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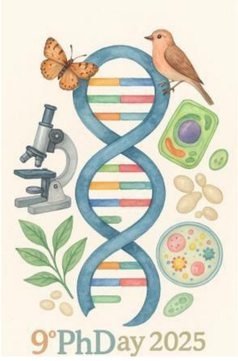

LIBRO DE ABSTRACTS

9ºPhDay Facultad de Ciencias Biológicas

9 de octubre de 2025

COLEGIO OFICIAL DE BIÓLOGOS DE LA COMUNIDAD DE MADRID

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Índice

Programa 9º PhDay Facultad Ciencias Biológicas UCM

Jueves, 9 de octubre en el Salón de actos de la Facultad de Ciencias Biológicas

9:00 - 9:15 Recepción y acreditación

9:15 - 9:30 Inauguración

9:30 - 10:00 Ponencia inaugural

Hic Sunt Dracones, el inventario de la biodiversidad en el siglo XXI

Francisco José Cabezas Fuentes
Profesor del Dpto. de Biodiversidad, Ecología y Evolución
Director del Herbario MACB

Sesión I - Biodiversidad y Conservación

10:00 - 10:10 Miriam García Torija
Analysis of the diversity of edaphic fungi and bacteria in ruderal communities in urban areas

10:10 - 10:20 Adrián Duro Peinó
The wolf´s diet in Europe: specialist wolves eat less livestock

10:20 - 10:30 Claudia Lansac Nieto
Searching for the culprits of drastic declines on a Colombian cloudforest amphibian community

10:30 - 10:40 Marta García Cobo
Island-like environments through the lens of meiofaunal diversity: a metabarcoding approach

10:40 - 10:50 Aida Vega Abellán
Assessing Parasite Prevalence and Health Status of the Eurasian Tree Sparrow (Passer montanus) in Green Urban Areas of a Southern European City

10:50 - 11:00 Sergio Alías Segura
Metataxonomic analysis reveals that the farming system has minimal effect on soil microbiome variation in cereal fields

11:00 - 11:10 Tessa Lynn Nester
Uncovering the complex interactions between invasive Gambusia holbrooki and endangered killifish populations of the Iberian Peninsula using eDNA techniques

11:10 - 12:00 *Coffee break* (cafetería de la Facultad)

Sesión II - Ecología y Evolución

12:00 - 12:10 Judit Sánchez Nogueras
Physico-chemical indicators of disconnected pools and dry riverbeds for the assessment of the ecological status of non-perennial rivers

12:10 - 12:20 Mar Casquero Muñoz
Patterns of growth and maturation in a Meroitic sample from Abri, Northern Sudan

12:20 - 12:30 Adrián Chinarro Sánchez
Deciphering the Evolution of the Pallial Fields of Ray-Finned Fishes

12:30 - 12:40 David Ricote Hernández
A New Perspective on Type-Token Distinction in the Genotype and Phenotype Concepts

12:40 - 12:50 Gabriella Lima Tabet Cruz
Asymmetrical patterns in eco-evolutionary networks of wild mammal immunity and zoonotic bacterial virulence

12:50 - 13:00 José María Lorente-Sorolla Pons
Diverse sex determination systems and ancient origins of reproductive genes in Sponges

13:00 - 13:10 Carlota Gracia Sancha
Whole Genome Sequencing reveals population structure of the deep-sea sponge Phakellia ventilabrum in the Northeast Atlantic and Mediterranean Sea

13:10 - 14:10 Comida

Sesión III - Biomedicina

14:15 - 14:25 Adriana Baca Muñoz
Modulation of Aging through Fecal Microbiota Transplantation in mice

14:25 - 14:35 Juan Lombardo Hernández
Toward an Integrative Understanding of Microbiota–Brain Communication: A Novel In Vitro Model of Neuron–Bacteria Interaction

14:35 - 14:45 Rut de la Vega Ruiz
Sex hormones and sex chromosomes shape hippocampal physiology in female mice: implications for spatial learning and memory

14:45 -14:55 Gonzalo Aparicio Rodríguez
Human brain transforms time into space for better memorization, prediction and decision-making

14:55 - 15:05 María del Mar Rodríguez San Pedro
Inflammatory impact of TET2 mutations in patients with chronic kidney disease

15:05 - 15:15 Karolina Tecza
VIP influences chondrocyte differentiation and regulates cartilage degeneration in osteoarthritis

15:15 - 15:25 Úrsula Díaz Dios
Unveiling the invisible maths of neuropathological aging

15:25 - 15:35 Pausa

Sesión IV - Biotecnología y Microbiología

15:35 - 15:45 Marina Usieto Albero
Beyond 60 °C: Validating Thermal Safety Against Anisakis in Traditional Cooking

15:45 - 15:55 Mirella Llamosi Fornes
Cooperation or conflict? Mixed biofilm models of Streptococcus pneumoniae–Aspergillus fumigatus in pulmonary co-infection

15:55 - 16:05 José David Toledo Guerrero
Effect of short-term high-CO2 treatments on the quality of highbush and rabbiteye blueberries during cold storage

16:05 - 16:15 Marta de Vicente Martínez
From organic wastes to single cell protein by Yarrowia lipolytica

16:15 - 16:25 Beatriz Pasero García
Microbial Valorization of Hydrothermal Liquefaction Wastewater

16:25 - 16:35 Inés Pareja Cerbán
Structural and functional studies of the enzybiotic VL-1L, the lysozyme of bacteriophage vB_PaeS_VL1 of Pseudomonas aeruginosa

16:35 - 16:45 Luis García Antón
The origins of scientific food control in Spain

16:45 - 17:45 Sesión Póster

Carlos Recio Añón
Genetic predisposition, dietary patterns and physical activity in the expression of obesity: an analysis in the school-age population of Andalusia (Spain)

María González Pascual
Pubertal somatic variation and age at menarche in XXI century Spanish girls

Sara Morán de Bustos
Comparative evaluation of the peripheral immune response in sheep experimentally infected subcutaneously or intranasally with Rift Valley fever virus

Cecilia Estefanía Suárez Arregui
Nutritional ultrasound diagnosis of sarcopenia in older adults in Madrid

Marlon Rafael Charris Rincón
Genetic diversity and ancestry in Colombian populations with a high level of admixture

Adrián García Deltell
Baermann vs faecal culture: comparison of two methodologies for detecting parasites in the faeces of wild fallow deer (Dama dama) in the Sierra de Albarracín, Teruel

Tamara González Illanes
Unveiling water effects: a comparative analysis in olive, almond and grapevine leaf surfaces grown under dryland or irrigation

Sara Vidal Notari
The Sleeping Beauty Awakening: Cellular Reprogramming upon Injury-Induced Regeneration in the Bladder Urothelium

Alba Méndez Alejandre
Inferring somatic mutations from single-cell transcriptomics in the human esophagus

Alba Cano Bustos
Beyond Telomeres: Unravelling the Function of CTC1 in Arabidopsis Meiosis

Carmen Erena Ortega
Mycobiota diversity in cereal seeds after four decades of storage

Andrea Miguel Batuecas
Optimization of primary mouse hepatocyte cultures for potential cell therapy in factor V deficiency

Carmen Duque Amado
Environmental DNA as an effective tool for the study and conservation of Parachondrostoma arrigonis (Teleostei: Leuciscidae) and for assessing co-occurring species

Javier Benítez de la Cruz
Engineering a Bioelectrical Interface: ENS Neurons and Bacterial Biofilms on a Microfluidic Chip

Itziar Jericó González
Low-coverage whole-genome sequencing and bioinformatic pipelines to explore genetic variation in Iberian blackcap populations

Paula de la Huerta Bengoechea
Yarrowia lipolytica as a dual platform for sustainable protein and tailored lipid production from carboxylates

Ainhoa Collada Marugán
Transient exposure to hyaluronic acid restores the structure and performance of pulmonary surfactant membrane complexes

Santiago Roque de Miguel Sanz
Investigation of PHA synthesis in the heterologous producer Escherichia coli W

Alba Macho Callejo
Root marks as diagnostic indicators in archaeological and forensic taphonomy

Natalia Elena Expósito de la Paz
Histone H4 acetylation as a molecular switch for somatic embryogenesis in Quercus suber

Tomás Torres Medina
The fossil hand of the Homo sp. from the Ruidera Middle Pleistocene site (Ciudad Real, Spain)

Ishtiak Malique Chowdhury
An efficient process strategy to co-produce microbial oil and carotenoids utilizing biowaste-derived sugar rich media

Marta Trujillo de la Cruz
Comparison of qPCR and LAMP for the detection of lupin in food matrices

Arturo Rodríguez Pascual
Changes in functional structure affect community stability: insights from a removal experiment

17:45 - 18:00 Entrega de premios

Abstracts

Comunicaciones orales

Sesión I. Biodiversidad y conservación

Analysis of the diversity of edaphic fungi and bacteria in ruderal communities in urban areas.

Miriam García Torija[1], Ana García Muñoz[2,3], José Antonio Molina[1], Raquel Pino-Bodas[2,3]

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Summary

Soil microbial communities play a fundamental role in ecosystem functioning, but their composition and diversity remain poorly understood in many environments, especially in Mediterranean urban areas. This study aims to characterise the taxonomic and functional diversity of soil microbial communities associated with four ruderal herbaceous communities in four green areas of the city of Madrid (Spain). This study was carried out using the metabarcoding method and the ITS2 region to characterise fungal diversity and the 16S region for bacterial diversity. The DADA2 pipeline was used to filter the reads and generate the ASVs present in each community. Taxonomic assignment was performed with the UNITE and Silva 138.1 databases, while the FungalTraits and Faprotax databases were used for classification into functional groups. Alpha diversity indices were calculated and generalised linear models were applied to evaluate differences between the different communities. NMDS analyses were used to explore the composition of the communities and ANOVA was used to assess whether different communities presented different abundances of functional groups. Our results indicate that the microbial communities associated with the four ruderal communities have different taxonomic and functional composition. These findings provide valuable insights into the role of soil microorganisms in Mediterranean urban ecosystems.

Keywords: Soil biodiversity, ruderal communities, urban microbiome, urban greenspaces.

The wolf´s diet in Europe: specialist wolves eat less livestock.

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Summary

The wolf (*Canis lupus*) is an apex predator and is often perceived as harmful to domestic ungulates, upon which they prey occasionally. We performed a bibliographical search for the available wolf diet studies in Europe to identify the main predictors that determine the wolf´s natural trophic niche, via a standardised Levin´s Index. We reclassified the trophic items (9 categories) found in 43 scientific papers and used the frequency of occurrence of only the natural trophic items (8) to calculate a “Natural Levin´s Index”. Akaike´s Information Criterion was used to select the most parsimonious models that explain the natural trophic niche breadth of the wolf, using the frequency of occurrence of domestic ungulates (FODU), biotic and abiotic variables as predictors. The best model showed that the wolf´s natural trophic niche breadth was narrower (more specialised) when domestic ungulate consumption was lesser and in areas with less vegetation cover, greater altitude and ruggedness. Thus, European wolves that consume more domestic ungulates possess a wider natural trophic niche breadth (more generalist diets). Finally, the FODU was significantly negatively correlated to an increase in wild ungulate species richness, thus proving that domestic ungulate consumption decreases significantly in areas of greater wild ungulate availability.

Keywords: Conflicts, Diet, Livestock, Wolves, Ungulates.

Searching for the culprits of drastic declines on a Colombian cloudforest amphibian community.

Claudia Lansac[1,2], Marta Miñarro[1,2], Ignacio De la Riva[1], Patricia A. Burrowes[1,3]

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[3]. Department of Biology, University of Puerto Rico, San Juan, P.O. Box 23360, Puerto Rico.

Summary

Climate change and infectious diseases are among the main Anthropocene stressors affecting amphibians. The Reserva Natural La Planada, located in the Andes of southern Colombia, allowed us to assess the effects of both factors in an amphibian community previously studied in 1986. In 2021, we replicated that study monitoring along stream and forest transects. We took climate and *Batrachochytrium dendrobatidis* infection data, a fungal pathogen responsible for amphibian severe declines and extinctions worldwide. We observed a 67% loss in species diversity, along with changes in relative abundance and community composition. We found a *Bd* prevalence of 30% affecting most species, but low infection intensities indicative of enzootic chytridiomycosis. Species identity was the strongest predictor of *Bd* infection, indicating a phylogenetic signal in host susceptibility. Because climatic data suggest temperature increase and precipitation variation, thermal-hydric tolerance experiments were conducted on four *Pristimantis* species to assess whether their physiological responses can explain their current abundance. Results suggest that the most common species tolerates and performs better at higher temperatures than those that have declined. We are currently investigating the *Bd* strain at the reserve and associations between the amphibian skin microbiome and *Bd* infection dynamics to explore how species survive disease outbreaks.

Keywords: neotropics, *Batrachochytrium dendrobatidis*, climate change, diversity

Island-like environments through the lens of meiofaunal diversity: a metabarcoding approach

Marta García-Cobo[1,2], Petra Cattano[3], Diego Fontaneto[2], Francesco Di Nezio[2], Fernando Pardos[1], Nuria Sánchez[1] & Alejandro Martínez[2]

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Summary

Island systems have long served as natural laboratories for ecology and evolution, enabling the development of theories of broad significance. Beyond actual islands, isolated habitats such as alpine lakes, caves, or deep-sea trenches function as “island-like environments”, offering to study processes of adaptation, speciation, and community assembly at multiple temporal and spatial scales. Problematically, most island biogeography research is biased towards a narrow set of organisms, predominantly vertebrates and hexapods, whereas meiofauna—remarkably rich in taxonomic, functional and phylogenetic diversity—remains unexplored as a model. Despite their richness and diversity, unbiased assessments of meiofaunal biodiversity patterns remain challenging. Metabarcoding provides a powerful entry point for studying meiofaunal diversity across habitats, producing large datasets efficiently. However, incomplete reference libraries and lack of trait annotation restrict taxonomic resolution and limit ecological inference. To mitigate this, we have developed a pipeline that places “unclassified” sequences within a reference tree, improving taxonomic assignment, retaining more sequence information, and enabling the calculation of functional and phylogenetic diversity metrics. Ultimately, the full potential of metabarcoding depends on integrative approaches: linking molecular surveys with traditional taxonomy and trait-based data. Here we propose a conceptual synthesis: using meiofaunal metabarcoding as a rapid, broad-scale entry point into meiofaunal diversity across island-like environments, followed by morphological and functional analyses to infer causal processes. We illustrate this approach with case studies from terrestrial gypsum caves from (Vena del Gesso, Italy), marine benthic samples from Antarctica and freshwater samples from an alpine lake (Lake Cadagno, Switzerland).

Keywords: metabarcoding, island-like environments, meiofauna, beta diversity

Assessing Parasite Prevalence and Health Status of the Eurasian Tree Sparrow (*Passer Montanus*) in Green Urban Areas of a Southern European City

Aida Vega [1]*, Michael J. Yabsley [2,3,4,] Sonia M. Hernández [2,3,4], Kayla B. Garrett [2,3] , José I. Aguirre [1] and Eva Banda [1]

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Summary

Urban environments generate new types of ecosystems whose ecological characteristics vary with local planning strategies. In Europe, the expansion of urban areas is a key conservation goal. However, the impact on wildlife health remains a relatively understudied area. The present study assesses the prevalence and parasite burden of Eurasian Tree Sparrows in five urban green areas in Madrid, Spain, over a period of four years. These green areas differed in their green infrastructure, providing a useful model to assess how green area design influences urban biodiversity. We examined parasite presence along with measures of body condition and immune status. Blood parasites were detected in 29% of individuals, and gastrointestinal parasites were found in 4% of birds. Notably, blood parasite prevalence was significantly higher in green areas characterized by the presence of stagnant, untreated water and muddy margins, which may be optimal breeding sites for vectors. Our findings highlight the role of water management in urban green areas as a key factor influencing parasite transmission. Incorporating parasite risk into green area planning can improve wildlife conservation and reduce potential health risks to humans in urban areas.

Keywords: water management, urban green area, urban biodiversity, public health, wildlife surveillance, vector-borne diseases.

Metataxonomic analysis reveals that the farming system has minimal effect on soil microbiome variation in cereal fields

Sergio Alías-Segura[1], Jéssica Gil-Serna[1], Belén Patiño[1]

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Summary

The soil microbiota, particularly mycotoxin-producing fungal communities, has garnered increasing attention owing to its implications for human and animal health. Mycotoxins commonly contaminate cereal crops and their by-products, with their associated health risks intensified by climate change. The growing demand for organic food, driven by perceptions of enhanced safety, contrasts with the inconclusive research on mycotoxin contamination in organic versus conventional cereals. In this study, we employed metataxonomics to investigate potential variations in fungal and bacterial community diversity between organic and conventional farming systems in cereal fields, with a focus on toxigenic fungi. Our analysis revealed that geographic location of the samples, rather than farming practice, was the primary driver of diversity differences. Furthermore, we found no significant evidence of differential abundance across toxigenic fungal groups between the two systems. To validate taxonomic assignments, we constructed a phylogenetic tree using sequences classified under the genus *Fusarium*. Additionally, we assessed the potential activity of biocontrol agents from certain bacterial genera against toxigenic fungi by analysing their co-occurrence patterns. Notably, we detected mycotoxigenic species of concern (e.g., potential producers of aflatoxins or trichothecenes) in cereal fields irrespective of the farming system.

Keywords: NGS; Mycotoxins; Fusarium; Organic; BCA

Uncovering the complex interactions between invasive *Gambusia holbrooki* and endangered killifish populations of the Iberian Peninsula using eDNA techniques

Nester, Tessa Lynn[1], López-Solano, Alfonso[1], Perea, Silvia[1], Doadrio, Ignacio[1]

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Summary

The invasive Eastern mosquitofish (*Gambusia holbrooki*) is considered a major threat to the native ichthyofauna of the Iberian Peninsula, particularly two endangered and endemic killifish: the Baetican toothcarp (*Aphanius baeticus*) and the Spanish toothcarp (*Aphanius iberus*). Since the introduction of *G. holbrooki*, both *A. baeticus* and *A. iberus* have suffered notable population declines, though the mechanisms driving this negative impact remain unclear. The present study applied environmental DNA (eDNA) techniques to assess possible interspecific interactions contributing to these population declines. Over three years, fecal and gut content samples were collected from co-occurring populations of *A. baeticus* and *G. holbrooki* in Cádiz, and over two years from coastal lagoons in Girona where *A. iberus* coexists with *G. holbrooki*. Additionally, a controlled mesocosm experiment explored potential ecological interactions across three treatments: species separated, cohabiting, and cohabiting with a barrier allowing only the passage of zooplankton. Results suggest that *G. holbrooki* may exert a multifaceted threat on *Aphanius* populations through a combination of interspecific interactions, including resource competition, predation and agonistic behavior. Given the widespread presence of *G. holbrooki*, invasive species management should be a conservation priority to safeguard the long-term viability of these endemic and endangered killifish within their native habitats.

Keywords: Environmental DNA (eDNA), Endangered killifish, Invasive species, Interspecific interactions

Sesión II. Ecología y evolución

Physico-chemical indicators of disconnected pools and dry riverbeds for the assessment of the ecological status of non-perennial rivers

Sánchez-Nogueras, J. [1], Arce, M.I. [2], Piñero-Fernández, M. [3], Quevedo-Ortiz, G. [3], Freixinos, Z. [2], de las Heras, P. [1], Bonada, N. [3], Cid, N.4, Sánchez-Campaña, C.[3], López-Rodríguez, N.[3], Soria, M.[3], Rodríguez-Lozano, P.[5], Ersoy, Z.[3], Roblas, N.[6], Verdugo, M.[6], Miñano-Martínez, J.[2], López-Pintor, A.[1], Morcillo, F.[1], Díaz-Redondo, M.[6], Suárez, M.L.[2], Vidal-Abarca, M.R.[2], López-Rodríguez, M.J.[7], Tierno de Figueroa, J.M.[8], Rovira, J.V.[1], Fortuño-Estrada, P. [3], Pérez-Lajarín, E.[1], Sánchez-Montoya, M.M. [1]

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Summary

Non-perennial rivers are fluvial ecosystems characterized by alternating flowing (lotic habitats), disconnected pools (lentic habitats) and dry riverbeds (terrestrial habitats) habitats. Research on these ecosystems have revealed their ecological importance for biodiversity, ecosystem processes, and ecosystem services. Despite their ecological significance, non-perennial rivers are often overlooked in scientific research and policy frameworks. In fact, the European Water Framework Directive (WFD) primarily addresses the flowing phase of rivers, leading to an incomplete assessment and management of non-perennial river systems. This study focused on the search for physico-chemical parameters as potential ecological indicators to assess the physico-chemical quality of non-perennial rivers during the dry phase (disconnected pools and dry riverbed sediments) we related several parameters to anthropogenic pressures (pH, conductivity, oxygen and nutrients). To this end, we monitored 65 disconnected pools and 61 dry riverbed sediments across different basins in Spain (Segura, Guadalquivir, Guadiana, Tajo, Jucar, Ebro, Menorca , and Catalan internal basins) along a multiple-stressor gradient. Additionally, we analyzed the geology of each study basin to determine its influence on the responses of physico-chemical parameters to the pressure gradient. These findings will allow advancing the proper assessment of non-perennial rivers, and will support the incorporation of the dry phase of rivers in ecosystem monitoring and assessment.

Keywords: Non-perennial rivers, Water Framework Directive, ecological assessment, physico-chemical parameters

Patterns of growth and maturation in a Meroitic sample from Abri, Northern Sudan

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Summary

The study of child growth and maturation is a sensitive tool for the assessment of the biological living standards of the larger population. We studied 33 well preserved skeletons from the Nubian cemetery of Amir Abdallah (Abri, Northern Sudan), dated to the Early Meroitic Period (3rd – 1st cent. BCE), ranging in estimated age from 0.125 to 19 years. Age was estimated from dental maturation, and the maximum lengths of the humerus, radius, femur and tibia were measured. Skeletal maturation was scored for those epiphyses associated with adolescence in skeletons older than 10 years of age. When compared to a modern, healthy North American series, 39%, 31%, 61% and 30.5% of the sample is under 2 standard deviations for the length distribution of the humerus, radius, femur, and tibia, respectively. Skeletal maturation shows a delay in entering the adolescent stage, when assessing the sample of skeletons in the second decade of life (N=11). These observations point to a relatively low biological standard of living of the children and adolescents in the Meroitic society represented by the cemetery of Amir Abdallah. Growth and maturation in Nubian samples have been studied previously at the sites of Wadi Halfa, Kulubnarti and Mis Island, and the present study represents a valuable addition to this body of research.

Keywords: Nubia, Meroitic, bioarchaeology, bone growth, adolescence

Deciphering the Evolution of the Pallial Fields of Ray-Finned Fishes: Comparative Organization of Telencephalic Regions in a Basal and a Derived Actinopterygian Fish

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Summary

The present study compares the telencephalic regions of two key actinopterygian models. As a basal model, we chose the bichir *Polypterus senegalus*, a cladistian fish phylogenetically close to the common osteichthyan ancestor. One of its most interesting features is the presence of an open-everted pallium with a pseudoventricle. As a derived model, we used *Carassius auratus*, a cyprinid teleost with great pallial complexity due to secondary fusion of its everted pallium. In this work, based on the analysis of their genoarchitecture, neurochemistry and connectomic, we revealed the similarities and differences between the main telencephalic territories in a rostrocaudal progression based on the distribution of highly conserved markers and their functional connectivity. The territories analyzed included the ventral telencephalic area in the subpallium and the dorsomedial and dorsolateral pallial areas in the pallium, which are rostrocaudally and functionally distinct in both models, as well as the putative amygdaloid territories of the dorsoventral pallium and posterior pallium in *C. auratus* and the supracommissural and postcommissural territories in *P. senegalus*. Our data provide evidence for a common ancestral telencephalic pattern with specific anatomical and functional features in each model. Our research is funded by the Ministry of Science, Innovation and Universities of Spain.

Keywords: evolution, pallium, telencephalon, actinopterygii, teleosts, cladistians.

A New Perspective on Type-Token Distinction in the Genotype and Phenotype Concepts

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Summary

The type-token distinction is a classical philosophical framework rarely applied to biological concepts. Here I propose that this distinction, when applied to genotype and phenotype, reveals a fundamental duplication: genotype and phenotype concepts each encompass both types and tokens, resulting in four distinct categories requiring theoretical consideration: genotype, phenotype, genotoken, and phenotoken. I demonstrate that genotokens (material instances of genotypes) generate their own identity and individuality through self-templating reproduction processes, independently of human classification. This self-organizing capacity suggests that genotokens function as natural kinds - classifications that reflect the structure of the natural world rather than human cognitive interests. By contrast, phenotokens require external observers for their classification into phenotypes. This perspective provides a novel resolution to the longstanding philosophical problem of natural kinds in biology. Genotokens maintain their identity through genealogical and material continuity across generations, constituting genuine natural classifications. This framework applies not only to genome sequences but extends to diverse inheritance systems including genetic membranes, chromatin modifications, centrosomes, and even cultural transmission patterns.

The core of my doctoral research centers on this diversity of inheritance systems: extending the genotype concept beyond genomic sequences and assimilating the theoretical consequences of this conceptual expansion.

Keywords: type-token distinction, genotype, natural kinds, biological inheritance, genotoken

Asymmetrical patterns in eco-evolutionary networks of wild mammal immunity and zoonotic bacterial virulence.

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Summary

Functional and molecular traits, such as those related to host immunity and pathogen virulence, shape host-parasite interactions. These complex interactions still require a multispecies approach. We addressed this by integrating phylogenetic, immunogenetic, and virulence data across 55 wild mammal species (11 orders) and 65 zoonotic bacteria to assess how trait combinations shape host-parasite networks. Host profiles included 39 protein families, 27 protein classes, and 18 biological processes related to innate immunity. Bacterial profiles included 31 virulence factors (e.g., β-haemolysin, secretion systems) and 12 functional mechanisms, such as motility, adhesion, and immune evasion. Bipartite network analysis revealed low modularity and high overlap in host-bacteria and host-immune factor networks. In contrast, bacterial virulence factors formed distinct functional modules aligned with host sharing, suggesting ecological and functional coherence among bacteria infecting similar hosts. Our results suggest conserved, specialised infection strategies among bacteria, contrasting with flexible, less conserved host immune traits. This functional asymmetry highlights divergent evolutionary pressures: bacteria evolve specificity to infect hosts, while hosts maintain broader immune responses. By identifying evolutionary and functional patterns in host defence and bacterial infectivity, our findings advance the understanding of zoonotic transmission dynamics. This study was supported by Serrapilheira Institute and Comunidad Autónoma de Madrid.

Keywords: innate immunity, immunogenetic, modularity, phylogenetic signal, virulence factor.

Diverse sex determination systems and ancient origins of reproductive genes in Sponges.

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Summary

Sex is a widespread biological feature that provides advantages at multiple evolutionary levels**.** In animals, sex determination can be genetic or environmental, with a wide variety of mechanisms across metazoans. Due to this diversity and plasticity of sexual reproduction in sponges, classical theory assumed that sex is environmentally determined, likely influenced by temperature acting on the expression of specific genes. Here, we used WGS and ddRADseq to investigate sex determination in eight sponge. We identified sex chromosomes in *Chondrosia reniformis* and *Oscarella lobularis*, as well as hundreds of sex-specific loci across the different species, pointing to different sexual systems. In these sponges, sex determination pathways appear to converge on a common set of genetic regulators involved in gonad fate maintenance and transposable element control. We also observed conserved synteny, particularly between *O. lobularis*, *C. reniformis*, and *P. ficiformis*. Evolutionary analysis of sex-related genes revealed that most have ancient origins, with many tracing back to early lineages such as cellular organisms and Eukaryota. Nonetheless, we found notable variation in species-specific sex genes, with *C.reniformis* showing recent innovation, and others like *H. panicea* exhibiting greater conservation—suggesting a combination of ancient retention and lineage-specific divergence in the evolution of reproductive gene families.

Keywords: Evolution, sponges, sex determination, genomics.

Genomic Insights into Species Delimitation of Atlanto-Mediterranean *Phakellia* spp.

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Summary

Deep-water sponge grounds are key structural and ecological components of benthic ecosystems. Within the Northeast (NE) Atlantic and the Mediterranean Sea, species of the genus *Phakellia* play an important role, yet their diversity and connectivity remain poorly understood. Here, we investigated 96 individuals of *Phakellia robusta* Bowerbank, 1866 and closely related *Phakellia* spp., sampled across depths of 50–1150 m. We applied an integrative approach combining genomic data (ddRADseq, 3392 SNPs), microbial community profiling (16S rRNA sequencing), and spicule morphology. Our results revealed four distinct genetic lineages, including two putative hybrid species with stronger genetic and microbiome similarity to *Phakellia* "molesta". Two gene flow events were identified: between *P. robusta* and *P.* sp1, and between *P.* sp1 and *P.* "molesta". Spicular analyses across lineages did not reveal species-specific diagnostic traits. Instead, spicule length and thickness varied significantly with depth. Greater silica availability in deeper habitats allowed for larger and thicker spicules, challenging classical taxonomic approaches that rely on morphology. Overall, our findings highlight the complexity of species delimitation in Phakellia spp. and demonstrate the value of integrative methods for understanding biodiversity in deep-sea sponge ecosystems, with important implications for conservation strategies.

Keywords: connectivity, ddRadseq, hybridization, microbiome, Phakellia.

Sesión III. Biomedicina

Modulation of Aging through Fecal Microbiota Transplantation in mice

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Summary

Gut microbiota communicates bidirectionally with homeostatic systems and is essential for health. With aging, these systems, the microbiota, and their interaction deteriorate, due to increased oxidative stress. Although the microbiota influences aging, it remains unclear whether fecal microbiota transplantation (FMT) from old animals could negatively affect adults. To address this, we evaluated the effects of FMT from aged mice on adult female mice, divided into three groups: one received FMT from old mice, another received FMT from adult mice, and a third served as control group. After two weeks, behavioral tests, and analysis of immune and oxidative stress markers were analyzed. FMT from old mice resulted in increased anxiety, reduced exploratory behavior, weakened immune responses, increased oxidative stress, and decreased longevity. In a second experiment, the effects of FMT from adult or long-lived donors were assessed in aged mice. Four groups were studied: control, handling control, FMT from adult donors, and FMT from long-lived donors. After two weeks, the same parameters were assessed. Mice receiving microbiota from long-lived donors showed improved behavior, immunity, and redox status, with reduced biological age and increased longevity. We conclude that FMT may modulate the aging process, biological age, and ultimately, the longevity achieved.

Keywords: microbiota, fecal transplant, immunity, oxidative stress, biological age

Toward an Integrative Understanding of Microbiota–Brain Communication: A Novel In Vitro Model of Neuron–Bacteria Interaction

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Summary

While it is well established that gut bacteria and brain neurons communicate via the microbiota–gut–brain axis, many fundamental questions in this field remain unresolved. Notably, current research approaches focus almost exclusively on molecular mechanisms—such as metabolites or hormones—while largely neglecting top-down, information-based frameworks. We argue that high-level, integrative approaches are essential for fully understanding the functional relevance of these mechanisms. In this study, we first developed an neuron–bacteria direct interaction methodology that enables rapid screening of the responses of neurons to various microbiota bacterial strains and conditions. Our results show that neurons in vitro can detect the presence of bacteria and actively reshape cell behavior. This includes distinct transcriptomic changes and alterations in intracellular signaling pathways in response to co-incubation with live probiotic strains. Notably, the neuronal response was both strain-specific and dependent on bacterial density. This work represents a proof of concept for advancing research on microbiota–brain communication and opens new avenues for exploring whether neuronal–bacterial interactions can be reprogrammed to modulate central nervous system function and address neuropsychiatric disorders.

Keywords: Gut-Brain axis, microbiota, *Lactiplantibacillus plantarum*, *Escherichia coli*, Bioelectricity

Sex hormones and sex chromosomes shape hippocampal physiology in female mice: implications for spatial learning and memory

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Summary

Despite increasing awareness of sex as a biological variable in neuroscience, most studies of hippocampal physiology still rely heavily on male mice. In this work, we aim to examine how female sex hormones and sex chromosomes (X and Y) contribute to neural activity in the dorsal CA1 (dCA1), a brain region essential for spatial learning and memory. We exploited the Four-Core Genotype (FCG) mouse model, in which biological sex is determined independently of sex chromosomes (X and Y), to perform acute extracellular recordings in awake, head-fixed phenotypic female mice (i.e., with ovaries) while monitoring the estrous cycle stage. This allows us to explore how natural hormonal fluctuations shape hippocampal activity and whether these effects differ depending on chromosomal sex (XX or XY). In addition, we include a cohort of ovariectomized females to study the role of peripheral estrogens, isolating the influence of the ovary from that of chromosomal sex. While previous work has largely overlooked the intersection of hormonal state and genetic sex in shaping brain activity, our approach attempts to fill this gap. Understanding these interactions is critical for better modeling of sex differences in cognitive function and ultimately for designing more inclusive and effective neuroscience research.

Keywords: sex chromosomes, estrogens, hippocampus, neurophysiology

Human brain transforms time into space for better memorization, prediction and decision-making

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Summary

Dynamic situations (i.e. those in which the subject and/or the elements in the environment move) are very common in nature and efficiently dealing with them is essential for survival. Humans cope with the inherent costs and difficulties of representing dynamic situations through time compaction, a cognitive mechanism that embeds time into space, yielding fast, low-cost and generalizable representations. However, the extent to which time compaction affects other cognitive functions is yet unknown. We have performed several cognitive tests in humans to test whether, and under which conditions, time compaction participates in memory, prediction and decision-making. Our results show that time compaction is used for memorization and recalling, predicting the outcome of a situation and making decisions in complex situations. However, the recurrence of this cognitive strategy seems to depend on contextual factors and task complexity. We further discuss the importance of time compaction for survival and evolution, as well as propose future research lines.

Keywords: Human cognition, Dynamic environments, Memory, Prediction, Decision making.

Inflammatory impact of TET2 mutations in patients with chronic kidney disease

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Summary

Chronic kidney disease (*CKD*) is associated with cardiovascular complications and accelerated aging, both linked to a pro-inflammatory state. Clonal hematopoiesis of indeterminate potential (*CHIP*), characterized by the expansion of mutated blood cells in the absence of overt hematologic disease, is another aging-related process, with TET2 being one of the most frequently mutated genes. This study aimed to identify *CHIP* mutations in TET2 in patients with *CKD* and to evaluate their association with inflammation. A cross-sectional study was conducted including 33 patients, 14 with advanced *CKD* (*ACKD*) and 19 on hemodialysis (*HD*), together with 17 healthy controls (*CT*). DNA was extracted from leukocytes and a region of the TET2 gene was amplified by PCR. Plasma inflammatory molecules were quantified using Luminex® technology. Four mutations (*rs34402524*, *rs146348065*, *rs2454206*, and *rs62621450*) were detected in patients and controls. Two of them (*rs146348065* and *rs62621450*) were associated with increased expression of TNFα and IL6, stable TGFβ levels, and higher TNFα/TNFRII, IL1α/IL1RI, and IL1β/IL1RI ratios. In *CKD* patients, TNFα and IL6 levels were significantly elevated compared to *CT*, while IL1α, IL1β, and TGFβ remained unchanged. Notably, TNFα/TNFRII and IL1α/IL1RI ratios were increased in *HD* versus *CT*, and IL1β/IL1RI was significantly higher in *ACKD* compared to *CT*. These findings suggest that *CKD* promotes a pro-inflammatory state similar to that induced by *CHIP* mutations, which may contribute to disease development and progression. This study was supported by projects PI20/01321 and PI23/01109, funded by Instituto de Salud Carlos III and managed by Fundación de Investigación Biomédica Hospital Doce de Octubre.

Keywords: Chronic kidney disease, CHIP, TET2 gene, inflammation

VIP influences chondrocyte differentiation and regulates cartilage degeneration in osteoarthritis.

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Summary

Osteoarthritis (OA) is a rheumatic disease and the leading cause of disability in the elderly. Since no effective treatments exist, new therapeutic approaches are need. Vasoactive intestinal peptide (VIP) has shown anti-inflammatory potential in multiple musculoskeletal pathologies. Chondrocytes (AC, articular chondrocytes) are the resident cells in articular cartilage. In OA, these cells produce inflammatory and catabolic mediators, destroying the extracellular matrix and releasing fragments such as fibronectin fragments (Fn-fs) that further promote degradation. AC cultured *in vitro* in monolayer tend to dedifferentiate, so three-dimensional cultures with biomaterials are used to avoid this and better mimic their natural microenvironment. Mesenchymal stem cells (MSC) are also proposed as potential tools for regenerating damaged cartilage. Therefore, we investigate the influence of VIP on MSC chondrogenesis. We also analyze its effects on cell proliferation, glycosaminoglycans (GAG) production and on the production of inflammatory and catabolic molecules, in AC from OA patients (OA-AC), in the presence of Fn-fs as proinflammatory stimulus. Our results show that VIP promotes chondrogenesis in MSC, by increasing chondrogenic gene expression. Likewise, VIP promotes cell proliferation and GAG production, and modulates the expression of C1R, MMP1 and MMP13 in OA-AC. Funding: Grant numbers RD21/0002/0004; RD24/0007/0014; PR17/24-31935; PR12/24-31568.

Keywords: osteoarthritis, VIP, chondrocytes, mesenchymal stem cells

Unveiling the Invisible Maths of Neuropathological Aging

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Summary

This thesis investigates the functional role of the gut microbiota in the physiopathology of neurodegenerative diseases, such as Alzheimer's and Parkinson's, through mathematical modelling and numerical simulation techniques. Based on the microbiota–gut–brain axis hypothesis, dynamic models are developed to represent the interactions between microbial metabolites, immune mediators, and neuroinflammatory processes. The study employs nonlinear differential equations and stochastic systems to simulate pathological trajectories under varying microbial profiles, validated against experimental and clinical data. A key objective is to use mathematical modelling and simulation to detect divergences between neurophysiological aging in individuals without neurodegeneration and neuropathological aging in affected patients. Computational simulations identify critical microbial compositions that exacerbate neurotoxic mechanisms, such as oxidative stress and protein aggregation. This approach enables the exploration of how specific microbiota variations may modulate neurodegenerative processes, offering potential implications for the design of microbiota-based therapeutic interventions, including prebiotics, probiotics, and personalized microbiome strategies. This interdisciplinary research provides a systems-level perspective on neurodegeneration, integrating microbiology, neuroscience, and mathematical modelling, and contributes to a better understanding of how microbial environments may influence the progression of chronic neurological disorders.

Keywords: Gut microbiota, Neurodegenerative diseases, Mathematical modelling, Numerical simulation, Neurophysiological vs. neuropathological aging

Sesión IV. Biotecnología y Microbiología

Beyond 60 °C: Validating Thermal Safety Against *Anisakis* in Traditional Cooking

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Summary

Anisakiasis is a human infection caused by consuming raw or undercooked fish containing viable third-stage *Anisakis* larvae (L3). EU regulations recommend cooking fish to an internal temperature of 60 °C or higher for at least one minute, but the fish quality can be affected. We recently developed and validated a thermal inactivation model capable of predicting parasite viability as a function of time and temperature exposure in lab conditions. Now, it is time to validate the model in infected fish at real cooking conditions and then use it to assess the risk of *Anisakis* infection in traditional recipes. For that, we used hake fillets infected with *Anisakis* L3 and exposed to various oven temperatures. Then, the risk of infection in fish recipes was assessed in thin and thick pieces of infected hake and cooked at 180 °C for different times. During both sets of experiments, temperature was recorded at different fish locations, model predictions were made and compared to visually observed larval survival. Excellent agreement between the predicted and experimental viability values was observed. Traditional fish recipes often did not achieve EU recommended temperature-time conditions. However, the model confirmed all studied recipes were safe in terms of larval inactivation.

Keywords: *Anisakis*, heat inactivation, hake, survival model

Cooperation or conflict? Mixed biofilm models of *Streptococcus pneumoniae–Aspergillus fumigatus* in pulmonary co-infection

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Summary

Co-infections between *Aspergillus fumigatus* and *Streptococcus pneumoniae* are rare but clinically relevant, especially in immunocompromised patients or those with chronic lung disease. These interactions can complicate diagnosis and treatment and worsen the prognosis. For this reason, the objective of this study is to develop a mixed biofilm between these two pathogens to understand how they interact in the lung. Three *in vitro* models have been analyzed in order to reproduce *in vivo* situations. The first model consists of forming the *A. fumigatus* biofilm and, once formed, adding *S. pneumoniae* for subsequent analysis at different times. The second model consists of forming the mixed biofilm of the bacterium and the fungus at the same time. And the third consists of forming the biofilm of pneumococcus and then adding *A. fumigatus*. Futhermore, in the case of *S. pneumoniae*, we used three different inoculum concentrations: one higher than the concentration of the fungus, one equal to it, and one lower than it. These three models attempt to reproduce situations that could occur in the context of a respiratory co-infection, providing a better understanding of how both pathogens interact and what implications this may have for persistence in these environments or for antimicrobial resistance.

Keywords: biofilm, *Aspergillus fumigatus*, pneumococcus, lung, resistance

Effect of short-term high-CO_2 treatments on the quality of highbush and rabbiteye blueberries during cold storage

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Summary

Worldwide consumption of blueberries has increased in recent years, largely due to their health-promoting properties. However, postharvest deterioration, particularly firmness loss and decay, remains a significant concern. This study aims to analyze the effects of applying high CO_2 concentrations (15% and 20%) for 3 d at 1 °C on maintaining the quality of highbush (cv. 'Duke') and rabbiteye (cv. 'Ochlockonee') blueberries during cold storage. Quality parameters evaluated included titratable acidity, pH, soluble solids content, weight loss, and decay. Additionally, firmness was assessed using mechanical parameters and the expression of genes related to cell wall modification (*XTH23*, *PL8*, *PG*, *PM3*, *EXP4*, and *GH5*). The results indicated that treatment efficacy varied between species. High CO_2 levels reduced decay in both cultivars, but only the highbush cultivar ('Duke') exhibited enhanced firmness. In 'Duke', CO_2 treatments affected the expression of *XTH23*, *PL8*, and *GH5*, while the role of *PG* and *PME* in firmness was minimal, with no significant differences between treatments. In 'Ochlockonee', CO_2 effectively reduced weight loss but did not improve firmness. These results highlight the need for tailored postharvest strategies for different blueberry species and cultivars and suggest that short-term high CO_2 treatments may effectively prolong the postharvest life of highbush blueberries.

Keywords: *Vaccinium*; CO_2; Cold storage; Mechanical properties; Gene expression.

From organic wastes to single cell protein by *Yarrowia lipolytica*

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Summary

Single cell proteins (SCP) are promising protein sources due to their balanced amino acid (AA) composition and potential in biopolymers production. Some yeast species can produce SCP using short-chain fatty acids (SCFAs) produced via anaerobic fermentation (AF) of organic wastes. This study evaluated two SCFA-rich digestates derived from AF of agricultural waste (AW) and depackaged food waste (DFW) as culture media for SCP production using two *Yarrowia lipolytica* strains (ACA DC50109 and EXF-11734). Fermentations were performed in a 50-L bioreactor containing 20 g/L of SCFAs, mainly acetate and butyrate. Synthetic digestate with similar SCFAs profile was used for comparison purposes. *Y. lipolytica* ACA DC50109 achieved the highest protein yield (0.62 vs 0.48 g/g dry biomass) and biomass concentration (11.52 vs 9.65 g/L) on DFW. While EXF-11734 reached the highest AA content (44% g AA/g biomass), with 70% essential AA prevailing in leucine, threonine and tryptophan. Compared to synthetic media, cells grown both in AW and DFW resulted in higher SCP content (g/g dry biomass) and 15% more essential AA. The complex composition of real digestates, rich in micronutrients and trace metals, mediated this enhancement. This work demonstrated the potential of utilizing real SCFAs-rich digestates as renewable media for SCP production.

Keywords: short-chain fatty acids, agricultural wastes, depackaged food waste, single cell protein, essential amino acids

Microbial Valorization of Hydrothermal Liquefaction Wastewater

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Summary

Within the concept of chasing for renewable sources for the production of biofuel and other industrial, high value-added chemicals, the use of anthropogenic waste as feedstock represents a solution to the problem of sustainable production and reduces the environmental and economic impact of waste disposal. Hydrothermal liquefaction (HTL) is an emerging physico-chemical procedure which involves the conversion, at high temperatures and pressures, of waste material into a bio-oil phase which may be further processed to be used as biofuel. Several by-products are obtained in this process: a gas fraction, mainly CO_2, a solid fraction or biochar and an aqueous fraction, which is often too toxic to be released to the environment. The main objective of this work is to valorise the hydrothermal liquefaction wastewater (HTWW) generated as by-product of HTL carried out on different raw materials, such as *Arthrospira platensis* biomass, cellulose, lignin, oils and conventional plastics. Characterization studies were performed on different HTWW samples, whose composition depends on the feedstock and HTL reaction conditions and indicates their potential for biological valorization. HTWW samples were subjected to enzymatic treatments with bacterial and fungal oxidoreductases reducing their toxicity and enabling the growth of microorganisms such as *Escherichia coli*, *Pseudomonas putida*, and *Yarrowia lipolytica* in media containing up to 55% HTWW. This lays the foundation for converting wastewater into valuable products such as polyhydroxyalkanoates (PHA), lipids, or other compounds of industrial interest.

Keywords: biofuels, wastewater, oxidoreductases, detoxification and valorization

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Structural and functional studies of the enzybiotic VL-1L, the lysozyme of bacteriophage vB_PaeS_VL1 of *Pseudomonas aeruginosa*

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Summary

The emergence of multi-resistant strains to antibiotics has encouraged the search for new antimicrobials as an alternative to treat infections. Phage lysins are a promising technological strategy to introduce a more precise approach to antimicrobial therapy. In this work, we have identified and characterised the antimicrobial activity of the endolysin encoded by the bacteriophage vB_PaeS_VL1 (VL1) from *Pseudomonas aeruginosa*, which we have named VL-1L. The enzyme, added exogenously, has high bactericidal activity at relatively low concentrations (2 micromolar) against *P. aeruginosa*. In addition, viability assays confirmed that VL-1L has bactericidal activity against other Gram-negative pathogens (*Escherichia coli*) but not against Gram-positive bacteria. Experiments have also been initiated to crystallise the protein in order to elucidate its three-dimensional structure. In any case, experiments with different mutants of the protein based on a theoretical structural model have identified amino acids essential for its peptidoglycan hydrolytic activity and suggest that the bactericidal activity of the enzyme is based primarily on its ability to interact with and alter the bacterial surface. In conclusion, VL-1L endolysin has biological characteristics that make it a potential antimicrobial candidate for treating infections against *P. aeruginosa* and other Gram-negative pathogens.

Keywords: antimicrobial resistance, endolysins, enzybiotics.

The origins of scientific food control in Spain.

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Summary

Scientific food control falls within the field of food safety, understood as access to safe and nutritionally complete foods. From the history of science, this paper analyzes how scientific knowledge, institutions, and state action shaped this field of knowledge applied to public health. In ancient times, concern for food was limited to the most populated cities and, later, to the most industrialized, focusing on product availability, shortage prevention, and preservation techniques. Under these circumstances, the population could consume dangerous, nutritionally altered products with altered organoleptic qualities, subject to purely commercial interests. This research examines the use of public and private measures to protect public health through food inspection and analysis mechanisms. In the mid-19th century, the role of the State began to take shape: when the first scientific studies were established by university academic institutions, creating the first professional links with this field and the first general state oversight mechanisms. We focus our study, starting in 1908 in Spain, on the role of municipal laboratories. These centers were pioneers in characterizing the chemical and nutritional composition of foods, hence their importance as a preliminary step in later verifying their adulteration.

Keywords: municipal laboratories, food safety, control, 19th century, altered products, analysis

Comunicaciones en formato póster

Genetic predisposition, dietary patterns and physical nativity in the expression of obesity; An analysis in the school-age population of Andalusia (Spain)

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Summary

This work presents preliminary results of a cross-sectional study conducted in a school population in Andalusia, aimed at analyzing the interaction between genetic predisposition and environmental factors in childhood obesity. The research includes detailed anthropometric assessment (body mass index, waist-to-height ratio, and body fat percentage), as well as physiological parameters such as blood pressure and forced vital capacity. Additionally, the study explores the relationship between the age of menarche onset and body composition in girls, considering its relevance as a biological marker associated with increased adiposity. Dietary habits were evaluated using the KIDMED questionnaire, which measures adherence to the Mediterranean diet, and the CEBQ, which analyzes eating behaviors related to satiety, emotional eating, and eating speed. The collected data will enable the exploration of associations between these habits, nutritional status, and cardiometabolic risk, as well as the identification of sex-specific risk patterns. The presentation will show the first significant findings linking body composition, blood pressure, biological maturation, and eating patterns, providing an integrated perspective on the determinants of childhood obesity and potential preventive interventions adapted to the school context.

Keywords: Childhood Obesity, Mediterranean Diet, SNPs, Body Composition, Eating Behavior

Pubertal somatic variation and age at menarche in XXI Century Spanish Girls

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Summary

Puberty is a transitional stage between childhood and adulthood. It begins with the activation of the hypothalamus-pituitary-gonad axis and manifests itself in five phases, with the fourth phase being the first menstruation or menarche. This biological event is influenced by genetic, nutritional, psychological and socio-environmental factors. The average age at which menstruation begins in Spain has gradually increased in line with improvements in living standards. The objective of this study is to provide updated data on this matter, given its significance in female health and as a measure of the biological well-being of the population. A sample of 800 girls between 9 and 16 years of age, recruited from schools in the Community of Madrid, was analysed. A range of data was collected, including family, anthropometric, maturational and menstrual history. The age at menarche was determined using the status quo and retrospective methods, applying probabilistic analysis in the first case. Statistical analysis was performed with IBM SPSS v25, obtaining an age at menarche of 11.696 years (11.627-11.949) by the probit method and 12.196 ± 1.20 years by the status quo method. A link was identified between earlier menarche and higher levels of adiposity.

Keywords: Menarcheal age, anthropometry, nutritional status, body fat percentage.

Comparative evaluation of the peripheral immune response in sheep experimentally infected subcutaneously or intranasally with riftvalley fever virus

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Summary

How the route of infection influences the immune response to Rift Valley fever virus (RVFV) in small ruminants remains unclear. We aim to compare the dynamics of specific antibodies, leukocyte subpopulations and immunomodulatory cytokines in sheep inoculated with RVFV by intranasal (IN) or subcutaneous (SC) routes. Seroconversion occurred earlier in the SC group. Increases of CD4+, WC1+ T cells and CD21+ B cells were observed only in the IN group with CD8+ cells peaked at 4 and 7 dpi in the IN and SC groups respectively. In the IN group, CD4+CD8+ levels were higher, and WC1+CD8- showed a significant increase at 21 dpi. Pro-inflammatory monocytes (CD45 CD14+CD16+) increased in the early stages of infection, with levels significantly higher at 1 dpi in the SC group. Classical monocytes (CD45 CD14+CD16+) showed a significant decrease in both groups. Cells with natural killer phenotype (CD45 CD14- CD16+CD8+) peaked at 7 dpi in the SC group, displaying significant differences compared to the IN group. Granulocytes (CD45$^+$ CD14$^-$CD16$^+$), likely neutrophils, increased initially in both groups with CD16 upregulation, suggesting activation. Serum levels of IFNγ, IL-17, IL-10 and IP-10 increased in the early stages, suggesting a role in viral clearance regardless of the route of inoculation.

Keywords: Rift Valley fever virus, zoonotic disease, vector-borne disease, disease dynamics, immune response in sheep.

Nutritional ultrasound diagnosis of sarcopenia in older adults in Madrid

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Summary

The World Health Organization (WHO) projects that Spain will be the oldest country in the world in 25 years (1). Sarcopenia, or significant loss of muscle mass, strength, and function, becomes particularly relevant in older adults (2, 3). To optimize its diagnosis and relationship with nutritional status, 100 adults with an average age of 87.54 years were analyzed in public nursing homes in the Community of Madrid. The analysis included ultrasound imaging of the quadriceps in the rectus femoris (RF) and vastus intermedius (VI) muscles, anthropometry, and the Mini Nutritional Assessment (MNA) questionnaire (4). Blood biomarkers were also examined. According to the MNA, 71% of participants were malnourished, while 58% were overweight or obese based on their BMI. Logistic regression models were applied to evaluate the predictive capacity of muscle ultrasound for detecting sarcopenia. The muscle areas obtained by ultrasound were then compared with those obtained by anthropometric equations adapted from Frisancho (5). The models showed areas under the ROC curve between 0.67 and 0.89 for the different ultrasound parameters, highlighting the RF muscle surface area, penation angle, and LV thickness. A positive correlation was found between ultrasound and anthropometric measurements.

Keywords: aging, malnutrition, body composition, muscle mass.

Genetic diversity and ancestry in Colombian populations with a high level of admixture

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Summary

Studying genomic diversity and ancestry can be challenging in highly mixed populations such as modern Colombian populations. The vast majority of genomic studies that are used to support advances in precision medicine have been conducted on European ancestry populations from the Global North. By now, it is well known that discoveries made based on studies of European populations do not translate well to diverse populations with distinct ancestry profiles. Patterns of genomic diversity within and between Colombian populations have important implications for complex common diseases, rare Mendelian diseases, and therapeutic treatment options (i.e. pharmacogenomics). We previously identified single nucleotide variants (SNVs) with anomalous ancestry patterns, i.e. SNVs that exist in Colombian populations at a higher frequency than expected based on the population’s genetic ancestry profile. Characterization of Colombian genomic diversity and association of that diversity with health outcomes will lead to the generation of an online database that users can interrogate to make predictions and generate hypotheses regarding genomic (precision) medicine in Colombia. Understanding genomic diversity in highly admixed populations such as Colombians is essential for the development of precision medicine strategies tailored to local ancestry profiles. Most genomic research to date has focused on individuals of European descent, limiting its relevance for Latin American populations. This study focuses on the genomic characterization of 250 individuals from Colombian caribbean, aiming to uncover patterns of diversity, ancestry, and clinically relevant variants. Genotyping will be performed using the Illumina Infinium Global Screening Array-24 v2.0, which includes over 665,000 markers across all autosomes, sex chromosomes (X and Y), and mitochondrial DNA. The array also contains curated content for pharmacogenomics, complex disease loci, and variants from ClinVar and GWAS catalogs. To ensure high-quality data, we implemented a robust, reproducible pipeline involving VCFtools, BCFtools, and PLINK, followed by statistical filtering and PCA. This approach enables the reliable identification of ancestry-informed variants related to disease risk and drug response. These results aim to lay the groundwork for the implementation of precision medicine in Colombia, tailored to its unique genetic diversity.

Keywords: Genomic diversity, Genetic ancestry, Population genomics, Precision medicine.

Baermann vs Faecal culture: comparison of two methodologies for detecting parasites in the faeces of Wild Fallow Deer (*Dama dama*) in the Sierra de Albarracín, Teruel

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Summary

Parasitic infections are an emerging problem in ungulates, with helminths such as *Chabertia* sp., *Nematodirus* sp., and *Dictyocaulus* sp. being particularly common in fallow deer (*Dama dama*). To evaluate wildlife health, coprological analyses are widely used, as they are minimally invasive, do not require capturing animals, and allow parasite detection.

The Baermann method relies on the thermotropism and hydrotropism of larvae, while faecal culture involves incubating samples on nutrient agar plates. Both are useful diagnostic tools for gastrointestinal parasites.

In this study, 20 faecal samples were analyzed with both methods to quantify parasitic forms and assess diagnostic performance. All samples were polyparasitized, with 7 species identified: *Chabertia* sp., *Nematodirus* sp., *Trichostrongylus* sp., *Varestrongylus* sp., *Muellerius* sp., *Protostrongylus* sp., and *Dictyocaulus* sp.

Results showed that the Baermann method exhibited higher sensitivity (≈80%) than faecal culture, while also being faster, requiring only 48 hours. Therefore, it proved more effective for detecting a broader abundance of larvae.

These findings highlight the Baermann method as a superior approach for monitoring gastrointestinal parasites in wildlife, offering greater diagnostic reliability and efficiency compared to faecal culture.

Keywords: *Dama dama*; Baermann; faecal culture; Albarracín (Teruel).

Unveiling water effects: a comparative analysis in olive, almond and grapevine leaf surfaces grown under dryland or irrigation

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Summary

Growing fruit trees in dryland and irrigated systems is common in Mediterranean agriculture. As irrigation increases to boost yields, challenges like water scarcity and climate change demand deeper understanding of plant responses at the epidermal level. This study compared leaf epidermal traits and water loss in almond trees (*Prunus dulcis* var. *Guara*), olive trees (*Olea europaea* var. *Arbequina*), and grapevines (*Vitis vinifera* var. *Monastrell*) in commercial Spanish orchards from 2023–2024. Parameters such as leaf wettability, surface free energy (γ), stomatal density, wax content and cuticular transpiration were estimated, as well as the stomatal conductance (G_s) and dark and light chlorophyll fluorescence. Different microscopic techniques were used to analyse the leaf topography and anatomy. Results revealed irrigated plants lost more water through their cuticles than dryland plants, with grapevine leaves showing the highest cuticular transpiration and olive leaves the lowest. Differences in cuticular thickness and surface morphology were more pronounced in grapevine and almond than in olive leaves. These findings highlight the importance of understanding epidermal responses to improve the agricultural systems in changing climate conditions.

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Keywords: agricultural systems, water efficiency, Mediterranean crops, leaf surfaces.

The Sleeping Beauty Awakening: Cellular Reprogramming upon Injury-Induced Regeneration in the Bladder Urothelium

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Summary

Some of the tissues with the highest impact in cancer remain largely most quiescent during normal, physiological adulthood. Studying the mechanisms of tissue regeneration under injury conditions can thus offer important insights on their cellular proliferative potential and on tumor cell-of-origin. The bladder urothelium is the source of bladder carcinoma (BLCA) and it is a paradigmatic case, as it is considered to show a high regenerative potential upon damage. It remains unknown whether this phenomenon is a result of clonal expansions from a scarce subpopulation of long-lived Krt14+ adult stem cells or whether it rather reflects induced widespread cellular reprogramming effects. Using inducible CreER/loxP mice, we have combined molecular characterizations with in vivo lineage tracing to track individual clone dynamics in the urothelium during homeostasis and in regeneration upon cyclophosphamide exposure. We have characterized the transcriptomic changes that drive the initiation, progression and termination of the regenerative response, and validate these findings at the protein level using immunofluorescence. A very rapid proliferative response to the damaging stimulus is observed, with localized-to-widespread pro-proliferative cellular phenotypes seen in a timescale of a couple of days, before the urothelium returns to quiescence. However, no clonal expansions are seen, a scenario consistent with cellular plasticity where vertical clone migration might mitigate the effects of chemical damage in the mouse urothelium.

Keywords: Regeneration, urothelium, lineage tracing, clonal expansion.

Inferring somatic mutations from single-cell transcriptomics in the human esophagus

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Summary

Somatic tissues have been found to accumulate mutations with age, some of which occur in cancer driver genes, giving mutant progenitor cells a competitive advantage that leads to clonal expansion in the tissue. The human esophagus exemplifies this phenomenon, becoming a mosaic of competing mutant clones over time. Novel algorithms for de novo mutant detection from single-cell transcriptomics (scRNA-seq) data could potentially contribute to unveiling mutant cell phenotypes and their clonal relationships in aged physiologically normal tissues. In this study we adopt and customize SComatic to test its ability to identify low-frequency mutations in the polyclonal human esophagus through analysis of a large public scRNA-seq dataset. Our analysis highlights the importance of a careful filtering workflow to remove potential technical and germline variants. After refinement, some potentially relevant somatic mutations were identified, including several alterations in genes implicated in cancer, which we are able to map to individual cellular transcriptomes and differentiation trajectories in the UMAP-embedding. Altogether, we showcase the limitations of scRNA-seq-derived mutation calling for genotype-phenotype inferences and establish a framework for investigating mutant clone behaviour in normal polyclonal tissues from scRNA-seq data, laying the groundwork for future studies.

Beyond Telomeres: Unravelling the Function of CTC1 in Arabidopsis Meiosis

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Summary

Telomeres are essential structures in eukaryotes, where nucleoprotein complexes protect chromosome ends from being recognized as double strand breaks (DSBs). In Arabidopsis thaliana, the CST complex, composed of CTC1, STN1, and TEN1, binds to the 3’ G-overhang of single stranded DNA (ssDNA). Mutants defective in CST components display telomere shortening, chromosome fusions, and extrachromosomal telomeric circles. These defects can affect meiosis, as telomere-LINC interactions during prophase I promote chromosome movements required for alignment, pairing, and recombination of homologous chromosomes.

CTC1 (Conserved Telomere maintenance Component 1) plays a critical role in telomere protection and in facilitating the completion of telomere replication. In the *ctc1* null mutant, mitotic anaphase bridges arise due to activation of the DNA damage response (DDR) pathway. To further assess its role, we analyzed the meiotic phenotype of the mutant. Our results show chromatin bridges in both meiotic divisions, which persist in the *ctc 1* spo11 double mutant. These likely result from telomere fusions due to loss of telomere structure. Additionally, abnormal chromosome segregation led to the formation of polyads and dyads, occasionally generating polyploid offspring. Our findings reveal the meiotic consequences of telomere loss and fusions and highlight their impact on chromosome dynamics and segregation during meiosis.

Keywords: meiosis, telomeres, CTC1, chromatin bridges.

Mycobiota diversity in cereal seeds after four decades of storage

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Summary

A comprehensive study of mycobiota in seeds stored in germplasm banks is crucial for preserving their health and preventing the spread of latent pathogens. To date, few studies have addressed fungal persistence in cereal seeds after decades of storage. Here we analyzed the mycobiota of 51 seed cereal samples (*Avena sativa*, *Hordeum vulgare*, *Secale cereale*, *Triticum aestivum*, and *Triticum turgidum*) conserved for about 40 years at the Spanish Plant Genetic Resources Centre (INIA-CSIC).

After surface sterilization using alcohol, five replicates of 10 seeds from each sample were incubated on rose bengal agar with dichloran and chloramphenicol at 28°C for one week. After isolation, fungal colonies were identified morphologically at the genus level using Barnett’s criteria.

A total of 14 genera were detected. *Alternaria* (60.8% of samples) was the most frequent, whereas *Fusarium* (20%), an important mycotoxigenic and phytopathogenic genus, was also present. *Alternaria* and *Cladosporium* co-occured in 40% of samples. This simultaneous development has been reported to have negative effects on human health. *Alternaria* also co-occurred with *Fusarium* (8%), posing an additional risk of mycotoxin contamination.

These results document fungal persistence in stored seeds, underscoring the relevance of mycotoxigenic genera and monitoring needs. Future work includes molecular identification of the isolates.

Keywords: mycobiota, seed banks, fungal diversity.

Optimization of primary mouse hepatocyte cultures for potential cell therapy in factor V deficiency

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Summary

Factor V (FV) is a key coagulation protein synthesised by hepatocytes. Its absence or dysfunction leads to FV deficiency, for which no specific treatment exists. Cell therapy is promising because it provides functional cells capable of restoring impaired functions and, potentially, re-establishing FV production.

This study aimed to determine the optimal functional window of primary mouse hepatocytes (PMH) cultured under 2D sandwich and 3D spheroids for potential application in transplantation.

PMHs were isolated from WT CBAXC57BL6 mice (both sexes) by hepatic perfusion and cultured in 2D sandwich and 3D spheroids. Functionality was assessed by FV coagulometric assays and urea and albumin production. Viability and proliferation were assessed, and associations between urea, albumin, and FV were analysed.

PMH were obtained from both sexes. Significant interactions were observed among sex, culture type, and time ($p< 0.05$), indicating strong overall variations. 3D cultures showed higher functionality in urea, albumin and FV ($p<0.05$), and sex-related differences were culture-dependent ($p<0.05$) for albumin and FV. Viability and proliferation also varied significantly with culture day ($p<;0.05$). Urea, albumin, and FV exhibited strong correlation ($r > 0.8$; $p<0.05$). Early culture days displayed balanced functionality, identifying this period as optimal for in vivo transplantation.

Keywords: Factor V deficiency, cell therapy, hepatocyte, 2D sandwich, spheroid.

Environmental DNA as an effective tool for the study and conservation of *Parachondrostoma arrigonis* (Teleostei: Leuciscidae) and for assessing co-occurring species.

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Summary

The Júcar River is one of the most important rivers in the Iberian Mediterranean hydrographic network and hosts unique freshwater biodiversity, including the Loína (*Parachondrostoma arrigonis* Steindachner, 1866), a cyprinid strictly endemic to this basin.

Over the last three decades, the Loina has experienced a dramatic decline of more than 80% in abundance and distribution led by the increased anthropogenic pressures in the Júcar basin. River channelization, dam regulation, water pollution, and habitat degradation are particularly intense in the middle and lower reaches of the Júcar, where the species is nearly extinct. Additionally, alien species have worsened its situation. Spatial segregation and hybridization with the translocated *Pseudochondrostoma polylepis* and predation by exotic species have greatly reduced its populations and historical range, leading to local extinctions. Currently, it has disappeared from the main river course and survives only in a few tributaries, where its populations are fragmented into seven isolated patches.

This study evaluates the potential of environmental DNA (eDNA) to update the distribution of P. arrigonis and to explore the composition of cohabitant fish species. Metabarcoding analyses using a fragment of the mitochondrial 12S allowed us to detect P. arrigonis and to characterize the accompanying fish assemblages.

Our results highlight the sensitivity of eDNA-based approaches for monitoring freshwater biodiversity. Furthermore, by providing updated information on the conservation status of *P. arrigonis*, this methodology offers valuable insights into community structure and invasive species interactions, highlighting its role as an essential tool for the conservation of threatened Iberian freshwater fish endemic species.

Keywords: communities, Cyprinidae, distribution range, Júcar basin, metabarcoding.

Engineering a Bioelectrical Interface: ENS Neurons and Bacterial Biofilms on a Microfluidic Chip

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Summary

The gut microbiota and the enteric nervous system (ENS) engage in complex, bidirectional communication that shapes host physiology and behaviour. While chemical and immune pathways are well established, direct bioelectrical interactions remain largely unexplored. Our long-term goal is to develop a functional microfluidic interface where ENS neurons and bacterial biofilms interact in real time, enabling simultaneous recording and stimulation.

We have recently characterized both components of this interface. For bacteria, we analysed *Lactiplantibacillus plantarum* biofilms using crystal violet and SYTO/propidium iodide assays. Thioflavin T (THT) proved to be a reliable fluorescent probe for monitoring membrane potential (Vmem). During biofilm development, we observed a progressive decrease in hyperpolarization, while exposure to the neurotransmitter GABA induced increased hyperpolarization and disrupted spatial homogeneity of the bioelectrical pattern.

For neurons, we established a cholinergic ENS model derived from murine neuronal tumor cells. This system was characterized by immunofluorescence and qPCR, confirming its suitability to study bioelectrical crosstalk with bacteria.

Together, these results provide the foundation for engineering a custom ENS–biofilm microfluidic platform, envisioned as a “functional microbiota–gut–brain organoid,” with broad implications for decoding gut–brain bioelectric communication and electroceutical therapies. Funded by an AEI grant including a predoctoral FPI fellowship (PID2023-147361NA-I00).

Keywords: Gut–Brain Axis, Enteric Nervous System (ENS), Bacterial Biofilms, Bioelectric Communication, *L. plantarum*, Electroceuticals

Low-coverage whole-genome sequencing and bioinformatic pipelines to explore genetic variation in Iberian blackcap populations

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Summary

Understanding the genetic basis of host–parasite interactions is essential to explore the evolutionary dynamics of avian malaria in natural populations. In my PhD project, I focus on the blackcap (*Sylvia atricapilla*), a widespread passerine bird in the Iberian Peninsula. I first analyzed a database containing prevalence and richness of malaria infections, as well as information on parasite genera and species. Based on this, I selected 20 populations maximizing variability in infection status and geography. Within these populations, individuals were chosen to represent both sexes, different infection states, and to minimize sampling of juveniles or related individuals. Blood samples preserved in ethanol were processed for DNA extraction using bead-based protocols at Secugen, and subsequently sequenced at low coverage at Macrogen. Raw sequencing data were processed through successive steps (.sam, .bam, .vcf) using bioinformatic pipelines with tools such as SAMtools, ANGSD, and PLINK on the Complutense University cluster (Brigit). Preliminary quality control analyses, including PCA, suggested that genetic variation is primarily structured by sex and secondarily by geography. Current efforts focus on refining genotyping quality, identifying candidate genetic variants under selection associated with infection patterns, reconstructing demographic history, and exploring the role of coinfections in shaping host–parasite dynamics in blackcap populations.

Keywords: Population genomics, blackcap, low-coverage sequencing, avian malaria, host-parasite interactions.

Yarrowia lipolytica as a dual platform for sustainable protein and tailored lipid production from carboxylates

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Summary

The rising global oil and protein demand intensifies environmental degradation, underscoring the need for sustainable alternatives such as yeast single-cell proteins (SCP). *Yarrowia lipolytica* is a promising candidate for both SCP and oil production from organic wastes.

Y. lipolytica ACA DC 50109 was used for SCP and oil production. Synthetic media was prepared with a yeast nitrogen base (7.5 g/L $(NH_4)_2SO_4$) and 29.2 g/L SCFAs based on previous reports. Real media (RM) derived from SCFA-rich autofermented digestates with 32.8 g/L of SCFAs was also used undiluted (URM) and diluted (50% v/v, 50RM). Shake flask cultures (100 mL) were incubated at 28 °C, pH 6.8 and 150 rpm. Promising conditions were scaled up to 1-L bioreactor. SCP and oil content were determined by BCA protein analysis and GC-FID, respectively.

In synthetic media, *Y. lipolytica* produced 15 % w/w SCP and fatty acid (FA) profile was dominated by C18:1t (28 % w/w). In shake flask fermentation with 50RM, SCP increased to 22 % w/w and predominant FA were C18:2c (29 % w/w) and C18:1t (25 % w/w). URM fermentation resulted in significant differences in the FA profile, with 32 % w/w C18:1t. Reactor results validated lipid and SCP levels. The different produced FA demonstrated the influence of the initial SCFAs and media composition on lipid synthesis, and highlights Y. lipolytica potential as SCP source.

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Keywords: *Yarrowia lipolytica*, single-cell proteins, short-chain fatty acids, lipids.

Changes in functional structure affect community stability: insights from a removal experiment

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Summary

Stability of biological communities is crucial for maintaining ecosystem functions and services in a changing environment. In this context, the implementation of an approach based on functional traits, as indicators of community response to changes in species composition can help elucidate the relationships between community structure, stability and ecosystem services. However, studies focusing on stability components from a functional trait-based perspective are scarce, despite the diversity of species' functional traits may drive the community's resistance and recovery. We selected five contrasting plant communities under semi-arid conditions, characterized by different dominant species and implemented removal treatments (7 plots per treatment) to modify the community structure, resulting in 35 plots per community (removal of the dominant species, of the 4 most acquisitives, of the 4 most conservatives, of 2 acquisitives and 2 conservatives and control). After one growing season, results showed that the removal of conservatives and the mixed treatment led to their replacement by acquisitive species, while the removal of acquisitives led to slow recovery. Finally, the dominant species removal treatment showed an increase in evenness as no subdominant species became dominant. These results underline the importance of functional traits in conservation work, highlighting their relevance as modulators of community recovery.

Keywords: functional structure, functional trait, recovery, stability.