 27 ± 1 °C during seven days. The macro-morphology of colonies and typical microstructures of each genus were characterized. Genomic DNA was extracted using the commercial Promega kit. The ITS region was amplified using the universal primers ITS1 and ITS4 by PCR with a standardized protocol. Amplifications were verified on an agarose gel (1% w/v) and electrophoretic run. The resulting products were sequenced using Sanger technology. The resulting reads were analyzed using BLAST searches, and identity was confirmed. Cross interactions between microorganisms were evaluated by dual-agar plates with APG, with three replicates per treatment. After 7 days at 27 ± 1 °C, the growth radius (cm) of the colonies was measured under different conditions: a) growth without competition and b) growth in interaction with another microorganism. Two indices were calculated from these values: i) the growth of each microorganism in competition and ii) the percentage of inhibition exerted by each microorganism on the others. *Mucor*, *Rhizopus* y *Trichoderma* produced the greatest inhibitory (%) and/or biocontrol effect on *Fusarium* (91.4%, 78.6% y 77.1%) and *Aspergillus* (70.6%, 82.4% y 76.5%), respectively. In addition, *Rhizopus* and *Mucor* (both belonging to Zygomycotas, Mucorales, Mucoraceae) inhibited each other reciprocally ($57 \pm 1.5\%$). While, average inhibitory effect of *Bacillus* and *Streptomyces* on the evaluated biota was $35 \pm 1\%$. It is important to point out that *Mucor* significantly inhibited fungal biocontrol agents such as *Gliocladium* (82.6%) and *Trichoderma* (64.3%). The competitive capacity recorded in *Mucor* allows to infer the relevance of its potential bio-ecological effects, since it acts as a bio-regulator of pathogenic microbial species, some beneficial ones that preserve the balance of the soil biota, and emerging reports has reported it as a cause agent of pathologies in crops of interest and in humans.

A19

PROTEOMIC PROFILE OF GERMINATION IN SOYBEAN SEEDS PRODUCED UNDER THERMO-HYDRIC STRESS CONDITIONS

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Thermo-hydric stress conditions (THS; high temperatures and water deficit) during the R6-R7 stages of soybean (*Glycine max* (L.) Merr.) are associated with chlorophyll retention in mature seeds, which compromises their physiological quality and results in reduced germinability. Additionally, previous studies have shown that high chlorophyll levels are associated with high concentrations of abscisic acid (ABA), similar to those found in immature seeds, where ABA acts as the primary agent inhibiting germination *in planta*. The objective of this work was to characterize the proteomic profile of soybean seeds generated under THS. Soybean seeds (cv. SRM 3410) produced in a greenhouse under THS (maximum mean temperature: 33.8 ± 5.9 °C; water level: 35-50% field capacity) during the R6-R7 period were evaluated and classified at harvest as green seeds (GS; with visible chlorophyll retention) and yellow seeds (YS; without visible chlorophyll retention); whereas non-stressed seeds of the same cultivar were used as controls (CS). Four replicates of fifty embryonic axes dissected from GS, YS, and CS were incubated in distilled water at 27 ± 1 °C. Once germination of the CS group was confirmed (9 h), the axes were powdered in liquid N₂ and subjected to a protein extraction protocol in HEPES buffer (pH 6.8) containing 1 M NaCl, 2 mM EDTA, and 3 mM Na₂S₂O₅, followed by precipitation in 0.39 g/mL (NH₄)₂SO₄ and resuspension in 50 mM NaAc. Proteins were identified via liquid chromatography followed by mass spectrometry (Q-Exactive HF) using Proteome Discoverer software and the Uniprot database (UP000008827). Protein lists for CS, YS, and GS were compared using BioVenn software, and the three groups of unique proteins for each sample were subsequently classified by Gene Ontology criteria using PANTHER. A total of 2094 (GS), 2003 (YS), and 1956 (CS) proteins were identified, of which 1977 were common to all three samples, while 121, 46, and 65 were exclusive to GS, YS, and CS, respectively. The characterization of unique proteins revealed an enrichment in categories related to cellular and metabolic processes. Furthermore, cellular processes played a predominant role in cellular organization and biogenesis in CS and YS, whereas GS focused primarily on mechanisms and metabolic pathways. Metabolic processes focused on primary cellular metabolism, organic substances, and nitrogenous compounds across CS, YS, and GS. These results suggest a developmental alteration in GS, characterized by an enrichment of processes related to primary cellular metabolism over those associated with cell expansion, synthesis, growth, and division that define germination.

A20

**STUDY OF FACTORS AFFECTING PATERNAL CHROMOSOME ELIMINATION AND
SUBSEQUENT PLANT DEVELOPMENT IN *WHEAT* × *MAIZE* CROSSES**

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This study aimed to optimize the production of double haploid (DH) wheat plants through intergeneric crosses with maize, a technique that allows the fixation of homozygosity in a single generation and accelerates plant breeding programs. Critical steps were refined, including flowering synchronization, post-pollination hormone application, embryo rescue and culture, and chromosome doubling. Sowing was carried out in staggered batches in greenhouse and field conditions to ensure the simultaneous availability of maize pollen and receptive wheat spikes. Wheat spikes were manually emasculated and directly pollinated with fresh maize pollen. After pollination, 2,4-dichlorophenoxyacetic acid (2,4-D) was applied using different delivery systems (T1: injection, T2: spot application, and T3: spraying), at single and double doses, 24–48 hours post-pollination. Embryos were rescued 15–20 days after pollination and cultured *in vitro* on Murashige–Skoog medium (½ MS) supplemented with sucrose and agar. The effect of adding activated charcoal (AC) on germination and seedling development was evaluated. Chromosome doubling was performed using colchicine (0.1%), applying a 6-hour root-immersion treatment to plants with 4–5 tillers, under a fume hood and with forced aeration to improve absorption. Plants were later recovered in pots and grown in greenhouse and field conditions until completing their life cycle. Hormonal treatment was confirmed as essential for embryo retention: without 2,4-D, caryopses abort prematurely. Double spraying (100 mg/L at 24 and 48 h post-pollination) proved to be the most efficient method, yielding 16.4% embryos and increasing the embryo/caryopsis and embryo/spike ratios. It was also the most practical method to apply. The addition of activated charcoal to the culture medium did not significantly affect germination or coleoptile length but improved root structure, producing more branched and vigorous root systems. Although embryo germination did not significantly increase, AC improved plant survival during colchicine-induced stress and resulted in a higher establishment rate in pots. As a result, 56% of the plants that completed the cycle originated from embryos germinated on AC-containing medium. Chromosome doubling efficiencies approached 85% when using the optimized methodology (0.1% colchicine for 5–6 h with aeration, plus trimming of root tips and leaves). During 2019–2022, over 10,000 caryopses from various wheat populations were rescued, yielding 337 embryos and 43 confirmed DH plants, of which 30 completed development and produced stable diploid seed. These lines are currently being multiplied for future agronomic and molecular evaluations. This project established an efficient platform for producing double haploid wheat lines via wheat × maize crosses, optimizing conditions and treatments, and providing a key biotechnological tool for breeding programs in Entre Ríos.

A21

**ALLELIC VARIATION OF ADAPTATION GENES IN COMMERCIAL VARIETIES AND
ADVANCED LINES OF *WHEAT***

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Wheat (*Triticum aestivum* L.) is one of the most important crops worldwide, and its yield depends on the interaction between environmental factors and genes regulating the floral transition. Vernalization genes (Vrn-A1, Vrn-B1 and Vrn-D1) and photoperiod response genes (Ppd-B1 and Ppd-D1) determine growth habit and sensitivity to day length, influencing cultivar adaptation and stability. Molecular markers enable the characterization of these genes and support selection in breeding programs. The aim of this study was to identify, allelic variation at these loci in 25 commercial varieties and 35 advanced lines from the INTA wheat breeding program. Alleles were identified by PCR using gene-specific primers to detect characteristic insertions and deletions in Vrn and Ppd genes. A KASP (Kompetitive Allele Specific PCR) marker was used to detect the Vrn-A1 (Rip3) SNP associated with vernalization requirement. Reference cultivars with winter or spring growth habit and with photoperiod sensitivity or insensitivity were included as controls. Among commercial varieties, 56% carried the recessive winter allele at Vrn-A1, 48% at Vrn-B1 and 78% at Vrn-D1. In contrast, advanced lines showed a higher proportion of spring alleles at Vrn-A1 (63%), while the winter allele was detected in 50% for Vrn-B1 and 71% for Vrn-D1. Regarding photoperiod genes, 23% of advanced lines were insensitive at Ppd-B1 and 89% at Ppd-D1, proportions similar to those observed in commercial varieties. The results reveal genetic variability in both commercial varieties and advanced lines. The higher frequency of spring alleles at Vrn-A1 in advanced lines suggests a shorter growth cycle, suitable for late sowing dates and warmer environments. A high proportion of winter alleles at Vrn-D1 indicates the persistence of germplasm with vernalization requirement, useful for regions with prolonged autumns. For Vrn-B1, 50% of advanced lines carried the winter allele, suggesting partial vernalization requirement and potential tolerance to spring sowing, although yield may be affected under insufficient cold exposure. Finally, the triple winter allele combination at Vrn loci was detected in 6% of advanced lines and 8% of commercial varieties, while 14% of advanced lines and 16% of commercial varieties showed low vernalization requirement. The high frequency of Ppd-D1 insensitivity highlights the phenological plasticity of the material, favoring adaptation across different latitudes. This study contributes to the local characterization of wheat adaptation genes, generating a valuable database to support crossing strategies and the selection of materials with greater stability and adaptive capacity across diverse environments.

A22

RELATIONSHIP BETWEEN MALE AGE AND SEMEN QUALITY

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Semen analysis (spermogram) is the initial basic study for evaluating the male factor in couples with reproductive problems. As men age, there is physiological involution of the testicles; spermatogonia are exposed to a greater number of external factors (radiation, pollutants, drugs, infections, inflammations) capable of producing an excessive increase in reactive oxygen species that could promote the formation of sperm with damage to their genetic material and plasma membrane, altering essential sperm parameters. The objective was to study the effect of male age on semen quality in a population of men who consulted with their partner for fertility problems. Descriptive and retrospective study carried out on men who attended the Andrology Laboratory of UHRMA (January 2019 to July 2025). 243 seminal samples were selected from men aged between 20 and 58 years without previous and current andrological conditions and/or pathologies, not consumers of cigarettes, drugs, no excess alcohol, no occupational exposure to toxic substances or extreme temperatures. Three groups were formed according to age: G1 (n=60) men aged 20–29 years, G2 (n=96) men aged 30–39 years, and G3 (n=87) men aged 40 years or older. Sperm volume (V) was measured using a graduated conical tube. Progressive sperm motility (PM) was assessed using the ISAS-LAB computerized system (Proiser). Sperm concentration (C) was determined in Makler chamber and hematoxylin staining was used to evaluate sperm morphology (M). Statistical analysis was performed using a Student's t-test ($p < 0.05$). A statistically significant difference was found in the percentage of MP and percentage of sperm with normal M between groups G1 and G3 and between groups G2 and G3. MP (G1: 71 ± 27.23 vs. G3: 65 ± 21.02 ; $p = 0.029$), (G2: 72 ± 16.86 vs. G3: 65 ± 21.02 ; $p = 0.038$). M (G1: 6.0 ± 1.67 vs. G3: 5.0 ± 1.74 ; $p = 0.036$), (G2: 5.8 ± 1.60 vs. G3: 5.0 ± 1.74 ; $p = 0.033$). No significant difference was found between the analyzed groups for the variables V and C. The analysis showed a decrease in sperm motility and a higher percentage of morphological alterations as the age of the man increased, possibly due to the influence of lifestyle, stress and greater exposure to environmental factors that could alter the normal development of spermatogenesis, generating a decrease in semen quality.

A23

NOSOCOMIAL OUTBREAK OF *Lodderomyces elongisporus* CAUSING FUNGEMIA

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Lodderomyces elongisporus, a yeast first isolated in 1952, has been documented as a pathogen with a notable increase in human infections since the 1970s. Initially misidentified as *Candida parapsilosis* due to morphological similarities, and later as *Saccharomyces elongisporus*, its current taxonomic placement was ultimately established through molecular techniques. Accurate identification of emerging pathogens and characterization of their antifungal susceptibility profiles are essential for optimal clinical management. Between February and March 2025, a fungemia outbreak caused by *Lodderomyces elongisporus* occurred at Hospital Provincial del Centenario, involving nine strains isolated from hospitalized patients. These patients shared common risk factors for invasive fungal infections, including central venous catheter use, recent invasive procedures, prolonged hospitalization, and immunosuppression due to underlying conditions such as systemic lupus erythematosus and gastric cancer. Initial diagnosis from blood cultures proved challenging. Colonies grown on CHROMagar-*Candida*® exhibited a green coloration that would permit presumptive identification as *Candida albicans* Complex, whereas microscopic examination on cornmeal agar and preliminary identification using the VITEK® automated system classified them as *Candida parapsilosis* Complex. Definitive identification of the isolates was ultimately achieved by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), confirming *Lodderomyces elongisporus*. This identification was further validated by sequencing the ITS and 26S ribosomal DNA regions. Additionally, phylogenomic analysis was conducted using whole-genome sequencing with Illumina technology and the MycoSNPs bioinformatics tool, demonstrating high clonal relatedness among strains and clustering them within a single clade. Antifungal susceptibility testing was performed according to the EUCAST (European Committee on Antimicrobial Susceptibility Testing) reference method, document EDef. 7.3.2, evaluating amphotericin B, fluconazole, voriconazole, posaconazole, caspofungin, anidulafungin, and micafungin. All strains exhibited low minimum inhibitory concentration (MIC) values across all tested antifungal agents. This outbreak underscores the critical importance of rigorous, multilayered diagnostic approaches for detecting yeast-like fungi exhibiting emerging pathogen behavior, particularly those capable of persisting in healthcare environments. These findings highlight the essential need for active epidemiological surveillance and integrated diagnostic strategies to ensure accurate pathogen identification and timely clinical intervention.

A24

**ANTIFUNGAL SUSCEPTIBILITY PROFILE OF HYALOPHYPHOMYCETES
RECOVERED FROM CLINICAL MATERIALS**

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Hyalohyphomycetes of the genera *Aspergillus* and *Fusarium* represent a significant threat to human health. They may cause allergic reactions and opportunistic diseases in people with weakened immune systems, and some species also generate toxins. The considerable variation in their response to antifungals is known, making it essential to study their susceptibility. There are currently no clinical cutoff points (standardized values) that would classify a strain as susceptible or resistant to treatment, but consensus exists to establish epidemiological cutoff points (ECOFFs). These make it possible to classify fungi according to the presence or absence of mechanisms of acquired resistance. The objective of this work was to analyze the sensitivity profiles of strains of the genera *Aspergillus* and *Fusarium* deposited in the culture collection of CEREMIC from clinical materials. 31 isolates of *Aspergillus* (9 *A. fumigatus*; 7 *A. flavus*; 7 *A. niger*; 2 *A. terreus*; 2 *A. ustus*, 1 *A. nidulans*, 2 *A. oryzae* and 1 *A. ochraceus*) and 16 strains of *Fusarium* (6 *F. oxysporum* and 10 *F. solani*) were studied. The antifungals tested were amphotericin B (ANF), itraconazole (ITZ), voriconazole (VCZ), posaconazole (PSZ). The methodology used was microdilution in broth described by EUCAST. They were classified as susceptible (S) or Resistant (R) taking into account the ECOFFs values. In the genus *Aspergillus* the following results were found: ANF: 58% of the strains were S and 42% R. ITZ 13% was S and 87% R. VCZ presented 74% of S and 23% R. PSZ, recorded 68% of S and 32% of R. In the genus *Fusarium*, ANF showed 62% S and 38% R. ITZ showed 6% S and 94% R. VCZ, 69% S and 31% R. PSZ: 19% S and 81% R. The results show that susceptible values for different genera and species vary depending on the AF tested. There was a general tendency for *Aspergillus* and *Fusarium* strains to be more susceptible to ANF and VCZ, but not to ITZ. However, for PSZ a higher proportion of susceptible strains of the genus *Aspergillus* was observed than of the genus *Fusarium*. Although there are no standardized clinical cutoff points, susceptibility studies allow us to know the behavior of these microorganisms, which is important in making therapeutic and preventive decisions.

A25

**SEARCH FOR S100A9 BINDING SITES IN SPERMATOZOA AND EVALUATION OF ITS
CHEMOTACTIC EFFECT**

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In previous studies, we detected the protein S100A9 in the tubal epithelium and in human oviductal secretions, and found that it modulates in vitro sperm capacitation parameters, such as protein tyrosine phosphorylation in spermatozoa. In the present study, potential sperm receptors for S100A9 were investigated, and the chemotactic effect of this protein on human spermatozoa was evaluated. Semen samples were obtained from normozoospermic donors and assessed according to WHO criteria (2021). Motile spermatozoa were recovered by swim-up. Spermatozoa were incubated in the presence of recombinant human S100A9 (hrS100A9) under capacitating conditions at 37 °C and 5% pCO₂. Binding of hrS100A9 to spermatozoa was evaluated by indirect immunofluorescence using a Cy3-conjugated anti-IgG secondary antibody. Counterstaining was performed with 4',6-diamidino-2-phenylindole. Three fluorescence patterns were observed: binding to the tail and midpiece; binding to the head, midpiece, and tail; or no binding. To detect sperm receptors, hrS100A9 was cross-linked with the sulfo-SBED reagent. Spermatozoa were incubated with the hrS100A9-sulfo-SBED complex and then exposed to UV light to form the labeled protein-receptor complex. A cell homogenate was prepared in Laemmli buffer, and an aliquot was treated with dithiothreitol to transfer the biotin label to the receptor. Samples were analyzed by 15% SDS-PAGE and electrotransferred onto a nitrocellulose membrane. Protein bands were detected by chemiluminescence, revealing two potential receptors (~76 kDa and ~60 kDa). For chemotaxis assays, special chambers provided by H. Guidobaldi (CCT CONICET) were used, in which protein gradients were generated and compared with the chemotactic effect of progesterone (positive control). The results of the chemotaxis assays (n = 4) showed no significant differences between groups treated with hrS100A9 (10–9 M: 7.82 ± 1.37% and 10–10 M: 4.83 ± 3.50%) and the progesterone control (7.91 ± 3.15%, p > 0.05). HrS100A9 at 10–9 M exhibited chemotactic activity similar to that of progesterone. Two potential receptors that may mediate the effects of S100A9 on sperm function were detected, but they have yet to be identified. Previous studies have shown that S100A9 interacts with Toll-like receptor 4 (TLR-4) and the receptor for advanced glycation end products (RAGE) in several cell types. The binding sites observed for S100A9 partially overlap with the reported localizations of TLR-4 and RAGE in spermatozoa. At least one of the hrS100A9 concentrations tested (10–9 M) exhibited an effect comparable to that of the known chemoattractant, indicating a potential chemotactic activity on human spermatozoa in vitro. S100A9 has been reported to exert a chemotactic effect on immune system cells.

A26

**STRAWBERRY DNA EXTRACTION AS AN ACTIVE LEARNING STRATEGY:
ENHANCING CONCEPTUAL ACQUISITION IN MEDICAL STUDENTS**

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Teaching molecular biology during the early years of a medical degree is often perceived as abstract and difficult to link with clinical practice. The objective of this research was to describe student academic outcomes after participating in an active learning experience. The methodological design was descriptive and cross-sectional with a quantitative approach. A DNA extraction practice using strawberries was implemented. The intervention was evaluated using pre- and post-test measurements among 98 second-year students enrolled in Biochemistry and Molecular Biology II, after providing informed consent. A questionnaire was used to address four key items: understanding the feasibility of DNA extraction and observation, the relationship between extraction and polymerase chain reaction (PCR), declared interest in the content, and self-perception of the ability to explain the procedure. Data analysis involved comparing independent proportions, estimating 95% confidence intervals (95% CI), and calculating effect sizes (Cohen's h). The results indicated that the proportion of students with a clear idea of how to perform the extraction increased from 33.6% to 95.9% (difference = 62.3 percentage points [pp]; h = 1.497). Those feeling very confident in explaining the process increased from 4.5% to 56.1% (difference = 51.6 pp; h = 1.264). Student valuation of the practice as "very interesting" rose from 66.4% to 95.9% (difference = 29.6 pp; h = 0.831), and understanding the link with PCR rose from 79.1% to 96.9% (difference = 17.8 pp; h = 0.598). These findings suggest that strawberry DNA extraction is an effective pedagogical strategy to improve conceptual acquisition, stimulate motivation, and foster the connection between theory and clinical applications in medical education.

A27

**INTERDISCIPLINARY PRIOR KNOWLEDGE FOR MEANINGFUL LEARNING OF
MORPHOLOGY IN BIOCHEMISTRY AND PHARMACY STUDENTS**

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Innovative pedagogical approaches that address curriculum design from a systemic perspective face the challenge of articulating content in an interdisciplinary manner. Currently, the curriculum for the Biochemistry and Pharmacy programs at the Faculty of Biochemical and Pharmaceutical Sciences of the National University of Rosario is organized into thematic units, with learning objectives and purposes limited to each discipline independently. Morphology, a subject taught in the second semester of the second year of both programs, integrates knowledge from diverse areas such as Biology, Organic Chemistry, General Chemistry, and Biological Chemistry. Interdisciplinarity in the training of health professionals demands an integrated understanding of fundamental concepts. In this regard, it is important to understand the prior knowledge of Pharmacy and Biochemistry students in order to explore points of convergence between these disciplines and to enrich the pedagogical approach from an integrative perspective. The objective of this study was to evaluate the interdisciplinary prior knowledge that students possess at the beginning of the Morphology course and to compare this fundamental knowledge for meaningful learning of Morphology between Pharmacy and Biochemistry students. The study was based on a quantitative, exploratory, and descriptive methodological design. A structured, anonymous, and voluntary questionnaire was administered to students from both programs at the beginning of the Morphology course in 2024 (n=43 for Biochemistry and n=22 for Pharmacy). The instrument consisted of multiple-choice questions related to knowledge of plasma membranes and organelles, water, peptides, proteins, carbohydrates, lipids, and types of organic compounds. Statistical analysis of the data employed proportion comparison tests using the EPIDAT 3.1 software. The results showed that students possessed knowledge of: plasma membrane structure (Pharmacy 95.5%; Biochemistry 97.7%)*; organelles (Pharmacy 86.4%; Biochemistry 88.4%)*; pH of water (Pharmacy 72.7%; Biochemistry 65.1%)*; amides and amines (Pharmacy 90.9%; Biochemistry 90.7%)*; alcohols, ketones, and aldehydes (Pharmacy 95.5%; Biochemistry 93%)*; and the composition of peptides and proteins (Pharmacy 100%; Biochemistry 90.7%)*. Lipid characteristics (Pharmacy 86.4%; Biochemistry 81.4%)*, *p>.05; no statistically significant differences were found between the two groups for the evaluated items. Conclusion: At the beginning of the Morphology course, students already possessed the interdisciplinary knowledge necessary for meaningful learning of this subject, with no statistically significant differences between the two programs; thus, identifying and sharing interdisciplinary points of convergence allows for the design of integrative pedagogical proposals that consider the curricular placement of the different disciplines.

A28

PHYTOCHEMICAL STUDY AND CHARACTERIZATION OF BIOACTIVE COMPOUNDS PRESENT IN THE FRUIT OF *Psidium guajava* L.

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Psidium guajava L., a tropical plant characterized by the presence of secondary metabolites with pharmacological properties, is used to treat diarrhea, vomiting, etc. It has a high content of essential oils, vitamins C and A, phenols, flavonoids, tannins and pectins. The aim of the present study is to investigate and characterize the bioactive compounds of the plant fruit. To achieve this, 7 g of fruit per 10 mL of solvent were used, applying extraction protocols by maceration or reflux heating. Simultaneously, three factors were modified at three levels: temperature (25, 60 and ~100 °C), solvent (water, ethanol:water (50:50) and ethanol 96%), and extraction time (5, 24 and 72 h). The extracts obtained from each protocol were dried by evaporation or lyophilization to calculate the yield of each dry extract. They were then dissolved in ethanol:water (2.2:1) and each solution was used for thin-layer chromatography (TLC) and spectrophotometric assays. The results showed differences in the mass yield obtained. The most efficient protocol, with a 12% yield, corresponded to maceration with ethanol at 25 °C for 24 h. Maceration with ethanol at 60 °C for 24 h also produced a high yield compared to the other protocols, indicating that the fruit is rich in moderately polar molecules, as aqueous extracts showed lower yields. On the other hand, longer extraction times did not improve the yield of compound extraction by maceration with water at 25 °C for 72 h. This may be attributed to the evaporation of certain compounds present in the fruit over prolonged extraction times, such as essential oils. In order to compare the chemical profiles of all prepared extracts, two normal-phase TLC experiments were carried out, spotting 200 µg of each sample and using three mobile phases; the optimal one was ethyl acetate: glacial acetic acid: methanol: aqueous formic acid (0.1%) (10:1:1:2.6). Chromatograms were initially observed under UV light at 254 and 365 nm. One chromatogram was developed with 2,2-diphenyl-1-picrylhydrazyl (DPPH), a free radical that accepts electrons, allowing the measurement of antioxidant capacity, generating yellow bands on a purple background and indicating the presence of antioxidants in all spotted samples. The other chromatogram was developed with Natural Product/ Polyethylene Glycol reagent, which demonstrated the presence of flavonoids in all extracts. Likewise, spectrophotometric analyses were performed to determine total phenolic content using the Folin-Ciocalteu reagent. All samples showed phenolic compounds at variable concentrations, with the extract obtained by reflux heating with ethanol:water (50:50) for 5 h being the richest in total phenols (0.11 mg/mL). These results demonstrate that *Psidium guajava* L. is a rich source of antioxidants, flavonoids and phenolic compounds.

A29

OPTIMIZATION OF FLAVONOID EXTRACTION FROM *Psidium guajava*. L LEAVES: STUDY OF THE ANTIOXIDANT ACTIVITY

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In this study, we analyzed leaf extracts of *Psidium guajava* L., a tropical species widely used in food, medicinal, and industrial applications. Its leaves contain bioactive compounds, primarily phenols and flavonoids, which are responsible for its well-known antioxidant activity. The extraction efficiency of flavonoids was evaluated using an experimental design considering three factors: temperature (25, 60, and ~100 °C), ethanol:water ratio (100:0, 50:50, and 0:100), and extraction time (5 and 24 h). In nine protocols, 0.7 g of dried and ground plant material was extracted with 10 mL of solvent under different conditions. At the end of the extraction, the plant material was separated by filtration, and the extracts were concentrated by evaporation or lyophilization, with yields ranging from 7.5 and 22%. The dry extracts were solubilized in ethanol:water mixture (50:50) and analyzed by thin-layer chromatography (TLC), using toluene:ethyl acetate:methanol:formic acid (75:25:25:6) as the mobile phase. The TLC plates were revealed using Natural Product–polyethyleneglycol (NP–PEG) and 2,2-diphenyl-1-picrylhydrazyl (DPPH). The plates, before and after derivatization, were documented under visible and UV light (254 and 365 nm) and analyzed by densitometry, absorbance, and fluorescence spectrophotometry using a CAMAG TLC Scanner. Under UV light, several bands attributable to unsaturated compounds were observed. NP–PEG derivatization revealed the presence of flavonoids and other phenolic compounds, while DPPH staining detected antioxidant compounds. The extracts were also analyzed spectrophotometrically to determine the percentage of total phenols (%TP) using the Folin–Ciocalteu method, with values ranging from 2 and 4%. A factorial analysis was performed to determine which protocol variables (temperature, solvent composition, or time) influenced the responses: extraction yield (%Y), %TP, and the number of peaks integrated by densitometry and spectrophotometry of the TLC plates. The results ($\alpha = 0.05$) showed that %Y depended on extraction time and ethanol proportion, with optimal conditions at 5 h and 50% ethanol. Variables associated with NP–PEG derivatization were influenced by time and ethanol percentage, with the maximum number of detected peaks at 5 h and 100% ethanol, respectively. Temperature did not significantly affect the measured responses, indicating that any of the tested values would be suitable for compound extraction. Antioxidant activity and %TP were not significantly affected by changes in the

tested variables, suggesting that all protocols were suitable for extracting flavonoids and antioxidants. Finally, an optimization was carried out to simultaneously maximize the dependent variables related to time and ethanol percentage, concluding that the best conditions were 5 h of extraction and 50% ethanol. Overall, these findings indicate that guajava leaves are a promising source of flavonoids and antioxidant metabolites, with great potential for future studies targeting biological applications in both food and medicine.

A30

ARSENIC TOXICITY ASSESSMENT USING THE *Allium cepa* TEST

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Arsenic (As) is naturally present in the earth's crust and is considered one of the most toxic environmental contaminants. Its presence in groundwater intended for human consumption constitutes a global public health emergency. In Argentina, several populations are exposed to water containing high levels of As, and the province of Santa Fe is one of the geographical areas affected by this issue, representing a significant health risk. The aim of this study was to evaluate the phyto-, cyto-, and genotoxic properties of As using the *Allium cepa* test. This is a sensitive, efficient, and cost-effective bioassay internationally validated as a tool for environmental biomonitoring. Homogeneous yellow onion bulbs (*Allium cepa* L.) were rooted in commercial mineral water for 72 h and subsequently exposed to various concentrations of As for 24 h: 0.01, 0.05, 0.1, 1, and 3 ppm (some of which are representative of concentrations found in groundwater); commercial mineral water was used as the negative control (5 bulbs per concentration). Arsenic solutions were prepared in mineral water from a commercial 1000 ppm As standard. The macroscopic parameter and indicator of phytotoxicity was, the elongation of the longest root, which was evaluated by measuring the difference in length before and after As exposure (ΔL). The microscopic parameters used, were the mitotic index (MI) determined as the sum of dividing cells (metaphase, anaphase, and telophase) per 1000 cells per slide (indicator of cytotoxicity), as well as the presence of chromosomal aberrations (CA) during anaphase-telophase (indicator of genotoxicity). For this purpose, chromosomes from the root apex were stained using Schiff's reagent and 2% acetic orcein. The meristematic region was then squashed on a microscope slide to obtain a single-cell layer, which was examined under a microscope at 400 $\times$ magnification. In this preliminary study, phytotoxicity assessment showed that at low As concentrations (<0.1 ppm), onion root growth was not affected. However, exposure to 1 and 3 ppm As resulted in a significant decrease in the elongation of the longest root (ΔL : 0.34 ± 0.21 and 0.36 ± 0.11 cm, respectively) compared with the control (1.28 ± 0.46 cm) ($p = 0.000024$). Cytotoxicity and genotoxicity analyses revealed a significantly lower MI in onions exposed to 0.1 (MI: 11.3 ± 3.5), 1 (MI: 8.3 ± 4.0), and 3 (MI: 7.3 ± 4.2) ppm As compared to controls (MI: 26.7 ± 4.5) ($p = 0.000122$). In contrast, no differences were observed between the control and the 0.01 and 0.05 ppm As treatments. Regarding CA, all As concentrations tested showed the presence of them. In conclusion, these results demonstrate the cyto- and genotoxic properties of As, even at low concentrations similar to those found in drinking water, and highlight the sensitivity of the *Allium cepa* bioassay as an environmental monitoring tool. Nevertheless, considering this is a preliminary study, an increased number of samples is required to consolidate the validity of the results and strengthen the interpretation of the observed effects.

A31

PRELIMINARY STUDY OF QUERCETIN ACTIVITY ON TRANSFUSION UNITS USING A FACTORIAL DESIGN

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Gamma radiation is very useful in blood banks to inactivate donor T lymphocytes, especially in the prevention of Graft-versus-Host Disease. However, it can induce the formation of Reactive Oxygen Species (ROS), producing oxidative stress and damage to the erythrocyte cell membrane, shortening its lifespan. The phytochemical quercetin (Q) has been shown to be a potent antioxidant with potential therapeutic effects as a protective and antithrombotic agent. The aim of this study is to investigate the variations in erythrocyte aggregation due to the effect of Q at different concentrations (5 and 10 μ M) on blood samples irradiated with gamma radiation at 0 and 25 Gy at two time points, 0 and 14 days. For this purpose, blood samples were collected from healthy adult volunteers in polyvinyl chloride bags containing CPDA as a preservative. Subsequently, the red blood cell concentrate was separated into different aliquots and supplemented with 5 or 10 μ M Q, as appropriate. Unsupplemented aliquots were also reserved for control. The aliquots were irradiated in duplicate with 0 and 25 Gy (Biobeam GM 8000) at the Regional Hemotherapy Center (Rosario). One fraction was analyzed immediately, and the other was stored at 4°C for 14 days. Digital image analysis and aggregation kinetics studies were performed using an optical chip aggregometer, calculating the percentage of isolated cells (%CA) and the Aggregation Index (IA), respectively. For digital analysis, samples were suspended in 0.25% autologous plasma, and digital microscopic images were recorded in quintuplicate. For aggregation kinetics, blood was reconstituted to 40% autologous plasma, and silectograms were recorded by quintuplicate. A balanced 2x2x3 factorial design was used to analyze the effect of radiation dose (two levels), elapsed

days (two levels), and the presence of Q (three levels) on %CA, thus studying the effect of each of these factors and, fundamentally, the interactions between them. The assumptions of normality and independence of the residuals and of homoscedasticity were verified. The proposed model was: $AC_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \epsilon_{ijk}$, where μ is the overall mean, α is the main effect of the day, β is the main effect of the radiation dose, γ is the main effect of Q and ϵ is the experimental error (the subscripts i, j and k are related to day, radiation dose and Q respectively). The main effect observed for the system under study was the significant three-way interaction, as well as all two-way interactions and main effects. It can be seen that the IA increases with the irradiated dose and over the time, while the %CA decreases in the irradiated samples. When analyzing the effect of Q (Q) in the irradiated samples, the %CA increases with the addition of Q10 (and to a lesser extent with Q5) compared to the non-supplemented sample, possibly indicating the anti-aggregatory and protective activity of Q. Further studies would be needed to establish the minimum Q concentration required to demonstrate its protective effect on erythrocytes and the mechanism by which it can reverse oxidative stress.

A32

APPLICATION OF A BACTERIAL GLYPHOSATE BIOSENSOR FOR QUANTIFICATION OF THE HERBICIDE IN ENVIRONMENTAL SAMPLES

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Phosphonates are organic compounds widely distributed in nature and characterized by the presence of a carbon-phosphorus (C-P) bond. Glyphosate (GP) is a synthetic phosphonate that has played a central role in modern agriculture due to its inhibitory effect on 5-enolpyruvylshikimate-3-phosphate synthase, a key enzyme of the plant shikimate pathway, thereby interfering with the synthesis of aromatic amino acids and essential secondary metabolites. The development of transgenic crops resistant to GP led to a substantial expansion in the use of glyphosate-based herbicides (GBHs), which has raised increasing environmental concerns. In our laboratory, several bacterial strains were isolated from soils exposed to high concentrations of GBHs. Among them, strains belonging to the genera *Achromobacter*, *Agrobacterium*, and *Ochrobactrum* showed the highest efficiency in GP degradation when used as the sole phosphorus source. The genome of one of these strains, designated *Agrobacterium tumefaciens* CHLDO, was fully sequenced, revealing the presence of a gene cluster known as *phn* involved in GP assimilation and degradation. *A. tumefaciens* CHLDO *phn* cluster encodes 15 proteins divided in 4 transcriptional units, among which there are PhnCDE2E1 involved in phosphonate assimilation, PhnGHIJKLO which are the core of the C-P lyase complex, the regulator PhnF and accessory proteins. Expression of *phnG* was strongly induced in the presence of GBHs compared to inorganic phosphate, suggesting its crucial role in phosphonate hydrolysis. The aim of this work was to quantify phosphonates in environmental samples using a biosensor based on *A. tumefaciens* CHLDO genetically modified by transformation with a plasmid carrying the *phnG* promoter fused to the green fluorescent protein (GFP) and a copy of the transcriptional repressor of the *phn* cluster, *phnF*. The constructed biosensor strain was able to detect phosphonates in a concentration range from 0.5 to 25 μ M. For quantification, soil samples supplemented with GBH (up to 400 mg/kg) were extracted with 0.6 M KOH, sonicated, and centrifuged. The resulting supernatants were used as the sole phosphorus source to generate biosensor growth curves in phosphorus-free minimal medium using a Synergy 2 (BioTek) microplate reader. Optical density and fluorescence (excitation 485 nm, emission 528 nm) were recorded every 30 minutes for 16 h. Growth-normalized fluorescence was analyzed to estimate GP concentrations using a calibration curve constructed with known GP concentrations. Our results demonstrate that the engineered *A. tumefaciens* CHLDO biosensor enables the detection and quantification of GP in soil samples under simulated environmental conditions, highlighting its potential as an alternative tool for phosphonate detection in complex environmental samples.

A33

EVALUATION OF THE EXPRESSION OF HGR AND HGR ISOFORMS OF GLUCOCORTICOID RECEPTORS IN HIV-INFECTED PATIENTS PRIOR TO TREATMENT

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Glucocorticoid activity is mediated by specific receptors, whose main isoforms are alpha (hGR α) and beta (hGR β). hGR α is the functional isoform responsible for hormone binding and glucocorticoid-mediated gene regulation. In contrast, hGR β lacks ligand-binding capacity and acts as a negative regulator of hGR α , attenuating its transcriptional effects. Serum factors associated with infections, such as IL-1 β , TNF- α , IL-6, and other inflammatory mediators, increase hGR β expression and are linked to glucocorticoid resistance at the cellular level. In HIV-positive patients, viral infection is associated with chronic immune activation, sustained inflammation, and endocrine alterations, mechanisms that involve glucocorticoid action. HIV infection has been reported to be accompanied by alterations in the production or action of adrenal steroids. Therefore, this study investigated the expression of hGR α and hGR β in lymphocytes from HIV-positive patients prior to treatment and

compared it with the expression observed in a group of healthy donors. Lymphocytes were obtained from venous blood samples of HIV-positive patients ($n = 16$) and healthy donors ($n = 16$) using a Ficoll density gradient, and total RNA was extracted. Reverse transcription was performed, and gene expression was analyzed by RT-PCR using SYBR Green-based reagents, with cyclophilin used as the reference gene. Relative expression levels of hGR α and hGR β were calculated using the $2^{-\Delta\Delta C_t}$ method, with the healthy donor group serving as the control. Statistical analysis was performed using Student's t-test. In the HIV-positive patient group, a significant decrease in the expression of both genes was observed compared to the control group ($p < 0.001$). hGR α expression in patients was $1.3 \pm 2.45\%$ of that observed in healthy controls, while hGR β expression was $25.9 \pm 95.4\%$ of control levels. The hGR α /hGR β ratio was 0.05. hGR β appeared to be expressed at a higher relative level than hGR α , and given its inhibitory effect on hGR α function, this imbalance may favor a persistent pro-inflammatory environment and a dysregulated immune response, consistent with glucocorticoid resistance. A low hGR α /hGR β ratio is associated with reduced sensitivity or resistance to glucocorticoids. Under infectious stress, the balance between the hGR α and hGR β isoforms of the glucocorticoid receptor becomes pathophysiologically relevant. The results suggest a critical alteration in the glucocorticoid response in the group of HIV-positive patients studied.

A34

EVALUATION OF LIPID AND HEMORHEOLOGICAL PROFILES IN DYSLIPIDEMIC PATIENTS OF DIFFERENT AGES RECEIVING *Ligaria cuneifolia* INFUSION

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Ligaria cuneifolia (R. et P.) Tiegh. –Loranthaceae– (*Lc*) is used in folk medicine to lower total plasma cholesterol (TCho) and increase blood fluidity. Objectives: To analyze the effect of oral administration of aqueous extract infusions from the leaves and stems of *Ligaria cuneifolia* (*Lc*) on the lipid and hemorheological profiles of dyslipidemic patients, differentiating the hypolipidemic impact across different age groups. Methodology: 20 patients were studied and divided by age into two groups of 10: 18 to 50 years old (G1) and over 50 years old (G2). After signing informed consent, venous blood was drawn for baseline (B) determinations. Each patient received lyophilized *Lc* extract and was instructed to consume it as an infusion (one 2.6 g sachet in 200 ml of hot water) three times per week. After 31 days, post-treatment (TLc) venous blood samples were obtained. Plasma determinations: TCho, HDL-Cho, and LDL-Cho were measured colorimetrically; fibrinogen (FB) and triglyceride (TG) concentrations were measured using enzymatic methods; all concentrations were expressed in mg/dL. Hemorheological parameters were evaluated in whole blood: erythrocyte aggregation by optical densitometry, obtaining the initial velocity of the process (V); blood and plasma viscosity were evaluated with a rotational viscometer, from which relative blood viscosity (RBV) was calculated. Statistical analysis: Wilcoxon test for paired data. Results (median and 95% CI): G1 TCho: B: 211 (198-250); TLc: 220 (177-243) ns; HDL-Cho: B: 57 (42-86); TLc: 58 (44-83) ns; LDL-Cho: B: 185 (135-203); TLc: 168 (101-179)*. RBV: B: 3.58 (3.29-3.91); TLc: 2.79 (2.36-3.45)*. TG: B: 118 (66-179); TLc: 77 (46-153)*; FB: B: 288 (203-544) ns; TLc: 280 (195-502) ns; V: B: 0.44 (0.42-0.775); TLc: 0.51 (0.40-1.85) ns. G2 TCho: B: 242 (205-250) vs TLc: 232 (180-261) ns; HDL-Cho: B: 59 (42-84); TLc: 63.5 (35-76) ns; LDL-Cho: B: 185 (140-203) vs TLc: 168 (101-181)**. RBV: B: 3.09 (2.19-3.72) vs TLc: 2.97 (1.64-3.79) ns. TG (mg/dL): B: 80 (66-343), TLc: 102 (42-118) ns; FB (mg/dL): B: 300 (190-410), TLc: 237 (187-359)*; V: B: 0.49 (0.3-1.13), TLc: 0.37 (0.26-1.09)*. (**p < 0.01 vs B; *p < 0.05 vs B; ns: non-significant vs B). In the patients studied, treatment with *Ligaria cuneifolia* in G1 resulted in a decrease in RBV, LDL-Cho, and TG levels. In G2, a decrease in LDL-Cho and fibrinogen levels, as well as in erythrocyte aggregation, was observed. Although the impact of *Lc* on the lipid profile differs by age group, an overall improvement in hemorheological parameters and lipid profile is observed, suggesting the use of *Lc* as an adjuvant in the prevention of cardiovascular disease.

A35

DETECTION OF MYCOBACTERIA IN THE CLINICAL LABORATORY OF THE DEPARTMENT OF MICROBIOLOGY, VIROLOGY AND PARASITOLOGY AT THE MEDICAL SCIENCES FACULTY, UNR

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Tuberculosis, mainly caused by *Mycobacterium tuberculosis*, is a public health problem in Argentina and worldwide. A definitive diagnosis is microbiological and involves microscopic observation techniques, culture, and molecular biology methods. Knowledge of local epidemiology is essential for accurate and early diagnosis. Objective: To determine the

current situation regarding the diagnosis of *Mycobacterium* in our laboratory, the available techniques, and their usefulness. Materials and Methods: A retrospective descriptive observational study of samples processed for the detection of mycobacteria at the laboratory of the Department of Microbiology, Virology and Parasitology, Faculty of Medical Sciences, UNR, between January 1st, 2022, and December 31st, 2023. Samples were classified according to collection site, sex, age, and diagnostic techniques used. Results: A total of 833 samples from 522 patients were analyzed; 58% male and 42% female, with a mean age of 46.8 years. Ninety-one percent were pulmonary samples. A total of 833 smear microscopies (AFB), 479 cultures, and 89 PCR tests were performed. Positivity rates were 12% for AFB smear, 19% for culture, and 63% for PCR. One hundred patients (19%) showed positivity by one or more techniques. When analyzing the relationship between diagnostic methods, it was determined that: 55 (55%) had both positive AFB smear and culture; 35 (35%) had negative AFB smear and positive culture; 5 (5%) had positive AFB smear and negative culture; and 5 (5%) had positive PCR with negative AFB smear. Conclusion: No single technique is sufficient for the microbiological diagnosis of tuberculosis; a combination of methods is required. Smear microscopy remains a diagnostic cornerstone, but the inclusion of molecular techniques is important for early detection and to address the challenge of drug resistance. Conducting local epidemiological studies is essential to guide practice in microbiology laboratories.

A36

ANOVAGINAL CARRIAGE OF *Streptococcus agalactiae* AMONG PREGNANT WOMEN

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Streptococcus agalactiae, also known as Group B beta-hemolytic *Streptococcus* (GBS), is a Gram-positive coccus that forms part of the normal gastrointestinal microbiota. It may intermittently colonize the vagina of pregnant women, with carriage rates reported in the international literature ranging from 10% to 40%, and in Argentina between 2% and 16%. GBS exhibits selective pathogenicity for pregnant individuals and newborns (NB), and it is a significant cause of maternal and neonatal morbidity and mortality. During childbirth, it can be transmitted from mother to child in approximately 50% of cases and may cause severe disease in both the newborn and the postpartum individual. Several factors are associated with an increased risk of neonatal GBS infection, including GBS bacteriuria during pregnancy, prolonged rupture of membranes, intrapartum fever, and a history of GBS infection in a previous pregnancy. In the absence of timely treatment, the incidence of neonatal sepsis is 3 cases per 1,000 live births. Since 2008, a national “universal screening in pregnant women” law has been in effect in our country, establishing mandatory screening for GBS in all pregnant women between 35 and 37 weeks of gestation. The aim of this study was to determine the prevalence of anovaginal GBS carriage in pregnant women. A cross-sectional observational study design was used. The results of processing anorectal and vaginal swabs from pregnant women were analyzed after informed consent was obtained, during weeks 35 to 37 of gestation, in patients attending the Department of Obstetrics and Gynecology at Hospital Provincial del Centenario, Rosario city, from June 1, 2023 to August 31, 2025. Samples were collected, preserved, and processed according to national guideline recommendations at the clinical laboratory of the Department of Microbiology, Virology and Parasitology, School of Medical Sciences, Universidad Nacional de Rosario. Absolute and relative frequencies were calculated. A total of 200 samples from 100 patients were obtained: 183 (91.5%) were negative and 17 (8.5%) were positive, corresponding to 14 carrier patients (14%). Among the positive samples, 8 (4%) were anal swabs and 9 (4.5%) were vaginal swabs; 3 patients tested positive in both samples. In the studied population, the prevalence of carriage was 14%. Nationally implemented preventive measures, including the detection of asymptomatic GBS carriers and the administration of intrapartum antimicrobial prophylaxis, have led to a marked reduction in severe GBS infections during the postpartum period, with a positive impact on maternal and infant morbidity and mortality. However, GBS infections still constitute a public health problem. Ensuring universal access for pregnant women to screening strategies and maintaining updated knowledge of local epidemiology are essential. Identifying colonization prevalence and antimicrobial resistance patterns is crucial to addressing this issue. This abstract presents the partial results of a four-year prospective study.

A37

MEASUREMENT OF ERYTHROCYTE OSMOTIC FRAGILITY AND ITS RELATIONSHIP TO NUTRITIONAL STATUS AND PHYSICAL ACTIVITY IN STUDENTS AT THE MEDICAL SCIENCES SCHOOL OF THE NATIONAL UNIVERSITY OF ROSARIO

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Several studies have highlighted increased sedentary lifestyles and poor nutrition with the growing prevalence of chronic noncommunicable diseases. Nutritional status and physical activity are some of the factors that modulate the physiological processes that enable adequate tissue perfusion. The integrity and functionality of erythrocytes is essential to ensure their deformability and flow through the microvascular circulation. Osmotic fragility (OF) is a sensitive indicator of erythrocyte membrane stability. We propose to analyze the relationship between OF, nutritional status, and physical activity intensity in

university students. Students from the medical sciences school of the national university of rosario were invited to participate on a voluntary basis after giving their informed consent. Blood samples were obtained by venipuncture after a 12-hour fast and were processed to determine osmotic fragility by photometry at 540 nm. The percentage of hemolysis was measured as a function of NaCl concentration, considering 100% hemolysis to occur at 0 mosm/kg, and then the mean osmotic fragility (X50) was calculated. Nutritional status was assessed using body mass index (BMI), classifying participants as normal weight (NW), overweight (OW), or obese (OB). Physical activity intensity was determined using a self-administered international questionnaire, following the recommendations of the World Confederation for Physical Therapy, and categorized according to METs as low (<600) (LI), moderate (600–1500) (MI), or high (>1500) (HI). Statistical analysis was performed using one-way ANOVA (MedCalc Software, version 11.3.0.0), establishing a significance level of $p < 0.05$. Results were expressed as mean $\pm$ standard deviation, and significant differences between groups were indicated with different superscript letters. The association between nutritional status and physical activity intensity did not reach statistical significance ($\chi^2 = 7.908$; $C = 0.319$; $p = 0.095$) although the observed trend suggests a possible relationship. The OB group was associated with higher OF, possibly linked to alterations in cell membrane composition and fluidity. In relation to physical activity, it was observed that OF tended to be higher in the low-intensity group. Although the difference was not significant, this would reinforce the role of exercise in preserving erythrocyte resistance. These results present OF as a possible indicator for assessing hemorheological health and highlight the influence of physical activity on an aspect of the health of the young population.

A38

ERYTHROCYTE DEFORMABILITY IN PATIENTS WITH HEMOPHILIA A: A COMPARISON WITH HEALTHY SUBJECTS

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Hemophilia A (HA) is a congenital coagulopathy characterized by a deficiency of Factor VIII (FVIII), which alters the hemostatic balance and promotes the occurrence of recurrent hemorrhagic episodes. Although FVIII is not directly involved in erythrocyte biomechanics, evidence suggests that the chronic inflammatory state, metabolic changes, and complications associated with severe and poorly controlled forms of the disease may induce secondary modifications in erythrocyte properties. Erythrocyte deformability (ED), which allows red blood cells to modify their shape to pass through narrow capillaries without compromising their integrity, is proposed as a parameter to study dysfunctions in microcirculation and oxygen transport in hemophiliac patients. This study aims to analyze erythrocyte deformability in patients with HA compared to healthy individuals. Participation was open to healthy subjects with normal FVIII levels aged between 18 and 65, and subjects diagnosed with HA within the same age range. Participation was voluntary, anonymous, and unpaid, subject to signing of an informed consent form by the participant. Filterability measurements were performed using a computerized instrument based on the technique described by Reid et al. Erythrocytes, suspended at a hematocrit of 10% in saline solution with 0.25% bovine albumin, were filtered under constant negative pressure (10 cm H₂O) through 13mm diameter polycarbonate membranes (Nucleopore, USA) with 5 μ m pores. The results are expressed as a filtration index (FI), calculated as: $FI = (t_s - t_0/t_0) \times (100/Hct)$. Where t_s is the passage time of the erythrocyte suspension at 10% Hct. t_0 is the passage time of the buffer. FI is an estimate of erythrocyte rigidity (inverse to ED). The results obtained were statistically evaluated using the one-way ANOVA test, with MedCalc Software (Version 11.3.0.0). The significance level of $p < 0.05$ was established. The FI was significantly lower in patients with HA ($n=7$) than in healthy controls ($n=28$) (9.19 ± 1.74 vs. 10.81 ± 1.79 ; $p = 0.039$). Given that a lower FI value reflects greater deformability, these findings suggest that erythrocytes from hemophilia patients have an increased ability to pass through narrow-pore filters compared to healthy subjects. Our results show that patients with HA have erythrocytes with greater deformability than controls. This unexpected finding could be interpreted as a pathophysiological adaptation aimed at promoting microcirculation and tissue oxygenation in the context of FVIII deficiency and bleeding risk. Future studies will be necessary to further investigate the underlying mechanisms, considering the influence of oxidative stress, chronic inflammation, and replacement therapies on erythrocyte biomechanics.

A39

IMPACT OF SLEEP HYGIENE ON ERYTHROCYTE DEFORMABILITY, PLASMA VISCOSITY, BLOOD VISCOSITY AND INFLAMMATORY MARKERS IN STUDENTS OF THE NATIONAL UNIVERSITY OF ROSARIO AGED 18–25 YEARS

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The digital era has transformed social and academic dynamics, generating greater vulnerability in university students to alterations in sleep habits, which represent a vital physiological process for maintaining physical, emotional and cognitive homeostasis. Chronic sleep deprivation induces oxidative stress and a subclinical inflammatory state, increasing mediators such as C-reactive protein, interleukin 6 and TNF-alpha. These processes may affect hemorheological parameters including

erythrocyte deformability, plasma viscosity and total blood viscosity, which are critical variables for microcirculatory perfusion. Previous studies conducted by our group demonstrated alterations in erythrocyte aggregation in students with partial sleep deprivation, prompting further analysis of additional rheological variables and inflammatory markers. The aim of the present study was to evaluate the relationship between sleep duration and changes in erythrocyte deformability, plasma viscosity, blood viscosity and acute phase reactants in students aged 18 to 25 years from the Universidad Nacional de Rosario. Volunteers recorded sleep hours in a weekly log and were grouped as <6 h (n=5), 6–7 h (n=6), 7–8 h (n=12) and >8 h (n=5) according to average daily sleep time. Erythrocyte deformability was determined by filtration index using a computerized instrument based on the technique described by Reid et al. Plasma and blood viscosity were measured with a cone-plate viscometer at 113 s^{-1} . C-reactive protein and erythrocyte sedimentation rate were determined using standard techniques. Fibrinogen was measured with a Col1 coagulometer. Statistical analysis was performed using one-way ANOVA, establishing a significance level of $p < 0.05$. Results were expressed as mean $\pm$ standard deviation. A significantly higher filtration index was observed in the >8 h group (28.8 ± 9.7) compared with the other groups (<6 h: 11.5 ± 3.8 ; 6–7 h: 15.5 ± 5.1 ; 7–8 h: 15.9 ± 6.7 ; $p < 0.05$), indicating reduced erythrocyte deformability. No significant differences were observed among groups in plasma viscosity, blood viscosity, fibrinogen, erythrocyte sedimentation rate or C-reactive protein. Longer sleep duration was associated with decreased erythrocyte deformability, which may reflect alterations in membrane mechanics and potential microcirculatory impairment. The absence of changes in viscosity and inflammatory markers suggests that sleep habit variations may not significantly impact these parameters in young individuals. Given the small sample size in each group, further studies are necessary to better understand the impact of sleep habits on hemorheology and cardiovascular risk factors.

A40

INCREASED BODY MASS INDEX IS ASSOCIATED WITH REDUCED ERYTHROCYTE DEFORMABILITY IN HEALTHY YOUNG ADULTS FROM THE UNIVERSIDAD NACIONAL DE ROSARIO (UNR)

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Erythrocyte deformability (ED) is a key determinant of microvascular perfusion. Impairment of this property compromises tissue oxygen delivery and increases susceptibility to hypoxia/ischemia, thereby contributing to cardiovascular risk (CVR). ED is regulated by both cellular and systemic factors. Relevant cellular determinants include erythrocyte morphology assessed by the Bessis morphological index (MI), intracellular viscosity reflected by mean corpuscular hemoglobin concentration (MCHC), and membrane lipid composition, particularly membrane cholesterol content (MCC). Clinical-metabolic parameters such as nutritional status expressed as body mass index (BMI), mean arterial pressure (MAP), levels of systemic inflammatory markers (C-reactive protein, CRP), and insulinemia could also modulate this property. The aim of this study was to evaluate the association between ED and these parameters in 68 students aged 18–25 years from UNR. Individuals with endocrine-metabolic disorders, underweight, or receiving pharmacological treatment were excluded. Anthropometric data were recorded to calculate BMI, and fasting venous blood samples were obtained. ED was assessed by the filtration index (FI), inversely proportional to deformability. MCC was determined by solvent lipid extraction, MI by optical microscopy, MCHC using an automated hematology analyzer, CRP by immunoturbidimetry, and insulin by immunoassay. MAP was calculated from sphygmomanometric measurements using a standardized formula. Associations between FI and the studied variables were analyzed using Spearman correlation, with $p < 0.05$ considered statistically significant. A positive and significant correlation was observed between BMI and FI ($r = 0.269$; $p = 0.028$), indicating reduced ED with increasing BMI. No significant associations were found for MCHC ($r = -0.116$; $p = 0.353$), MCC ($r = 0.111$; $p = 0.361$), MAP ($r = -0.059$; $p = 0.645$), CRP ($r = 0.050$; $p = 0.802$), insulin ($r = -0.194$; $p = 0.273$), or MI ($r = -0.021$; $p = 0.879$). These findings suggest that excess body weight is associated with early hemorheological alterations in otherwise healthy young adults, a mechanism seldom considered in obesity-related CVR, which is traditionally attributed to insulin resistance, dyslipidemia, hypertension, and chronic low-grade inflammation. Altered erythrocyte rheology may therefore represent an additional pathophysiological pathway contributing to impaired microvascular oxygen delivery and could serve as an early marker of cardiometabolic risk. Larger cohorts and longitudinal studies are warranted to validate these observations.

A41

KNOWLEDGE AND ACTION BUILDING FOR DENGUE PREVENTION: AN INTERSECTORAL EDUCATIONAL PROPOSAL

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The *Aedes aegypti* mosquito, responsible for transmitting dengue fever, develops mainly in urban areas. Its control depends largely on the elimination of breeding sites, a key action for preventing disease. In this context, citizen participation is essential, since in many cases, are home themselves those that offer favorable conditions for mosquito proliferation. Since 2009, Argentina has experienced increasingly severe dengue outbreaks, and, in response to the largest epidemic recorded in years 2023-2024, an inter-institutional project was implemented, led by the Costa Ciencia Interactive Museum (MICC), the

University of Buenos Aires (UBA), and the National Scientific and Technical Research Council (CONICET), with the participation of two Secondary Schools for Youth and Adults (No. 29 and No. 42), the Concordia Teacher Training Institute (IPC), and the municipal health department. Within the framework of this project, teachers from the schools and members of the MICC received training on dengue prevention and vector biology from researchers at UBA and CONICET. The teachers then gave classes in various subjects, and the students, guided by their teachers, created oviposition sensors (ovitraps) to record the egg-laying activity of *A. aegypti*. The students placed the ovitraps in their homes, in shaded and preferably vegetated areas, and distributed them throughout various parts of the city. A total of seventy-four locations were surveyed, each with a sensor monitored weekly for two and a half months, coinciding with the beginning of the *A. aegypti* population peak. The MICC and IPC supervised the fieldwork and the weekly egg count. With the obtained data, the students created graphs and maps that demonstrated the widespread presence of the mosquito in the city. Prevention and control measures were implemented at the homes where the sensors were placed, targeting potential breeding sites. These measures were also replicated in neighboring homes and areas surrounding the participating schools. This experience allowed us to address the problem from environmental, social, and scientific perspectives, actively involving students, teachers from different subjects, directors, student teachers, and MICC interns, thus consolidating collaborative and multidisciplinary work in the face of this important and current public health problem.

A42

PFAS IN ARGENTINA: GLOBAL ISSUE, LOCAL CHALLENGES

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Per- and polyfluoroalkyl substances (PFAS) are a group of synthetic chemical compounds that, due to their unique properties, are widely used in a variety of applications and products. They are also highly persistent and bioaccumulative. This study presents a compilation of research quantifying PFAS in the country, along with a summary of their potential health and environmental effects, bioremediation techniques for contaminated areas, and methods for their removal. The literature review was conducted using tools such as Google, ScienceDirect, Google Scholar, and PubMed, covering publications from 2000 to the present. According to the UNEP (United Nations Environment Programme), there is a lack of information on these substances in Latin America and the Caribbean. The findings show a concentration of measurements in the Río de la Plata area, leaving a large geographic area and population unaccounted for. In Argentina, PFAS concentrations in water range from 0.35 ng/L in the Argentine Sea to 27 ng/L in the Río de la Plata. For comparison, average values in ocean waters are approximately 0.11 ng/L, while the USEPA has set maximum levels in drinking water at 4 ng/L.

A43

ORAL HEALTH AND SEXUALLY TRANSMITTED INFECTIONS IN ADOLESCENTS: KNOWLEDGE, PERCEPTIONS AND CARE PRACTICES

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According to the World Health Organization (WHO), more than one million people acquire a sexually transmitted infection (STI) every day, and more than half of them are under 25 years of age. The oral cavity may present signs and symptoms or act as a route of transmission, although this is generally unknown. The aim of this study was to analyze the knowledge, perceptions, sources of information and oral self-examination practices of adolescents in relation to STIs and their possible manifestations in the oral cavity. A descriptive, observational, cross-sectional study was conducted in 319 students aged 13 to 17 years from two technical schools in the central district of Rosario. Knowledge and practices were collected through voluntary, anonymous, semi-structured online questionnaires. The data were analyzed using Chi-square tests and odds ratio (OR) calculations, with a significance level of set at $p < 0.05$. Most of the participants were male (85.6%). Dental care was received in through the public sector (44.5%), health insurance (37.9%) and prepaid health services (17.6%). The analysis showed that general knowledge about STIs and awareness that they can cause oral lesions increases significantly with age ($p=0.007$) and ($p=0.0039$) respectively. Self-observation of the oral cavity was a frequent practice among adolescents, with no statistically significant differences ($p=0.45$). In prevention, 42.9% recognized that condoms are not the only method to prevent transmission, with differences by age ($p=0.0083$). The most cited source of information was "Don't know/No answer" responses, followed by school (90) and school and family (13), while health professionals were the least mentioned source (2). A significant association was found between information source and level of knowledge ($p<0.001$). Those who knew what STIs are (66.14%) recognized oral sex as a route of transmission (41.38%), in contrast to 24.76% who did not have this knowledge ($p<0.001$). A total of 229 adolescents expressed interest in receiving more information citing "the importance of knowing and preventing." The analysis on interest and knowledge showed that those with less knowledge about STIs were the most interested in receiving information ($p<0.001$), indicating a clear perceived need. As age increases, the probability of knowing what STIs are increased by 43% ($OR=1.43$; $p=0.045$). The study showed that adolescents' knowledge about STIs and their oral manifestations is limited, although it improves with age. Oral self-observation is common, but is not associated with greater STI knowledge. The school emerged as a key source of knowledge, while those with the lowest level of

knowledge were the most likely to demand information, revealing a significant educational gap. These findings highlight the need to implement educational workshops addressing the relationship between oral health and STIs in order to promote the development of self-care behaviors during adolescence.

A44

DEVELOPMENT OF A METHOD FOR QUANTIFYING *STREPTOCOCCUS MUTANS* COLONIES ON DENTAL HEAT POLYMERIZABLE ACRYLIC RESIN SURFACES

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Streptococcus mutans (Sm) is the primary etiological agent in the initiation of dental caries due to its biofilm-forming capacity, as well as its acidogenicity and aciduricity. This biofilm can develop on soft tissue surfaces, teeth, and both fixed and removable restorative surfaces, which are particularly susceptible to colonization in retentive areas. Preventive practices include mechanical oral hygiene and the use of antiseptics and disinfectants aimed at reducing bacterial load. The aim of this study was identifying a method capable of quantifying the germicidal effect of commercially available solutions commonly indicated for disinfecting the surfaces of prosthetic devices fabricated with heat-polymerizable acrylic resin. Sixty (n=60) samples of this resin were prepared, of which 30 underwent a polishing protocol (RP) and the other 30 received an abrasion protocol (RA). Samples were sterilized with ethylene oxide, incubated with Sm (ATCC® 25175) in tryptic soybean broth for 48 hours at 37°C, washed 5 times with sterile distilled water, and then divided into 3 groups exposed to different treatments: G1 control: rinsing with sterile distilled water; G2: immersion in 0.12% chlorhexidine digluconate; and G3: immersion in a solution containing 34% sodium bicarbonate, 10% potassium monopersulfate, 10% sodium perborate monohydrate, 6% sodium polyphosphate, and 1.5% sodium lauryl sulfoacetate. After treatment, samples were rinsed with sterile distilled water, and surfaces were vigorously swabbed. Each swab was immersed in 0.5 M phosphate buffer, and serial dilutions (1:10, 1:100, 1:1000) were prepared in phosphate buffer. Aliquots of 100 µL from each dilution were plated on Counting Agar (Britania®) and incubated at 37°C ±2 in a 5% CO₂ enriched atmosphere for 48 hours. After this period, direct CFU counts were performed. In the control group, colony counting was impossible at all dilutions due to excessive growth. In G2, between 600 and 1000 CFUs were obtained, whereas in G3, counts ranged between 50 and 500 CFUs. The results obtained are promising with respect to the applicability of the method for the intended objectives. Increasing the number of trials is necessary to allow for statistical evaluation of the findings.

A45

EFFECT OF LAYING HEN HOUSING SYSTEMS ON THE pH AND ELECTRICAL CONDUCTANCE OF EGG ALBUMEN

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The egg is a food product of excellent nutritional quality, offering great versatility for use in the food industry. Currently, consumers are increasingly interested in aspects such as food safety, product quality, price, animal welfare, and environmental care. In this context, interest in the welfare of laying hens has grown, and cage housing systems are often considered deficient, which has driven an increase in floor-raised poultry farming. To ensure egg quality, it is crucial to understand how different housing systems affect their physicochemical properties. In particular, pH and electrical conductance (EC) serve as indicators of internal egg quality. The objective of this study was to evaluate the effect of the laying hen housing system (cage vs. floor) on the pH and EC of the egg albumen. A study was conducted with a population of 500 Lohmann Brown hens. The population was divided into two groups, maintaining identical sanitary and feeding conditions, with the housing type as the sole variable. The Cage Group (CG) consisted of 250 hens housed individually in cages. The Floor Group (FG) comprised the remaining 250 hens, housed in a barn with manual nesting boxes available for laying. Both facilities belong to the Faculty of Veterinary Sciences at the National University of Rosario. For the analysis, 40 eggs were randomly sampled from each group. The pH of the albumen was determined directly using an Orion digital pH meter (model SA 720). Similarly, EC was measured directly using a Navi conductometer (model D3-51). Data were analyzed using a Student's t-test to determine if observed differences were statistically significant. The average pH values were 8.633 ± 0.14 for the CG and 8.479 ± 0.16 for the FG. Regarding EC, the CG showed an average value of 0.757 ± 0.059 mS/m, while the FG had a value of 0.866 ± 0.029 mS/m. Statistical analysis revealed that the differences found in both measurements were significant ($p < 0.05$). The pH and EC of the albumen were found to be higher in eggs from hens housed in cages. The results demonstrate that the housing system significantly affects the pH and EC of the egg albumen. Specifically, in this study, it was observed that the pH of eggs from the CG was 1.8% higher and the EC was 22.6% higher compared to eggs from the FG. These findings suggest that the albumen of eggs from the CG possesses a higher ionic strength, which could indicate higher shell permeability. These increases in pH and EC negatively affect techno-functional properties such as foaming and gelling capacity. Future research could further explore the relationship between these physicochemical parameters and the shelf life or final quality of the egg.

A46

EGG WHITE FOAMS: EFFECT OF LAYING HEN HOUSING SYSTEMS

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Eggs are a food product of excellent nutritional quality and great versatility for the food industry. Egg white is widely used as an effective foaming agent in various bakery products due to its excellent foaming properties. Current consumer demand focuses on safety, quality, price, animal welfare, and environmental care, among other factors. Consequently, interest in the welfare of laying hens has grown; cage systems are considered to have deficiencies in this regard, leading to a rise in the use of floor-based housing systems. To guarantee egg quality, it is essential to investigate how the type of housing affects their physicochemical and functional properties, such as the foaming capacity of the albumin. The objective of this study was to evaluate the effect of the laying hen housing system (cage vs. floor) on the foaming capacity and stability of egg white foams. A population of 500 Lohmann Brown hens was used, divided into two groups with identical sanitary and feeding conditions, differing only in their housing system. The Cage Group (CG) consisted of 250 hens housed individually in 30 x 50 x 37 cm cages. The Floor Group (FG) included the remaining 250 hens, housed in a barn with manual nesting boxes. Both facilities belong to the Faculty of Veterinary Sciences at the National University of Rosario. Forty eggs were randomly selected from each group to evaluate their foaming capacity. To obtain the foams, 10 mL of egg white were stirred in a graduated cylinder using a rotary tool for one minute. The maximum foam volume was measured immediately after whipping. Analysis of variance (ANOVA) was used to determine if the observed differences were statistically significant. Foam stability was evaluated by measuring the amount of drained liquid as a function of time and the drainage rate, using non-linear regression for statistical analysis. The results for maximum foam volume were 23.08 ± 2.39 mL for the CG and 24.8 ± 2.34 mL for the FG, showing statistically significant differences for this variable ($p < 0.05$) in favor of the FG. Regarding stability, the results for the amount of drained liquid and the drainage rate showed no statistically significant differences. The CG presented a drainage of 7.655 ± 1.014 mL at a rate of 0.077, while the FG had a drainage of 8.145 ± 1.045 mL at a rate of 0.075. The findings of this study indicate that the housing system affects the foaming capacity of egg whites. Foaming capacity was 7.4% higher in floor-housed birds. Although foams from floor-housed hens showed a higher final drained volume, those from the cage group—while producing a smaller initial amount of foam—proved to be more stable in the long term. These results suggest that floor housing improves foaming capacity, but cage housing favors foam stability; therefore, it cannot be inferred that the housing system has a negative influence on this egg property, which is so vital for the food industry.

A47

PRESENCIA DE *PUMA CONCOLOR* EN LA CUENCA DEL ARROYO SALADILLO, SANTA FE, ARGENTINA

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The puma (*Puma concolor* Linnaeus, 1771) is particularly sensitive to the expansion of human activities, which may reflect the population contraction it experienced during the twentieth century. However, since the 1990s a possible "recolonization" has been suggested based on various lines of evidence indicating its presence in several sectors of southern Santa Fe, highlighting the importance of monitoring its occurrence and interactions with human activities. The aim of this contribution is to analyze the current population status of the puma in the Arroyo Saladillo basin. To evaluate the presence of the species and its potential conflicts, semi-structured surveys were conducted with local producers, who were contacted through veterinarians and agronomists from the region. These surveys were conducted in person and included closed and open-ended questions directed to individuals who had recorded sightings or experienced conflicts with pumas in the area. A total of fifteen cases occurring between 2019 and 2025 were reported. The results indicate the presence of the puma in eight localities within the basin, with the highest frequency recorded in the commune of Villa Mugueta, where four records were documented. In nine cases the presence of the animal was confirmed through direct observation, whereas in the remaining cases evidence consisted of tracks or third-party testimonies. Regarding the consequences associated with the presence of the species, eight respondents reported livestock injuries. Preventive measures included fencing, the use of sentinel animals such as donkeys (*Equus asinus*) and dogs (*Canis lupus familiaris*), and changes in livestock management. The species was most frequently recorded in mixed farming and/or livestock areas near the Arroyo Saladillo. All interviewees reported the presence of potential prey such as the large hairy armadillo (*Chaetophractus villosus*), the European hare (*Lepus europaeus*), small mammals and birds. A total of 45.5% of respondents do not perceive the puma as a productive problem, whereas the remainder consider it a conflict. All respondents stated that they had not received any institutional guidance regarding the management of the species. Although all participants recognized the importance of conserving *P. concolor* due to its ecological role, most considered its recolonization unfeasible due to human pressure and the expansion of the agricultural frontier. It is concluded that the species is present in the region and that the Arroyo Saladillo may be functioning as a biological corridor; however, its presence generates productive conflicts and the lack of public policies or institutional support programs limits both producers' management capacity and the conservation of the species.

A48

DISTRIBUTION OF RABIES IN DOMESTIC AND SYNANTHROPIC ANIMALS IN URBAN AREAS OF THE PROVINCE OF SANTA FE DURING THE PERIOD 2015-2025

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Zoonotic diseases pose a significant public health challenge. In urban areas, close contact between humans and domestic and synanthropic animals increases the risk of transmission. In the Province of Santa Fe, a notification system has been implemented for registered professionals since 2015, allowing them to report notifiable diseases. This study aims to describe the distribution of rabies in domestic and synanthropic animals in Santa Fe, based on reports made through the notification system, during the period 2015-2025, characterizing the distribution by species and geographic origin. It was also of interest to analyze the geographical distribution according to the first (1°C) or second (2°C) district of the College of Veterinary Physicians of Santa Fe. A cross-sectional observational study was conducted using data obtained from the Santa Fe Food Safety Agency's alert system from mid-2019 until the end of the first half of 2025. Relative and absolute frequencies were used for description, and Fisher's exact test was used for comparisons. During the study period, there were 236 reports, of which 65 (27.5%) were for rabies. Of the rabies reports, 90.77% involved bats, and the remaining 6 involved dogs and cats. A peak in reports was observed in 2020-2022. Eighty percent of the reports were filed in the 1°C, and the remaining 20% in the 2°C. In the 1°C, the departments that contributed the most reports were La Capital (43.08%), followed by Castellanos (18.46%), and Las Colonias (10.77%). In the 2°, the Constitución department accounted for 10.77% of the total reports and had the highest concentration of reports in the 2°C. Complaints filed regarding dogs and cats were distributed equally between both districts; while complaints regarding bats were distributed unevenly, thus, of the total complaints regarding bats, 83.05% were made in the 1°C and the remaining 16.95% in the 2°C, this disparity had a statistically significant trend ($p=0.088$). Regarding confirmation: 100% of reported cases in bats were confirmed, compared to only 50% of those in dogs and cats ($p=0.0004$). The 100% prevalence of rabies in bats underscores the importance of surveillance in this species. The geographic distribution of diseases varies significantly, with a higher number of reported cases in the 1st century. The differences in confirmation rates between species for rabies suggest that active surveillance and awareness are crucial, especially in dogs and cats, to avoid underreporting or misdiagnosis. These findings highlight the need for surveillance and control programs targeted at specific species and regions to mitigate the risk of transmission of these zoonoses to the human population.

A49

NOTIFIABLE DISEASES IN THE PROVINCE OF SANTA FE: REPORTS DURING THE PERIOD 2015-2025

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Epidemiological surveillance is an essential public health tool, as it allows for the development of effective health prevention and promotion measures. In the Province of Santa Fe, the alert button system has been implemented since 2015, enabling veterinary professionals to report notifiable diseases. The objective of this study was to describe the frequency of reports from urban areas submitted by veterinary professionals throughout the province of Santa Fe via the Alert Button system, from its inception until the end of the first half of 2025. A cross-sectional observational study was conducted using data obtained from the alert button system of the Santa Fe Food Safety Agency. Data were collected on the year of the report, the animal species, the reported disease, and the Veterinary College district where it was filed. Descriptive data analysis was performed using relative frequencies, and the difference of proportions test was used to compare proportions. During the study period, there were 236 disease reports. The breakdown by species was as follows: canines: 61.02%; bats: 25%; cats: 7.20%; and birds: 6.78%. The reports were not consistent, with the highest number occurring in 2024, followed by 2021, and then 2017 and 2020. In 2024, the majority of reports concerned canines, and 80.4% of these cases involved leptospirosis. In 2021, canines and bats contributed in a prevalent and similar manner. This year, the main diseases reported were leptospirosis (23.3%) and rabies (56.7%). In 2020, the animals most frequently reported were bats, cats, and dogs, and the most prevalent diseases were rabies (56.67%) and leptospirosis (23.33%). Finally, in 2017, the species contributing the most to the reports were canines, birds, and bats, and the most prevalent diseases were leptospirosis (33.33%), chlamydia (29.63%), and rabies (25.93%). Throughout the study period, of the total reports in the 1st District (C1) (155), 53.55% were for leptospirosis; while in the 2nd District (C2) (81), leptospirosis accounted for 37.04% ($p=0.023$). Similarly, 33.6% of the reports in C1 were for rabies, while in C2, this figure was 16.1% ($p=0.007$). Finally, of all reports in C2, 12.35% were for chlamydia, no reports of chlamydia were found in C1. These results indicate limited and inconsistent participation of veterinarians in reporting these diseases. It is crucial to raise awareness among professionals about the importance of their participation in epidemiological surveillance.

A50

DESCRIPTION OF VARIABLES RECORDED DURING A RABIES VACCINATION CAMPAIGN IN ZAVALLA, ARGENTINA

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Rabies is an endemic and mandatory notifiable disease in Argentina. The National Service for Agrifood Health and Quality (SENASA) has established a national prevention program that mandates annual vaccination of dogs and cats from three months of age. The Animal Health and Welfare Department of the National University of Rosario collaborates with local municipalities in organizing rabies vaccination campaigns aimed at protecting animal health and, consequently, public health. These campaigns are provided free of charge to animal owners and promote the participation of senior Veterinary Medicine students as volunteers, thereby reinforcing their understanding of the veterinarian's social role. The records generated through these activities constitute a valuable source of information for characterizing the targeted animal populations and for supporting evidence-based public health strategies. The aim of this study was to characterize the population attending a rabies vaccination campaign conducted in Zavalla on April 5, 2025. A cross-sectional descriptive analysis was performed based on duplicate official vaccination certificates, and data were entered into a Microsoft Excel database specifically designed for this purpose. Variables recorded included owner information (name, address, locality), animal characteristics (species, name, breed, sex, neuter status), and vaccine-related data (brand, batch number, expiration date). A total of 111 vaccine doses (Providean®) were administered, 86 to dogs and 25 to cats. Among dogs, 24 were intact males, 21 neutered males, 13 intact females, and 28 neutered females; 37 were classified as purebred and 49 as mixed breed. All cats were classified as Domestic Shorthair, including 11 intact males, 6 neutered males, 2 intact females, and 6 neutered females. Data were recorded for 65 owners (42 women, 22 men, 1 unspecified), with variability in the number of animals presented per owner. According to national census data, Zavalla has 6,378 inhabitants; however, the lack of reliable data on the local dog and cat population limits estimation of vaccination coverage and underscores the need for systematic companion animal surveillance. Periodic vaccination campaigns, together with strengthened public health policies, are therefore essential to sustain rabies prevention and promote responsible dog and cat ownership.

A51

DOG HEMOPATHOGENS INVESTIGATION IN SANTA FE AND CORDOBA PROVINCES (ARGENTINA): BACTERIA OF *Anaplasmataceae*, *Rickettsia* AND PROTOZOA OF *Apicomplexa*

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Detecting hemopathogens in dogs and cats presents a constant challenge for veterinarians. These agents are geographically widespread; climate change causes variations in vector populations that transmit them. The aim of this study was to detect bacteria of the *Anaplasmataceae* family and *Rickettsia* genus, and *Apicomplexa* protozoa in dogs from southwestern of Santa Fe and southeastern of Córdoba. Samples of blood submitted by clinicians to the laboratory, from different locations of Santa Fe (Chañar Ladeado, Berabevú and Casilda) and Córdoba (Camilo Aldao, Cruz Alta, Corral de Bustos, Isla Verde, Monte Maíz and Cavanagh), between 2021 and 2025, with a request for hematological analysis and detection of hemopathogens, were selected. Extracted DNA of these samples were sent to Immunology and Parasitology Laboratory of INTA Rafaela, where three conventional PCR were performed: 1- *Anaplasmataceae* (16S rDNA): GE2-F2 (5'-GTT AGT GGC AGA CGG GTG AGT-3') and HE3 (5'-TAT AGG TAC CGT CAT TATCTT CCC TAT-3'); 2- *Rickettsia* spp. (gltA): CS 239 (5'-GAT GAT GTC TGA AGA TAT GAA ACA AAT-3') and CS 1069 (5'-CTG CTC GTC TAT TTTACT TCT TAAAGT-3'), and 3- *Apicomplexa* (18S rDNA): BAB 143-167 (5'-CCG TGC TAA TTG TAG GGC TAATAC A-3') and BAB 694-667 (5'-GCT TGA AACACT CTA RTT TTC TCA AAG-3'). Positive samples for *Anaplasmataceae* were tested to identify *Ehrlichia canis* with a real-time PCR using the primers EC rev (5'-CCC GAGACCGTA TTC ACC G-3') and AE_for (5'-CGC AAG GYT KAG CTA ATC CRT AAA AGT -3') and TaqMan® EC_probe (5'-TGT TCT CTG AAA CTC GAG -3'). Negative (nuclease-free water) and positive controls (DNA of *Anaplasma marginale*, *Babesia bigemina*, *Ehrlichia canis* and *Rickettsia parkeri*) gave expected results. *Ehrlichia canis* DNA was detected in 5 samples from Isla Verde (2/5), Cruz Alta (1/8), Cavanagh (1/2) and Casilda (1/1). One sample from Berabevú (1/1) was positive for *Apicomplexa*; it is being sequenced to determine genus/species. In 2016, 70 samples from healthy dogs of this region were studied, and *A. platys* was detected in 15.7% of animals, *Babesia vogeli* in 7% and *E. canis* was not detected. The present research (2021-2025) revealed that 12.5% of studied dogs were infected with *E. canis* and 2.5% with *Apicomplexa*. In both studies, no bacteria of the genus *Rickettsia* were detected.

A52

**TOTAL PHENOLS OF PLANT SPECIES WITH FORAGE POTENTIAL FROM THE
UPPER DELTA OF THE PARANÁ RIVER**

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Phenolic compounds are part of the secondary metabolism of plants and possess a chemical structure characterized by an aromatic ring (phenol) and at least one hydroxyl group, which provides redox characteristics. It is of interest to determine the concentration of total phenols (TP) in species with foraging potential consumed by livestock, as these could influence the efficiency of their utilization within the ruminal environment. Previous studies conducted on Mulberry leaf samples showed seasonal variations in TP concentration relative to the time of year of sampling. The objective of this work was to quantify the total phenol content in plant species with foraging potential from the islands of the Upper Paraná River Delta. Samples were taken from the herbaceous species *Vigna luteola* (VL); the shrubs *Lippia alba* (LA) and *Baccharis salicifolia* (BS); the trees *Salix humboldtiana* (SH), *Tessaria integrifolia* (TI), *Vachellia caven* (AC), and *Gleditsia triacanthos* (GT); and three hays of *Medicago sativa* (alfalfa: HA16, HA18, and HA3). Plant species samples were collected periodically during their growth cycle on islands of the Paraná Delta across from the City of Rosario (Km 430 of the navigation channel). The determination of TP was performed using the Folin-Ciocalteu (FC) spectrophotometric method, using Gallic Acid (GA) as a standard. An aqueous extract was prepared using 0.5 g of dry sample and 10 ml of 60% (w/v) ethanol. The mixture was stirred for 3 hours at room temperature in the dark, centrifuged at 4000 rpm for 20 minutes, and filtered. The residue was resuspended, centrifuged, filtered, and incorporated into the first supernatant. Then, 100 µl of the aqueous extract were reacted with 500 µl of FC reagent and 4 ml of 1M Na₂CO₃ for 90 minutes, and measured at 765 nm in a Hitachi U-1500 spectrophotometer. Results were compared with a 0.04 g/l GA standard. TP content was determined in duplicate and analyzed by ANOVA and Fisher test. The results were expressed in mg of gallic acid equivalents (GAE) per 100g of DM (Dry Matter) and were as follows: BS 187.08±6.40 a; TI 194.98±12.84 a; HA3 217.81±18.40 ab; GT 245.32±13.25 abc; HA18 246.20±29.22 abc; HA16 282.16±14.52 bcd; AC 287.27±25.47 cde; SH 287.45±19.14 cde; LA 336.06±17.76 de; VL 351.77±39.15 e (a; b; c; d; e: different letters indicate significant differences, $p < 0.05$). The lowest TP concentration was observed in BS and TI, which differed significantly from the rest, except for HA3, GT, and HA18. The highest TP concentration was observed in VL, which showed significant differences from the rest, except for AC, SH, and LA. Regarding the studied hays, a significant difference was observed between HA3 and HA16. These results show that although the TP concentration among the analyzed plant species was variable, it is similar to or even higher than that of a forage species widely used in ruminant nutrition, such as HA. Furthermore, these findings encourage further study during the collection period to evaluate possible variations in TP concentration during the different stages of the growth cycle of the studied species.

A53

**SURVEY OF SPONTANEOUS PLANT FLORA IN THE “FLORINDO DONATI”
PROTECTED NATURAL AREA (CASILDA, SANTA FE, ARGENTINA)**

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The systematic survey of spontaneous plant flora in the “Florindo Donati” Protected Natural Area (Santa Fe, Argentina) was conducted between March and December 2024 using a sampling design based on three transects, including field observation, specimen collection, herborization, and taxonomic identification. The objective of this study was to identify, record, and characterize the spontaneous plant species present in the area, distinguishing between native and exotic taxa, in order to contribute to floristic knowledge and biodiversity conservation. A total of 36 angiosperm species were recorded, comprising 21 native and 15 exotic species, belonging to 4 monocotyledons and 31 dicotyledons. Among the native species, *Eryngium coronatum*, *Chaptalia nutans*, and *Modiolastrum malviflorum* were identified as indicators of well-conserved Pampean environments, while invasive exotic species such as *Gleditsia triacanthos*, *Xanthium spinosum*, and *Convolvulus arvensis* were recorded, representing a potential threat to local biodiversity. All collected specimens were herborized and incorporated into the Herbarium of the Agrotechnical School (UNR). This study provides a preliminary floristic inventory that supports conservation and management of the protected area and also represents a valuable educational resource for Natural Sciences teaching. Continued surveys will allow the expansion of floristic knowledge and monitoring of invasive species in the region.

A54

THE INFLUENCE OF ARTIFICIAL INTELLIGENCE APPLICATIONS IN INITIAL
TEACHER EDUCATION IN BIOLOGY

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Artificial Intelligence (AI) is no longer a future prospect but has become an everyday tool in various areas of social life, including education. Its accessibility has directly impacted teaching and learning processes, transforming not only daily classroom practices but also initial teacher education. In this context, the Secondary Education Biology Teacher Training Program faces the challenge of critically incorporating these technologies without losing sight of the pedagogical and ethical foundations that guide their use. During the 2025 academic year, we set out to analyze how AI-based applications are being used by pre-service teachers, particularly in the field of Biology, and to examine the implications of these practices for their professional development. The analysis addressed different dimensions of AI use: the positive and negative changes it introduces in learning processes, the level of conceptual appropriation achieved by future teachers, and the frequent overuse of digital tools without sufficient pedagogical reflection. In this regard, we problematized the way AI generates automated protocols for the production and application of content, which are often adopted literally by students. We also examined the possibilities and limitations of these tools in the development of teaching resources, considering criteria such as relevance, contextualization, and curricular coherence. The proposal aims to promote a responsible, creative, and situated use of AI, understood not as a replacement for teacher reflection but as a tool that can enhance it. From the perspective of initial teacher education, it is essential to create spaces for debate and critical analysis in order to review the strengths and weaknesses of these emerging technologies and to encourage their planned integration based on clear pedagogical foundations. Through work with students from different years of the teacher training program, we analyzed diverse experiences ranging from the instrumental use of AI to complete specific tasks, to more complex proposals such as the design of teaching sequences that integrate curricular content with technological tools. The inclusion of AI in Biology teacher education raises urgent questions regarding the role of the future teacher, the meaning of technology-mediated teaching, and the construction of meaningful knowledge. This reflection is crucial to ensuring quality education in which technology serves autonomous pedagogical thinking rather than replacing it.

A55

RUMEN DEGRADABLE FRACTIONS OF *Lippia alba* DURING ITS GROWTH CYCLE

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Lippia alba (Mill.) N.E.Br. ex Britton & Wilson, an aromatic, perennial shrub of the *Vervaceae* family, known as "purple sage". Native to the American continent, in our area it is found on the islands of the Paraná River Delta. In recent years, information has been generated on native food resources consumed by ruminant herbivores grazing on the islands of the upper Paraná River Delta; however, the available information remains limited, especially regarding chemical composition, digestibility in ruminants, etc. This work proposes to compare *in sacco* rumen degradable fractions of *Lippia alba* (LA) during its vegetative growth period. We worked with leaf samples, obtained at regular intervals, during the spring-summer growth period of 2019-2020, on Mástiles Island located at km 430 of the Paraná River. After collection, the dry matter content (DM %) was measured, subsequently they were dried at 60°C, ground and sieved (2 mm). The ruminal degradability of dry matter (RDDM %) was determined for each sample at 0, 3, 6, 12, 24 and 48 h of *in sacco* incubation, in four Pampinta breed sheep. The data obtained were fitted to the model of Orskov and McDonald (1979): $RDDM \% = a + b(1 - e^{-ct})$, where **a**: rapidly degradable fraction, **b**: slowly degradable fraction, **c**: degradation rate of **b** and **a + b**: potentially degradable fraction. The results were analyzed using ANOVA and Tukey's test ($P > 0.05$). The average value (SD) of the dry matter of the LA samples was 25.5 (3.5) %. The rapidly degradable fraction (a), the slowly degradable fraction (b), the degradation rate of b (c) and the potentially degradable fraction (a + b) of the *Lippia alba* samples were in **LA1**: 19.05; 54.01; 73.06 and 0.086344; in **LA2**: 20.42; 52.90; 73.32 and 0.095937; in **LA3**: 27.54; 55.82; 83.36 and 0.110328; in **LA4**: 16.30; 50.34; 66.64 and 0.086344 and in **LA5**: 19.35; 52.38; 71.73 and 0.081547, respectively. The RDDM 48h was 69.12; 71.85; 78.86; 64.81 and 67.43 % in LA1, LA2, LA3, LA4 and LA5, respectively. Differences were observed between the LA samples in the rapidly and potentially degradable fractions, while there was no difference in the slowly degradable fraction and in the rate of degradation. The 48-hour dry matter degradability (RDDM 48h) was lowest in LA1, LA4, and LA5, intermediate in LA2, and highest in LA3. The ruminal degradation rate was the same in all samples, suggesting a similar degradation dynamic throughout the vegetative period, although variations in extent were observed; however, these were not related to the plant's growth period. *Lippia alba* can be considered a native food resource for ruminant herbivores that is rapidly degradable and has high potential degradability in the rumen *in sacco*, as all samples exceeded the 60% rumen degradable dry matter threshold.

A56

**TEACHING INNOVATION AND SKILLS DEVELOPMENT IN THE ORIENTATION
CYCLE OF THE VETERINARY MEDICINE DEGREE PROGRAM EDUCATIONAL**

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In the current context, university teachers face unprecedented challenges in higher education, which requires deep reflection and analysis of educational processes. This transformation is necessary and goes beyond mere updating, involving a review of curricula and the adoption of innovative teaching methodologies to significantly improve the quality of teaching-learning processes and the professional quality of educators themselves. These challenges arise from multiple factors, such as the need for future professionals to adapt to a globalized, competitive, and constantly changing society. Pedagogical innovation involves the development of new teaching strategies and resources that promote more active and motivating teaching. The aim is to move from a model focused on the transmission of content by the teacher to one where the student is the active protagonist of their own learning. The Department of Agricultural Economics and Rural Administration proposes changes in the program and teaching strategies for the orientation cycle, relying on the application of Problem-Based Learning (PBL), where a real or simulated situation is created with the aim of recreating a business situation or analyzing a company fact. One of the fundamental purposes of this strategy is to promote the development of complex skills and competencies for professional fulfillment. PBL aims to promote student-centered learning, making students responsible for "learning to learn," which is related to the development of cross-curricular skills. These types of innovative methodologies in the university setting represent a profound transformation of teaching-learning processes, which seek to go beyond traditional models focused on the transmission of information by the teacher. In addition, this technique is characterized by being student-centered, encouraging student participation and autonomy, and preparing students for the challenges of a constantly changing society. Students work in small groups to achieve a common goal, acquiring social and collaborative skills. Innovative methodologies are not just new tools, but a change in pedagogical approach that seeks to empower students, connect them with reality, and incorporate the complex skills necessary for professional development. They involve a continuous effort of reflection and adaptation on the part of teachers and institutions, integrating technology in an intentional and effective way to create meaningful, creative, and motivating learning experiences. The use of active methodologies is crucial to improve university learning in the current context, driving significant change in educational processes. Innovation, knowledge update and teaching strategies are essential to provide quality education and to develop essential skills and competencies such as critical thinking, problem solving, creativity, communication, collaborative work, and decision making.