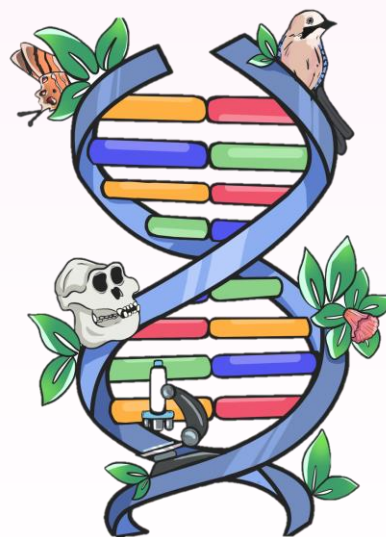


# Libro de Abstracts

8<sup>th</sup> PhDay  
Biología

3 de octubre 2024



COLEGIO  
OFICIAL DE  
**BIÓLOGOS**  
DE LA COMUNIDAD DE  
MADRID





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Carmen Ureña Lara





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# 8<sup>th</sup> PhDay Biología

9:00 – 9:15 [Recepción y acreditación](#)

9:15 – 9:30 [Inauguración](#): **Fernando Gascón Inchausti** (Director de la Escuela de Doctorado UCM) y **M. Esther Pérez Corona** (Vicedecana de Investigación y Doctorado)

9:30 – 10:00 [Ponencia inaugural](#): **Antonio González Martín** (Profesor de la Universidad Complutense de Madrid)  
**Aportaciones de la paleogenómica a la biología evolutiva**

## Sesión I

- 10:00 – 10:15 **Elisa Quarta**  
Nutritional iron deficiency effects on microbiota-gut-brain axis
- 10:15 – 10:30 **Marwane Bourqia Ramzi**  
From the Microbiome to the Electrome: Implications for the Microbiota-Gut-Brain Axis
- 10:30 – 10:45 **Gemma Valera Arévalo**  
Biomarkers of cardiovascular and thrombotic risk in chronic kidney disease
- 10:45 – 11:00 **María Rubert Hernández**  
Modulation of cannabinoid receptor 2 expression and activity in the breast tumor microenvironment
- 11:00 – 11:15 **Natalia Elena Expósito de la Paz**  
Targeting epigenetic modifications to improve somatic embryogenesis: the role of H4 acetylation
- 11:15 – 11:30 **Carmen Soler Zamora**  
Designing a novel biological water quality index: implementing metabarcoding and machine learning techniques using Arcellinida as a model

## Sesión II

- 12:00 – 12:15 **Luna Ballestero García**  
Antimicrobial activity of enterocins L50A and L50B against *Clostridoides difficile*: understanding the mechanisms of Fecal Microbiota Transfer
- 12:15 – 12:30 **Amaya de Cos Gandoy**  
Bacterial community structure and diversity patterns of mountain rock basins from the Sierra de Guadarrama National Park
- 12:30 – 12:45 **Alicia Portela Estévez**  
Origin and history of Agote people: a Genomics perspective
- 12:45 – 13:00 **Albert Carné Constans**  
A race against extinction: the challenge to overcome the Linnean amphibian shortfall in tropical biodiversity hotspots.
- 13:00 – 13:15 **Sandra Navas Sastre**  
Effect of forest management in taxonomic, functional and phylogenetic diversity of Mediterranean Scot pine (*Pinus sylvestris*) understory plant communities.
- 13:15 – 13:30 **Darío Fidalgo Casares**  
How do hippos grow? ([online](#))

## Sesión III

- 14:30 – 14:45 **Miguel López Cano**  
Reconstrucción serial de falanges: Estudio en Hominini
- 14:45 – 15:00 **Mario Benítez Prián**  
Can the strangest amphibians save us? Diversity and molecular evolution of antimicrobial peptides in caecilians.
- 15:00 – 15:15 **Mercè Palacios López**  
Unraveling the migratory behaviour of hoopoes (*Upupa epops*): a multidisciplinary journey through eco-immunology, genomics, stable isotopes analysis and satellite tracking
- 15:15 – 15:30 **Ángela Aguado-Lara**  
Euphorbiaceae Afrotropicales en la Lista EDGE: Tesoros Evolutivos al Borde de la Extinción
- 15:30 – 15:45 **Jaume Xavier Soler Mari**  
Analysis of the endemicity of the Dianic territory. Implications for the conservation of species and habitats
- 15:45 – 16:00 **Lucía Villaescusa González**  
Ethnobotany and medical applications in Acalypha: a global review with taxonomic assessment



Salón de actos  
Facultad de C.C. Biológicas  
UCM



Jueves, 3 de octubre  
9:00 - 18:00

16:00 – 17:00

## Sesión Póster

**Alejandro Arriero-Cabañero**

Transplantation of predegenerated peripheral nerves after complete spinal cord transection in rats: Effect of neural precursor cells and pharmacological treatment with the sulfoglycolipid Tol-5

**Manuel Francisco Blanco Roldán**

Effects of insoluble solids and lignocellulose-derived inhibitors on *Kluyveromyces marxianus* CECT 10875 on fermentation performance.

**Mar Casquero Muñoz**

Biomechanical analysis of physical activity in a merotic cemetery from northern Sudan

**Adrián Duro Peinó**

Determinantes ecológicos del tamaño territorial del gato montés (*Felis silvestris*) en Europa.

**Alejandra Fernández Hernández**

The arabidopsis pat1 proteins differentially regulate plant responses to abiotic stress

**Nuria García Martínez-Illescas**

Short exposure to nanomolar cannabinoids promotes breast cancer differentiation

**Irene García Toledo**

Descifrar el efecto de diferentes dietas a lo largo de la vida en las alteraciones motoras y cognitivas causadas por la desregulación de TDP-43

**Gloria Gómez Montesino**

Effect of pegylation on pulmonary surfactant-driven interfacial vehiculation of drug delivery systems

**Tamara González Illanes**

Response of sweet cherry leaves to foliar application of calcite and kaolinite

**Guillermo González Salso**

Melanoma-derived extracellular vesicles promote t cell exhaustion that can be reverted using immunoregulatory micromRNAs

**Sergio Izquierdo Gea**

Intraspecific genomic and phenotypic diversity in *Yarrowia lipolytica*, an industrially relevant yeast.

**Javier Lescure Rodríguez**

Study of climate adaptations in cranial morphology using geometric morphometry

**Juan Lombardo Hernández**

In vitro co-culture of cortical neurons and probiotic bacteria *Lactiplantibacillus plantarum* induces morphological, structural, and transcriptomic changes in neural cells

**Carla Maya López**

El envejecimiento renal es una cuestión de género.

**Tessa Lynn Nester**

eDNA techniques unveil the dietary and distribution patterns of the invasive Eastern mosquitofish in Spain: Insights for Endangered toothcarp conservation

**David Aurelio Oropesa Olmedo**

Desiccation in Mediterranean oak acorns: does morphology influence germination rate?

**Covadonga Pérez García**

Rise of pneumococcal serotype 3 is associated with clade 1- $\alpha$ /GPSC12 involving enhanced evasion of the host immune response and disease potential

**Pedro Rebollo**

Forest diversity modulates differential species responses to disturbances in Iberian forests

**Arturo Rodríguez Pascual**

Una evaluación de los principales mecanismos detrás de la relación entre biodiversidad y estabilidad a través de escalas (BIOSTAR: BIODiversidad STabilidad Relaciones)

**Luis Javier Sánchez Martínez**

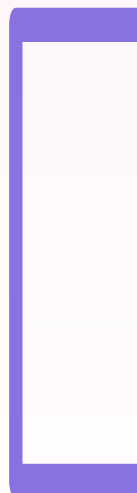
Application of artificial intelligence to improve the treatment of acute child malnutrition in emergency contexts

17:30 [Entrega de premios](#) por **Juan E. Jiménez Pinillos** (Secretario del COEMB) y [clausura](#)



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# Resúmenes



# Comunicaciones Orales





### Nutritional iron deficiency effects on microbiota-gut-brain axis

Elisa Quarta<sup>1</sup>, Marwane Bourqqia-Ramzi<sup>1</sup>, David Munoz-Rodriguez<sup>1</sup>, María Teresa García-Esteban<sup>1</sup>, Antonio Murciano-Cespedosa<sup>1</sup>, Álvaro Mateos-Gonzalez<sup>2</sup>, Jesús Mansilla-Guardiola<sup>1</sup>, Juan Lombardo-Hernandez<sup>1</sup>, Simona Baroni<sup>3</sup>, Simonetta Geninatti Crich<sup>3</sup>, Stefano Geuna<sup>3</sup>, Luca Maria Munaron<sup>3</sup>, Deborah Chiabrand<sup>3</sup>, Celia Herrera-Rincon<sup>1</sup>

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**Keywords:** iron deficiency, microbiota-gut-brain axis, bacteria, bioelectricity, iron chelation

#### Summary

Iron deficiency (ID) is the most common nutritional deficiency worldwide, affecting both gut bacteria metabolism and cellular biochemistry. However, its impact on the microbiota-gut-brain axis (MGB) is not well understood. Early-life ID-related gut dysbiosis is linked to neurodevelopmental disorders like autism and ADHD. Investigating ID's effects on bacterial signaling can help develop interventions to reduce neurodevelopmental risks. This study examined how *Escherichia coli* (*E. coli*) and *Limosilactobacillus reuteri* (*L. reuteri*), key human microbiota species, respond to ID conditions created using the iron chelator 2,2'-Bipyridyl (BP). We assessed and modeled their growth and cultivability and explored their bioelectric profiles using the voltage-sensitive dye DiBAC4(3). Results showed *L. reuteri*'s growth and cultivability remained unchanged under ID, while *E. coli* exhibited reduced growth and cultivability. Notably, *E. coli*'s bioelectric profile was altered, showing increased cell depolarization under ID. These findings highlight the diverse responses of gut bacteria to iron deficiency and emphasize the complexity of gut microbiota interactions. Understanding this variability is essential for elucidating the role of microbiota in health and diseases related to nutritional iron imbalance and neurological disorders.

# From the Microbiome to the Electrome: Implications for the Microbiota–Gut–Brain Axis

Marwane Bourqqa-Ramzi <sup>1,2</sup>, Jesús Mansilla-Guardiola <sup>1,3</sup>, David Muñoz-Rodríguez <sup>1</sup>, Elisa Quarta <sup>1,4</sup>, Juan Lombardo-Hernandez <sup>1</sup>, Antonio Murciano-Cespedosa <sup>1,5</sup>, Francisco José Conejero-Meca <sup>1</sup>, Álvaro Mateos González <sup>1,6</sup>, Stefano Geuna <sup>7</sup>, María Teresa Garcia-Esteban <sup>3</sup>, and Celia Herrera-Rincon <sup>\*1</sup>.

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**Keywords:** membrane potential; microbiota–gut–brain axis; growth phase; neurotransmitters; Gram-positive; Gram-negative

## Summary

The gut microbiome plays a fundamental role in metabolism, as well as in the immune and nervous systems. Microbial imbalance (dysbiosis) can lead to physical and mental pathologies. This study investigated the bioelectrical profile of two bacterial species characteristic of the gut microbiome: *Escherichia coli* (a Gram-negative bacillus) and *Enterococcus faecalis* (a Gram-positive coccus). We validated the fluorescent probe DiBAC4(3) to measure changes in membrane potential and examined the effects of neurotransmitters glutamate and GABA on  $V_{mem}$ . Results showed distinct bioelectrical profiles for each species, with neural stimuli inducing  $V_{mem}$  changes without affecting bacterial growth, viability, or cultivability. These findings contribute to understanding bacterial responses to external stimuli and suggest potential therapeutic applications in modulating bacterial bioelectricity.

Moreover, the differential responses observed between *E. coli* and *E. faecalis* highlight the complexity of microbial interactions within the gut environment. The unique  $V_{mem}$  changes triggered by neurotransmitters suggest a sophisticated level of communication between the gut microbiome and the host's nervous system. Future research could explore how these bioelectrical interactions influence overall gut health and disease, potentially opening new avenues for microbiome-targeted therapies. Understanding these mechanisms is crucial for developing strategies to manipulate the gut microbiome, aiming to restore balance and treat dysbiosis-related conditions through bioelectric modulation.

## Biomarkers of cardiovascular and thrombotic risk in chronic kidney disease

Gemma Valera Arévalo<sup>1</sup>, Jara Caro Espada<sup>3</sup>, María Del Mar Rodríguez San Pedro<sup>1</sup>, Claudia Yuste Lozano<sup>3</sup>, Matilde Alique Aguilar<sup>2</sup>, Andrea Figuer Rubio<sup>2</sup>, Natalia Guerra Pérez<sup>1</sup>, Rafael Ramírez Chamond<sup>2</sup>, Enrique Morales Ruiz<sup>3</sup>, Julia Carracedo Añón<sup>1</sup>

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**Keywords:** chronic kidney disease, endothelial damage, glycocalyx, microvesicle, tissue factor

### Summary

Chronic kidney disease (CKD) is associated with cardiovascular, thrombotic and haemorrhagic diseases, preceded by endothelial dysfunction, as well as endothelial glycocalyx damage and alterations in coagulation systems. The aim of the study is to evaluate possible biomarkers of early cardiovascular risk in patients with CKD.

In a cross-sectional study of 91 CKD patients (23 with advanced chronic kidney disease (ACKD), 25 on haemodialysis (HD), 23 on peritoneal dialysis (PD) and 20 transplant recipients (TX)) the amount of two endothelial glycocalyx molecules (perlecan and decorin) in plasma was assessed by ELISA. The amount of endothelium-derived microvesicles (EMVs) and platelet-derived microvesicles (PMVs), and the expression of tissue factor (TF) in both were assessed in plasma from 116 subjects (40 ACKD, 40 HD, 40 PD and 40 TX). Analysis was performed in plasma by direct immunofluorescence and flow cytometry. Statistical analysis: SPSS 21.0

Patients with CKD have higher plasma perlecan and decorin levels. ACKD is associated with increased TF expression, HD with increased MVEs and PD with elevated levels of PMVs. The parameters studied could be proposed as early biomarkers of cardiovascular risk in patients with CKD.

## Modulation of cannabinoid receptor 2 expression and activity in the breast tumor microenvironment

María Rubert<sup>1</sup>, Marta Seijo-Vila<sup>1</sup>, Nuria G. Martínez-Illescas<sup>1</sup>, Isabel Tundidor<sup>1</sup>, Sandra Blasco-Benito<sup>2</sup>, Cecilia J. Hillard C.<sup>3</sup>, María Teresa Grande<sup>4</sup>, Julián Romero<sup>4</sup>, María Salazar Roa<sup>1</sup>, Cristina Sánchez<sup>1</sup>, Eduardo Pérez-Gómez<sup>1</sup>.

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**Keywords:** breast cancer, tumor microenvironment, immune cells, cannabinoid receptor 2

### Summary

The breast tumor microenvironment (BTME) is a complex entity where breast cancer (BC) cells establish dynamic interactions with other non-cellular and cellular components. Among them, immune cells (ICs) are especially relevant since they can have both, pro or antitumorigenic effect depending on the context. These cells are known to express the immunomodulatory cannabinoid receptor 2 (CB<sub>2</sub>R), whose activation has been shown to produce immunosuppressive effects in different scenarios. On the other hand, activation of this receptor in BC cells triggers antitumor responses. However, little is known about its role in the BTME.

Considering the above, we conducted *in vitro* and *in vivo* experiments to determine the consequences of the modulation of CB<sub>2</sub>R expression and activity in the context of BC. *In vivo*, lack of BTME-CB<sub>2</sub>R slows down tumor growth and alters BTME composition and function. *In vitro*, activation of CB<sub>2</sub>R in isolated immune cells decreases their killing capacity, an effect that is masked in co-culture as the antitumor effect resulting from cancer cell CB<sub>2</sub>R activation prevails.

Thus, although CB<sub>2</sub>R expression in the BTME favors cancer progression, its general activation in tumors may tip the balance towards antitumor responses, and therefore might not interfere with immunomodulatory therapeutic approaches (i.e. immunotherapy).

### Targeting epigenetic modifications to improve somatic embryogenesis: the role of h4 acetylation

De la Paz, Natalia.E<sup>1</sup>, Carneros, Elena<sup>1</sup>; Testillano, Pilar S.<sup>1</sup>.

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**Keywords:** somatic embryogenesis, SAHA, histone deacetylases, H4 acetylation, *Quercus suber*.

#### Summary

Cork oak (*Quercus suber* L.) is a tree with remarkable economic and ecological value threatened by deforestation, diseases, and challenging natural regeneration. Somatic embryogenesis is a powerful biotechnological tool with applications in regeneration and propagation programs. Despite its potential, the high cell death and low induction rates limit its use. Understanding the regulatory pathway of cellular reprogramming and embryogenesis induction is crucial to improve its manipulation. In this study, we analyzed the dynamics of H4 acetylation, a significant histone post-translational modification, during somatic embryogenesis in *Q. suber*. Changes in global levels of this epigenetic mark, along with the expression profiles of regulating enzymes, have been characterized. Furthermore, the effect of Suberoylanilide Hydroxamic Acid (SAHA), a histone deacetylase inhibitor has been also evaluated. Our results showed that embryo development is associated with H4 acetylation, correlating with the upregulation of the histone acetyltransferases (*QsHAC1-like/QsHAM1-like*) and the repression of histone deacetylases (*QsHDA2/QsHDA15*) during embryo development. Moreover, the use of SAHA in embryogenic cultures led to a 55% increase in embryo production compared to control. These results offer new insights into the role of histone epigenetic marks and introduce new possibilities to improve plant *in vitro* regeneration in forest species.

## Designing a novel biological water quality index: implementing metabarcoding and machine learning techniques using Arcellinida as a model

Carmen Soler-Zamora<sup>1,2\*</sup>, Gema González-Palomino<sup>2</sup>, Patrizia Vannucchi<sup>2</sup>, Bertrand Fournier<sup>3</sup>, Julio Luzón-Ortega<sup>2</sup>, Enrique Lara<sup>1</sup>

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**Keywords:** Bioindication, Arcellinida, Machine-Learning, Metabarcoding, Protist

### Summary

Anthropogenic pressures have a significant impact on freshwater ecosystems, particularly in arid climates. Bioindication stands as the predominant method for monitoring environmental quality in these ecosystems. Various biomonitoring protocols have been developed; however, they suffer from complex procedures and a lack of taxonomic precision, resulting in limited sensitivity.

Exploring novel biological indicators present in all lentic environments is imperative. Additionally, metabarcoding-based protocols have greater sensitivity, efficiency, cost-effectiveness, reproducibility and eliminate dependence on taxonomic expertise.

In this project, we developed a biomonitoring protocol to screen Arcellinida diversity (=lobose testate amoebae) based on metabarcoding. Arcellinida are widely distributed in inland water bodies, display significant ecological niche specialization, and demonstrate swift reactions to environmental disruptions. These make Arcellinida outstanding bioindicators.

The primary goal of this project is to set an innovative metabarcoding-based protocol for rapid and reliable monitoring of water quality in lentic systems. We applied this protocol across three river basins (Guadiana, Guadalquivir and Segura) to reveal the Arcellinida communities' composition. Furthermore, we will utilize machine learning methodologies to formulate environmental quality indices, with the aim of incorporating this approach into Spanish legislation for assessing the environmental health of freshwater lentic ecosystems, which are presently confronted with substantial threats.

## Antimicrobial activity of enterocins L50A and L50B against *Clostridioides difficile*: understanding the mechanisms of Fecal Microbiota Transfer

Luna Ballester<sup>1</sup>, Raquel Barbero-Herranz<sup>1</sup>, Juan Borrero<sup>3</sup>, Rosa del Campo<sup>1,2</sup>, Ana Blanco-Moreno<sup>1,2</sup>, José Avendaño<sup>1,2</sup>

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**Keywords:** Bacteriocins, *Clostridioides difficile*, *Enterococcus lactis*, Fecal Microbiota Transfer, Microbiota.

### Summary

Fecal Microbiota Transfer (FMT) is an effective treatment for recurrent *Clostridioides difficile* infections. Recent data indicate the importance of microbial metabolites, like bacteriocins, in the success of FMT. This study aimed to identify bacteriocin-producing strains against *C. difficile* within the microbiota of donors of FMT program at the Ramón y Cajal U. Hospital.

Stool samples from three certified donors were cultured on general and selective media under anaerobic conditions. After 48h of incubation at 37°C, different colonies were tested for antimicrobial activity against *C. difficile* ATCC 9689 strain and two hypervirulent clinical isolates (ribotypes 027 and 078). Isolates with antimicrobial activity were identified by mass spectrometry (MALDI-TOF) and genetically characterized by whole-genome sequencing.

An isolate *Enterococcus lactis* sequence type 94 (ST94) showed the highest antimicrobial activity, with genes coding for enterocins L50A and L50B identified in its genome. Production of both enterocins was validated through chromatographic purification and mass spectrometry (MALDI-TOF/MS) analysis of the active compounds from the supernatant of an overnight culture of this isolate. The Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) against *C. difficile* ATCC 9689 was determined by microdilution, being 0.125 µg/mL for Enterocin L50A<sup>®</sup> and 0.5 µg/mL for Enterocin L50B<sup>®</sup>.

## Bacterial community structure and diversity patterns of mountain rock basins from the Sierra de Guadarrama National Park

Amaya de Cos-Gandoy<sup>1</sup>, Andrea Serrano-Bellón<sup>2</sup>, María Macías-Daza<sup>2</sup>, Blanca Pérez-Uz<sup>2</sup>, Richard A.J. Williams<sup>2</sup>, Abel Sánchez-Jiménez<sup>1</sup>, Mercedes Martín-Cereceda<sup>2</sup>

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<sup>2</sup>. Department of Genetics, Physiology and Microbiology, Faculty of Biology, Complutense University of Madrid, 28040 Madrid, Spain.

**Keywords:** Bacterial assemblages; heterogeneity; national park; rain-fed rock basins; replicates

### Summary

Bacterial microbiomes influence global carbon and nutrient cycling as the environment changes. Rain-fed rock basins are ephemeral aquatic systems, potentially subject to extreme environmental stress, that host a variety of biological communities, including bacteria. However, bacterial communities are barely described in these habitats. This study describes the diversity and distribution patterns of the bacterial communities in rain-fed granite mountain rock basins located in the Sierra de Guadarrama National Park, Spain, using high-throughput sequencing of 16-S RNA. Five replicates of sediment were collected from three basins. A highly diverse community of 3,174 OTUs belonging to 32 phyla was detected. 50% of OTUs were shared among basins, and under 10% were basin-exclusive OTUs, suggesting a robust global bacterial meta-community colonizes the basins. Additionally, 6% of the OTUs were replicate-exclusive and at least four replicates were required to catalogue 90% of the community, which emphasizes the heterogeneity of these habitats. Both environmental filtering and random dispersal are likely to be involved in the arrangement of the bacterial communities. The taxa identified are versatile in metabolism and some have biotechnological potential. The taxonomic affiliation of many of the OTUs found suggests that rain-fed rock basins could be a resource for mining of novel biocompounds.



### Origin and history of Agote people: a Genomics perspective

Alicia Portela Estévez<sup>1</sup>, Georgios Athanasiadis<sup>2</sup>, César Fortes-Lima<sup>3</sup>, Alín Acuña Alonzo<sup>4</sup>, Araxi Urrutia Odabachian<sup>4</sup>, Javier Lescure<sup>1</sup> and Antonio González Martín<sup>1</sup>.

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**Keywords:** Agote people, Bozate, Social marginalization, Genomics, Inbreeding

#### Summary

Agote people represent one of the most mysterious Western European populations. Although nowadays most of them are located in Bozate, Arizkun, Navarra, their true origin and history remain unknown, related to a hard social marginalization until the last century. There are several hypothesis that try to explain this phenomena (Jewish, Saracen, Viking, Gothic or Catharian origin, leprosy patients...), but they lack scientific rigor. The aim of this study is identify agote's origin, history and the reason of their discrimination. For this purpose, 125 genetic samples from present-day individuals from Bozate, Baztan and Navarra were genotyped through Axiom Genome-Wide Human Origins 1 array (~620,000 SNPs per individual). Data were analysed with computational tools to explore population structure, demographic history, haplotype-based clustering and admixture events. Results show that Agote people have genetic similarity with near populations and a bottleneck occurred around the year 1.224, which falls within the period of Albigensian Crusade (1.209 – 1.244) that took place in South France against Catharian people. Hence, agotes would be a Catharian group of people that fled from the Albigensian Crusade. Thus, the origin of their discrimination would have religious motivations. Finally, they show high kinship coefficient, probably due to the social isolation.

## A race against extinction: the challenge to overcome the Linnean amphibian shortfall in tropical biodiversity hotspots

Albert Carné<sup>1, 2, 3\*</sup> & David R. Vieites<sup>3</sup>

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<sup>3</sup>Integrative Marine Ecology group, Department of Ecology and Marine Resources, Instituto de Investigaciones Marinas (IIM), CSIC, Vigo, Spain

**Keywords:** Tropical hotspots, species delimitation, amphibians, undescribed diversity, Linnean and Wallacean shortfalls

### Summary

There is an urgent need to explore, describe, and preserve as many species as possible to prevent their decline. Tropical biodiversity hotspots harbor most of the known land diversity and vast amounts of undiscovered and undescribed species.

By analyzing 10,873 mitochondrial sequences using species delimitation algorithms and integrating all previously published bioacoustics, distributional, morphological, and nuclear data, we quantify the taxonomically unassessed amphibian species richness in Madagascar.

Besides the 413 described species, we identified 408 divergent lineages, 310 of which fit the category of candidate species, while 98 are considered deep conspecific lineages. These figures suggest that species richness could be twice the currently recognized. Geographically, most of these candidate species occur in well-studied areas within the island.

Despite being one of the best-studied and explored tropical countries worldwide for amphibians, many species are awaiting a taxonomic assessment in Madagascar. Paradoxically, this unassessed diversity concentrates on highly explored regions, emphasizing the importance of exploring and inventorying new areas, as they will likely harbor many new species yet to be discovered. We expect similar patterns across less-studied tropical realms and encourage researchers to perform such studies in different clades before this neglected biodiversity becomes irremediably lost.

### Effect of forest management in the taxonomic and functional diversity of Mediterranean Scot pine understory plant communities

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**Keywords:** forest management, plant biodiversity conservation, plant communities, Mediterranean Scot pine

#### Summary

Scot pine forests (*Pinus sylvestris*) in the Spanish Central System constitute, together with the relictic betic populations, the Southwestern limit of the species distribution. These forests have been subject to various types of management since ancient times.

Nowadays, there has been a great interest in developing management approaches that simultaneously support biodiversity, production, and optimize the benefits of climate mitigation. However, the direct and indirect effects that forest management has on biodiversity are not yet fully understood.

Thus, our objective is to assess the effects that different forest management practices have on the plant biodiversity taking into account the taxonomic, functional and phylogenetic composition of the Scot pine understory plant communities. For that we selected two locations in differently managed pine forests where a total of 64 floristics inventories were performed during 2022.

Our results show significant differences in taxonomic and functional diversity between pine forests subjected to more intensive management versus those managed with techniques that generate homogeneous stands. The latter forests are more diverse and maintain a higher conservation value

In a global change context where southern populations of Scots pine are threatened, our results highlight the importance of management focused on the conservation of species and communities.

### How do hippos grow?

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**Keywords:** *Hippopotamus amphibius*, Ontogeny, Life-history, Geometric morphometrics, Skull.

#### Summary

The characterisation of the battery of biological processes related to the generation of the diversity of phenotypes found among mammals is a widely discussed topic that requires a great deal of effort to study. This work aim to advance our understanding of these phenomena by examining how life-history traits influence the cranial morphology of the common hippopotamus (*Hippopotamus amphibius*), focusing on an ontogenetic perspective. By analysing a large database of 3D digitized skulls and jaws from over 198 individuals across 20 developmental stages, we applied geometric morphometrics and integrated life-history data approach. Key findings reveal that the primary variation in skull and mandible shape aligns with typical mammalian developmental patterns. Significant morphological changes occur during early infancy, coinciding with weaning, and during puberty, aligning with reproductive maturation. Skull morphology stabilizes earlier than the mandible, indicating additional biological factors at play. A notable late-stage modification in the male mandible suggests a link to the development of secondary sexual characteristics, specifically lower canine hypertrophy. This research highlights the intricate relationship between life-history traits and cranial ontogeny, providing insights into the evolutionary biology of large mammals.

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## Serial Reconstruction of Hand Phalanges

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**Keywords:** Hand, 3D Geometric Morphometric, Hominini, Seriality, Reconstruction.

### Summary

Manual digits, with proximo-distal and radio-ulnar homology in primates, can be analysed following a serial morphological approach. In the hominin fossil record, hand bones are scarce and rarely found in anatomical articulation. Therefore, this study aims to analyse the seriality in the proximal and intermediate phalanges of current and extinct Hominini species to validate a new reconstruction methodology.

For this purpose, we designed a template (27 true landmarks and 128 curved semi-landmarks) for proximal and intermediate phalanges of digits II-V, applied to *Homo sapiens* (n=125), *Homo neanderthalensis* (n=9), *Homo naledi* (n=9), *Australopithecus sediba* (n=2), and *Pan troglodytes* (n=122). Missing data were estimated using mirror symmetry or TPS. We used Principal Component Analysis to quantify morphological variability and examine each phalanx deformation vector. Every reconstruction was validated by comparing the estimated to the original data using Procrustes Distance and the Mann-Whitney U test.

The results show differences in serial deformation vectors between *Pan* and *Homo*. Within hominins, it depends on the digit. Reconstructions based on elements of the same anatomical level are closer to the originals than those from proximal to intermediate or vice versa, highlighting the importance of homology.

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## Can the strangest amphibians save us? diversity and molecular evolution of antimicrobial peptides in caecilians

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**Keywords:** AMP; Gymnophiona; genome; transcriptome; antimicrobial activity prediction.

### Summary

Antimicrobial peptides (AMPs) are essential components of the vertebrate innate immunity, offering broad-spectrum antimicrobial activity and evading pathogen resistance. Despite amphibians being a major source of AMPs, most studies focus on frogs, with caecilians (Gymnophiona) being largely neglected. Our study aims to explore the AMP diversity and evolutionary dynamics in caecilians, using genomic and transcriptomic data from eight representative species.

We identified over 400 candidate AMPs, classified into 29 peptide families, through bioinformatic analyses. Four peptide families primarily exhibit primary antimicrobial activity, while the others may play secondary roles. Phylogenetic analyses revealed gene duplications, convergent evolution, and signatures of positive selection in five AMP families, highlighting evolutionary adaptations that could be related with antimicrobial activity. Using artificial intelligence (AI) approaches, several peptides showed strong antimicrobial potential and no cytotoxicity, making them promising therapeutic candidates. Additionally, structural analysis indicated links between peptide 3D conformation and function.

These findings suggest that caecilians, with their distinct evolutionary history, represent an unexplored source of bioactive peptides with pharmaceutical potential. *In silico* approaches offer a cost-effective method to identify new therapeutic agents, providing a valuable preliminary step before undertaking more expensive experimental validation. This research highlights the biomedical potential of caecilian AMPs in the fight against antibiotic resistance.

## Unraveling the migratory behaviour of hoopoes (*Upupa epops*): a multidisciplinary journey through eco-immunology, genomics, stable isotopes analysis and satellite tracking

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**Keywords:** birds, migration, evolution, physiology, transcriptomics.

### Summary

Every year, billions of birds perform seasonal migration movements, a spectacular behaviour that has been studied for decades, but many aspects of which are still poorly understood. In many species, there is variation in migratory behaviour, resulting in partially migratory populations where migratory and resident individuals coexist. This scenario allows for the investigation of the evolutionary causes and consequences of migratory strategies, as well as the origin and maintenance of behavioural variation in an ecological context. New technological advances are challenging many paradigms about animal migration, and a multitude of approaches have been applied to study this topic: comparing the morphology of migrants and residents, their immunology and physiology, their reproductive success, monitoring individuals using remote tracking, studying population genetics, and, more recently, genomics and transcriptomics. We introduce here a methodological framework to consolidate all these techniques in an integrative study using the Eurasian hoopoe (*Upupa epops*) as a model. This non-passerine bird species has partially migratory populations in the Iberian Peninsula. In addition, we show the first results and future directions of my PhD project, combining the well-known concepts about migration with the most recent technology to unravel this behaviour which has fascinated biologists and non-biologists for centuries.

## Euphorbiaceae Afrotropicales en la Lista EDGE: Tesoros Evolutivos al Borde de la Extinción

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**Keywords:** Biogeografía, Conservación, Euphorbiaceae, Filogenómica, África Tropical

### Summary

A pesar de que África tiene mayor tamaño que Sudamérica, presenta menor número de especies de plantas vasculares (47% menos). Esta diferencia se denomina el patrón de biodiversidad 'Odd-Man-Out'. La familia Euphorbiaceae es un claro ejemplo de esta disparidad y se caracteriza por un ratio especies/géneros muy alto: c. 80% de los géneros presentan menos de 10 especies, mientras que el resto son hiperdiversos con una distribución pantropical. En este estudio, nos enfocamos en 66 géneros afrotropicales (20 géneros monotípicos o con 1 especie africana) que agrupan 202 especies. Nuestros objetivos son: i) reconstruir las relaciones filogenéticas y la edad de divergencia de cada linaje basándonos en los datos genómicos obtenidos (HybSeq), ii) reconstruir el nicho climático utilizando proyecciones paleoclimáticas, iii) explorar el 'patrimonio evolutivo' (pérdida gradual de caracteres biológicos, como parte de la diversidad filogenética), iv) implementar modelos multi-clado basados en inferencia bayesiana e inteligencia artificial supervisada para explorar patrones biogeográficos y de diversificación, v) estimar el estado de conservación de las especies utilizando criterios IUCN-EDGE (Evolutionary Distinct, Globally Endangered) para establecer la priorización del esfuerzo de conservación. Nuestros resultados preliminares son un 85% de muestreo molecular (174) y 51% de informes IUCN completados hasta la fecha (144).



## Analysis of the endemism of the Dianic territory. Implications for the conservation of species and habitats

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**Keywords:** Endemism, Biogeography, Conservation, Dianic Territory, Taxonomy

### Summary

The territory of our study includes most of the Baetic mountains of limestone nature that reach the provinces of Valencia and Alicante. Includes thermo to supra-Mediterranean territories of the Valencian counties of La Costera, La Vall d'Albaida, La Safor, La Ribera Baixa, El Comtat, La Marina Alta, La Marina Baixa and L'Alcoià.

We are not aware of any recent update on the number of endemic plant taxa in the study area. Some indirect data taken from Valencian authors such as G. Mateo and M. B. Crespo suggest of a range between 30-50 taxa

We are aimed to address the following aspects: (1) defining the endemic dianic element; (2) studying the taxonomy of Dianic endemic taxa; (3) establishing phylogenetic relationships with species close to the Dianic endemic element; (4) assessing the threat degree of Dianic endemic taxa based on population studies, (5) modeling the evolution of the populations of threatened taxa in different scenarios of global change and in the face of future changes in the land use; and (6) proposing management and conservation measures for the taxa presenting the highest threat degree.

## Ethnobotany and medical applications in *Acalypha*: a global review with taxonomic assessment

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**Keywords:** Ethnobotany, Euphorbiaceae, pharmacology, taxonomy, tropical botany

### Summary

Throughout history, humans have used plants for different purposes, including disease prevention and treatment. Understanding why and how communities have used and continue to use plants is valuable as part of human history and can help identify new pharmacologically interesting compounds and conservation priorities. However, many of them belong to groups that are only imperfectly known. The lack of good taxonomic knowledge hinders confirming the identity of the species.

The genus *Acalypha* L. (Euphorbiaceae), with ca. 500 accepted species and a pantropical distribution, includes many species with reported human uses. However, the information available is limited due to a lack of basic taxonomic knowledge for most species, frequent specimen misidentification, and many names now considered synonyms. Understanding *Acalypha*'s ethnobotanical diversity relies on comprehensive taxonomy.

We present a detailed review of the ethnobotany of *Acalypha* species with medicinal interest. We compiled and classified scientific literature on ethnobotanical and experimental studies of *Acalypha*, at a global scale. Importantly, we assess the taxonomy of the plants studied, evaluate the reliability of published studies and standardize recorded uses to facilitate future research. This review, part of a broader monographic study of the genus, paves the way for targeted investigation on *Acalypha* and its medicinal potential.



# Pósteres



## Transplantation of predegenerated peripheral nerves after complete spinal cord transection in rats: Effect of neural precursor cells and pharmacological treatment with the sulfoglycolipid Tol-51

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**Keywords:** Traumatic spinal cord injury, predegenerated peripheral nerve, neural precursor cells, Tol-51, axonal regeneration, modified BBB scale

### Summary

Background: After brain trauma or spinal cord injury (SCI), the regenerative capacity of the central nervous system (CNS) is severely limited. This limitation stems in large part from the failure of axonal regeneration and the formation of glial scars. However, the introduction of a combinatorial treatment involving PPN and stem cells after SCI must address the additional challenge of glial scar formation, which inhibits regenerating axons from integrating into the neural circuitry. We hypothesize that Tol-51, a synthetic sulphoglycolipid that inhibits glial scar, could be beneficial in a combinatorial treatment approach for SCI. Therefore, the objective of this project was to evaluate axonal regeneration and improvements in locomotor function following SCI in rats using a combination of PPN, NPCs, and Tol-51. Methods: One month after complete spinal cord transection a 7 mm spinal cord segment containing the scar tissue was removed and replaced with segments of pre-degenerated sciatic nerves. This treatment was combined with injection of NPCs and Tol-51 into the spinal cord anterior and posterior of the PPN transplant. Conclusions: Our data demonstrate that PPN implants plus NPCs and Tol-51 allow successful axonal regeneration in the CNS, however the problem of establishing functional connections of regenerating axons for a clinically significant recovery after SCI requires further studies.

## Effects of insoluble solids and lignocellulose-derived inhibitors on *Kluyveromyces marxianus* CECT 10875 on fermentation performance

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**Keywords:** Non-conventional yeast, lignocellulose fermentation, bio-refineries, thermotolerance.

### Summary

*Kluyveromyces marxianus* is a non-conventional yeast with promising applications in lignocellulosic-based bio-refineries. This microorganism can ferment at temperatures between 40-45 °C, and assimilate a wide range of carbon sources. However, fermentation of lignocellulosic-derived media is challenging and the increase of *K. marxianus*' cell robustness against lignocellulosic-derived inhibitors (LDI) is required. In this work, the tolerance of *K. marxianus* CECT 10875 against a synthetic mix of LDI (0-100% v/v), insoluble solids (0-60% w/w), and different temperatures (30 °C, 36 °C, and 42 °C) was studied with a Box-Behnken experimental design. The presence of 60% w/w of insoluble solids and 100% v/v of the LDI mix severely affects fermentation performance. Ethanol and cell concentration decreased from 20.3 to 3.0 g/L and 4.9 to 0.5 g/L, respectively, compared with the control condition after 48 hours of fermentation. The combination of both stressors additionally increases intracellular stress, with a 6-fold increment in ROS level when 50% v/v of LDI and 30% w/w of insoluble solids are present. These results confirm the synergic effect of insoluble solids and LDI and set the basis for further study of the mechanisms involved in cell tolerance, which can be targeted in the future to engineer *K. marxianus* genetically.

## Biomechanical analysis of physical activity in a meroitic cemetery from northern Sudan

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**Keywords:** Nubia, Meroitic, biomechanics, Cross-sectional geometry, sexual differences

### Summary

We present the biomechanical study of long bones of the Nubian cemetery of Amir Abdallah (Sudan). The objective is to explore the levels of ambulatory activity and upper limb workload from the analysis of cross-sectional geometric properties of tibia and humeri. Only adult skeletons were selected (n=155), and osteological sex was estimated through metric analyses of the pelvic bone. Tibiae and humeri were scanned with a surface scan, and solid cross-sectional images were obtained at the mid-shaft. Biomechanical parameters were obtained with the BoneJ software, and statistical analyses were carried out to estimate differences between sexes in the shape index ( $I_{max}/I_{min}$ ), and bilateral asymmetry of the second polar moment of area ( $J$ ). There were no differences between sexes for the shape index of the tibia (male=2.21, female=2.11,  $p=0.157$ ), which indicates that there were no differences in ambulatory activity between sexes. In comparative terms, this value is similar to urban current populations. No significant differences were observed between sexes for humeral asymmetry (male=10.33, female=11.64,  $p=0.703$ ), which indicates the absence of sexual differences in physical tasks involving the development of humeral asymmetry. We discuss the information that these results offer regarding the social structure of the Meroitic society represented by this cemetery.

## Ecological Determinants of the European Wildcat's (*Felis silvestris*) Home-range size

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**Keywords:** Home-Range, Minimum Convex Polygon, Wildcat, Spatial ecology, Conservation

### Summary

A study was conducted on the ecological determinants that shape European wildcat's Home-Range (HR) size. A bibliographic review was performed to obtain metadata of wildcat HR size in 31 European sites (11 countries). The data were standardized to the Minimum Convex Polygon 95% method (MCP95). The response variables (HR size of males, females and both combined) were studied based on different predictor variables: biotic, abiotic and landscape variables (CORINE). Data on the presence/absence of different species of potential prey, ungulates and competitors, were obtained from the Global Biodiversity Information Facility (GBIF). Predictor variables were obtained using Geographic Information Systems (GIS), from a buffer equal to the number of individuals studied in each area times the mean of their respective HR size. Using Akaike's Information Criterion (AIC), the most parsimonious General Linear Models (GLM) were constructed and selected. According to the most parsimonious model, male HRs increased as did female HRs and mean annual temperature. Female HRs decreased in areas of elevated competitor, rodent and ungulate species richness. Finally, considering both sexes combined, HR size decreased in areas of increasing latitude, abundant forest cover, high mean annual precipitation and high mean Normalized Digital Vegetation Index.

## The arabidopsis PAT1 proteins differentially regulate plant responses to abiotic stress

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**Keywords:** Arabidopsis, decapping, PAT1, abiotic stress,

### Summary

The sessile nature of plants has led to the development of sophisticated adaptative responses to cope with adverse environmental conditions, such as freezing, drought, or soil salinity, that constrain plant growth and development. These adaptive responses are mostly controlled through masive changes in gene expression, which are regulated at different levels. When considering the post-transcriptional regulation of gene expresión in response to abiotic stresses, mRNA degradation constitutes a fundamental step, as it determines the levels of a given transcript. In plants, the 5'-3' mRNA degradation pathway is the most relevant, as it controls the stability of 68% of transcripts. In this pathway, the 5' cap of mRNAs is removed by the decapping machinery, generating substrates for exoribonucleases that completely hydrolyze the transcripts. PAT1 is an essential component of the decapping machinery, which acts as an activator of DCP2, the functional decapping enzyme in the machinery. Interestingly, in contrast to yeast and other eucaryotes, Arabidopsis has three functional PAT1 proteins, named PAT1, PAT1H1 and PAT1H2. In this study, we have analyzed the possible role of these proteins in plant tolerance to abiotic stress (cold, drought and high salt).



## Short exposure to nanomolar cannabinoids promotes breast cancer cell differentiation

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**Keywords:** Breast cancer, tumor differentiation, organoids, cannabinoids, differentiation therapy.

### Summary

Cancer is a heterogeneous disease, due to differences in the the organ of origin and the intrinsic tumor variability. Mutations in cancer, along with alteration in the epigenetic landscape, are key drivers of tumor progression, invasiveness and metastasis, especially on poorly differentiated scenarios. Dedifferentiated cells often resist to conventional cytotoxic therapies that target proliferation, which opens the door to complementary approaches based on cancer differentiation. Breast cancer is the most diagnosed cancer worldwide and the second leading cause of death in women. Most breast cancer-related deaths occur due to relapse or metastasis, linked to poorly differentiated tumors and partial responses to current therapies. In our lab, we aim to develop differentiation-based strategies to complement chemotherapy.

In this project, we demonstrate that cannabinoids, at low doses and short exposures, act as pro-differentiation agents in breast cancer. Using organoids derived from mouse models and patient biopsies, we show here that cannabinoids induce long-term differentiation, reducing cancer cell invasiveness and self-renewal, and promoting a basal-to-luminal switch. These changes notably impair tumor aggressiveness, suggesting that cannabinoids may cooperate with existing breast cancer therapies to efficiently reduce the possibility of relapse or metastasis.

## Deciphering the effect of different diets throughout life on motor and cognitive impairments caused by TDP-43 deregulation

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**Keywords:** TDP-43, ALS-FTD, Diets, Multi-omics, Metabolism.

### Summary

TDP-43 proteinopathies are complex neurodegenerative diseases that are characterized by the cytoplasmic mislocalization of TDP-43. One external factor that may significantly influence these diseases is the metabolic changes associated with their age of onset. These metabolic alterations could play a crucial role in the pathophysiology of these disorders, although their mechanism remains unknown.

We conducted an exhaustive study using a mouse model carrying a point mutation in the Tardbp gene (M323K), which exhibits cognitive and motor deficits alongside TDP-43 cytoplasmic mislocalization. Mice were subjected to three different diets from 6 weeks to 9-12 months of age. We longitudinally evaluated the impact of diets on disease progression through motor and cognitive tests, and analyzed proteins using western blot and immunohistochemistry, focusing on TDP-43 localization in the nervous system. A multi-omic approach was used to identify key metabolic pathways, combined with brain glucose metabolism studies using 18F-FDG PET.

The results show a clear reduction in cognitive deficits with a caloric restriction diet. We observed change in the localization of TDP-43 in mutants on the restricted diet, along with a differential synapse-related pathway regulation.

This study highlights the direct link between diet/metabolism and cognitive alterations in a murine TDP-43 proteinopathy model.

## Effect of pegylation on pulmonary surfactant-driven interfacial vehiculization of drug delivery systems

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**Keywords:** PEGylation, pulmonary surfactant, surfactant function, interfacial activity, vehiculization.

### Summary

You may also add a couple of lines naming your funding entity, always respecting the words limitation (Optional). Coating the surface of nanoparticles with polyethylene glycol (PEG), or "PEGylation", is a well-established approach to improve the efficiency of drug and gene delivery to target cells and tissues. Different PEGylated nanoparticles have been designed for pulmonary drug delivery since PEGylation protects nanocarriers from pulmonary immune system, enhances mucopenetration and facilitates sustained drug release. However, PEGylation may interfere with the interfacial vehiculization of nanoparticles along the air/liquid interface of the respiratory airways as it is promoted by pulmonary surfactant, a lipoprotein complex that facilitates the work of breathing by forming films that decrease the surface tension at the alveolar surface. Therefore, the aim of this work was to assess the effect of PEGylation on the interfacial vehiculization of liposomes composed of dipalmitoylphosphatidylcholine and lysophosphatidylcholine. To that end, we characterized the interfacial activity of PEGylated liposomes, its interaction with surfactant components and its vehiculization by surfactant using two surface balance-based set ups: an adsorption Wilhelmy balance and a double-balance setup connected through the interface. Finally, to evaluate whether the incorporation of PEGylated nanomaterials could compromise surfactant function, we investigated their impact into surfactant performance using a captive bubble surfactometer.

## Response of sweet cherry leaves to foliar application of calcite and kaolinite

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**Keywords:** mineral formulations; foliar absorption; adjuvants; nutrient elements; plant physiology.

### Summary

Foliar application of mineral formulations may enhance crop yield and quality and help alleviate stress factors which are becoming more frequent worldwide. Calcite ( $\text{CaCO}_3$ ) and kaolinite ( $\text{Al}_2\text{Si}_2\text{O}_5(\text{OH})_4$ ) are being supplied in crop areas as routine treatments, although their impact is little known. In this study, we evaluated the effect of treating cherry leaves (*Prunus avium* var. Sweetheart) with mineral suspensions (5, 10, 15% (w/v)) of approximately 1.5  $\mu\text{m}$  particle size, with and without 0.1% surfactant (Genapol X-80). The trial was developed at the end of the summer in a commercial cherry tree plantation in Jumilla (Spain). The stomatal conductance ( $G_s$ ) and leaf temperature ( $T_{\text{leaf}}$ ) were monitored for a 1-month period. Also, chlorophyll fluorescence and leaf tissue mineral element concentrations were determined at the end of the experiment. Regarding to the results, chlorophyll fluorescence was not affected by foliar treatments, but short-term effects on  $G_s$  and  $T_{\text{leaf}}$  were recorded. We also observed changes in the nutrient balance of some elements such as calcium (Ca), aluminium (Al) and silicon (Si). The obtained results provide evidence for the response of plant leaves to the foliar application of mineral particles, but further investigations are required for characterizing and improving the effectiveness of such treatments.

## Melanoma-derived extracellular vesicles promote t cell exhaustion that can be reverted using immunoregulatory micrnas

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**Keywords:** T cell function, microRNAs, melanoma, Small Extracellular vesicles (sEVs), nanoimmunotherapy

### Summary

Tumors have developed different mechanisms to evade immune surveillance. Melanoma is the skin cancer that exhibits the highest mortality rate due to its ability to metastasize to distant organs. Tumor cells have been shown to release small extracellular vesicles (sEVs) that dampen antitumoral responses, in particular by promoting lymphocyte function impairment and exhaustion. In this context, immunotherapies have arisen as promising therapeutic alternatives to improve patient outcome, however not all patients respond to these therapies.

In this context, we have set up an immunosuppression in vitro model to isolate human melanoma cell-derived sEVs and study the functional impact on primary T helper lymphocytes. In addition, to reverse T cell immunosuppression mediated by melanoma sEVs, we generated gold nanoparticles loaded with immunoregulatory microRNAs (miRNA-AuNPs).

sEVs from two highly metastatic human melanoma cell lines (SKMEL103 and A375MA2) were found to have an impact on T cell activation and promote differential expression of depletion markers such as PD-1, TIM-3 or CTLA-4. On the other hand, miRNA-AuNPs were able to partially reverse the immune impairment mediated by sEVs and promote the maintained expression of T cell activation markers such as CD25 or CD69.

## Intraspecific genomic and phenotypic diversity in *Yarrowia lipolytica*, an industrially relevant yeast

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**Keywords:** *Yarrowia*, yeast, population genomics, Illumina sequencing, phenotypic diversity

### Summary

*Yarrowia lipolytica* is a non-conventional yeast commonly used as a biotechnological chassis in several bioprocesses. However, research on this yeast focuses on a few strains, limiting our understanding of its ecology, evolution and industrial potential. Here, whole-genome sequencing was used to analyze 140 strains of *Y. lipolytica*, representing the geographical and ecological diversity of the species. The analysis revealed four distinct lineages and several admixed strains, with genetic diversity and phylogenetic data indicating varying levels of complexity within populations. A significant clonal group was identified, mainly associated with human-related environments like dairy products. High fixation indexes (0.5-0.8) suggest substantial genetic differences among populations. Phenotypic analysis of a subset of strains in over 40 conditions revealed that different lineages showcase specific adaptations to certain environments. Notably, admixed strains performed better across more conditions, suggesting a broader ecological niche due to diverse genetic backgrounds. This study offers new insights into the population structure of *Y. lipolytica*, which could guide future bioprospecting and enhance the application of this species in biotechnology by leveraging its genetic diversity for emerging challenges.

## Study of climate adaptations in cranial morphology using geometric morphometry

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**Keywords:** Biological Anthropology, Human Variability, Geometrical Morphometry, Climate Adaptation, Arid Climate.

### Summary

Since the expansion of *Homo sapiens* across the globe, our species has had to face different climatic realities, having to adapt to survive. This climatic stress may have acted as an evolutionary force that, together with other factors, contributed to shape the cranial morphology of the different populations.

In our work we propose the study of human variability in cranial morphology, as well as its relationship with climatic variables. We included populations from different archaeological contexts, distributed throughout the African continent, Central America and the Iberian Peninsula, covering a wide climatic range.

We evaluated both intra-population variability, studying the range of distribution of the individuals of each population with respect to the centroid, and the relationship between climate and skull morphology, by applying a Two-Block Partial Least Squares analysis to study the covariation between the climatic variables and the set of cranial landmarks used.

We have been able to detect an association between the climate in which a population develops and its internal variability (i.e., diversity among individuals), as well as a significant relationship between cranial shape and climatic variables, which allows us to increase our knowledge about the adaptation of our species to the environment in which it lives.

## In vitro co-culture of cortical neurons and probiotic bacteria *Lactiplantibacillus plantarum* induces morphological, structural, and transcriptomic changes in neural cells

Juan Lombardo-Hernández<sup>1</sup>, Riccardo Aucello<sup>2</sup>, David Muñoz-Rodríguez<sup>1</sup>, Elisa Quarta<sup>1</sup>, Cristian Botta<sup>3</sup>, Luca Cocolin<sup>3</sup>, Antonio Murciano<sup>1</sup>, María Teresa Garcia-Esteban<sup>5</sup> and Celia Herrera-Rincón<sup>1</sup>.

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**Keywords:** microbiota, cortical neurons, gut-brain axis, bioelectricity, neurological diseases

### Summary

The role of bacterial communities within the microbiota in maintaining organismal homeostasis is a growing area of interest. While the influence of the microbiota on the gut-brain axis is well-established, direct interactions between bacteria and neurons remain largely unexplored. This study establishes an in vitro co-culture model combining *Lactiplantibacillus plantarum* with cortical neurons to investigate these interactions. We demonstrate that bacterial-neuronal co-culture is feasible and introduce a novel platform for the detailed analysis of their communication. Our results indicate that *L. plantarum* adheres to neurons, with bacterial adhesion increasing in a time-dependent manner. Furthermore, neurons in co-culture exhibit significant structural and functional alterations, including the modulation of proteins essential for neuroplasticity, such as Synapsin1 and pCREB. Real-time calcium imaging further reveals that co-cultured neurons display enhanced cytosolic Ca<sup>2+</sup> signaling in response to bacterial presence. Transcriptional analyses suggest an upregulation of genes associated with inflammation, stress response, bioelectricity, and cellular signaling in co-cultured neurons. These findings provide evidence of bidirectional communication between neurons and bacteria, presenting a novel example of cross-kingdom signaling. This model offers a valuable framework for studying biological information exchange across distinct cellular domains and may enhance our understanding of neuron-bacteria interactions in both physiological and pathological conditions.



## Kidney aging is a gender issue

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**Keywords:** kidney disease, aging, gender, sex

### Summary

Increasing global life expectancy has contributed to population aging and to the increased prevalence of age-related pathologies, including kidney disease. Since gender is an influential factor in both longevity and nephropathies, with women having the highest life expectancy and prevalence of chronic kidney disease, renal aging can also be influenced by sex.

Aging was associated with a worsening of renal function (renal aging) in mice, which was especially striking between 18 and 24 months and greater in males than in females. Renal aging was associated with increased glomerular size, inflammation (leukocyte infiltration) and renal fibrosis, as well as increased renal expression of genes encoding proinflammatory and profibrotic factors and decreased expression of genes encoding nephroprotective factors. Better conservation of renal function in older females was associated with lower renal inflammation, lower gene expression of certain chemokines (such as MCP-1) and increased gene expression of the nephroprotective factor PGC-1 $\alpha$ .

In conclusion, sex seems to influence the rate of renal aging and our data identified harmful factors, such as MCP-1, and nephroprotectors, such as PGC-1 $\alpha$ , which could be related to the different rate of renal aging between sexes.

## eDNA techniques unveil the dietary and distribution patterns of the invasive Eastern mosquitofish in Spain: Insights for Endangered toothcarp conservation

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**Keywords:** Environmental DNA; Endangered killifish; Invasive species; Eastern mosquitofish; Conservation management

### Summary

Environmental DNA (eDNA) techniques have emerged as a promising tool in conservation biology, aiding in species monitoring, early detection of invasive species, and dietary analyses. The Eastern mosquitofish (*Gambusia holbrooki*), introduced to Spain in the 1920s for malaria control, now poses a significant threat to two endangered and endemic killifish species: the Baetican toothcarp (*Aphanius baeticus*) and the Spanish toothcarp (*Aphanius iberus*). Employing eDNA methods, the present study aims to uncover whether the negative impact that *G. holbrooki* has on toothcarp populations is due to a competition for resources or predation. Our findings reveal that both competition and predation are likely and that *G. holbrooki* presents a widespread distribution range. These results underscore the invaluable role of eDNA in revealing ecological interactions and informing conservation management, highlighting the urgent need for targeted strategies, including invasive species control and habitat restoration, to ensure the long-term survival of *A. baeticus* and *A. iberus* across their native range.

## Desiccation in Mediterranean oak acorns: does morphology influence germination rate?

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**Keywords:** Acorn, desiccation, germination rate, Mediterranean oak, *Quercus*, recalcitrant seeds.

### Summary

The relationship between weight and size of the acorns can be an important factor in the loss of moisture and therefore affect the germination rate of *Quercus* acorns. The acorns of Mediterranean oaks are considered to be recalcitrant seeds, so biological and climatic processes are important to maintain a constant moisture content in the seeds, as a drop in moisture content of up to 25-30% can affect their viability. This study hypothesises that the more elongated and narrower seeds lose moisture more easily and are therefore more sensitive to germination rate during periods of desiccation. The aim of this study is to find out whether the morphological traits of the acorns, mainly width and length are variables that might influence seed desiccation and thus limit the germination rate. For this purpose, seeds of different shape and size from different *Quercus* species (*Q. ilex*, *Q. pyrenaica*, *Q. faginea*, *Q. suber* and *Q. coccifera*) are exposed to different drying times and subsequently germinated under constant humidity conditions. In this way, the amount of moisture lost by the acorns as a function of time exposed to dryness, their length and width are recorded and related to germination capacity.

## Rise of pneumococcal serotype 3 is associated with clade 1- $\alpha$ /GPSC12 involving enhanced evasion of the host immune response and disease potential

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**Keywords:** Streptococcus pneumoniae, serotype 3, PCV-13, H3N2 influenza virus, LytA

### Summary

*Streptococcus pneumoniae* serotype 3 has become the leading cause of IPD in children and adults. Despite being a vaccine serotype, the 13-valent pneumococcal conjugate vaccine has failed to reduce the disease burden due to serotype 3. Therefore, it is necessary to characterise which lineages are circulating and whether there are differences in pathogenicity between them to clarify the reasons for this apparent lack of protection by PCV-13.

Bioinformatic analysis show that the predominant lineage before the introduction of PCV-13 was CC260/GPSC83/ST260. Selective pressure from the vaccine gradually led to its replacement by CC180/GPSC12/ST180. This is a lineage consisting of several clades and sequencetypes, most belonging to Clade I- $\alpha$ /ST180. Strains of this clade adhere better to the lung epithelium and better evade opsonophagocytosis. The increased virulence of this clade may be due to a point mutation in the virulence factor LytA (His166-Tyr) that increases its enzymatic activity, a change that was observed in all strains of this clade.

In addition, an association between CC180/GPSC12/ST180 strains and H3N2 influenza has been observed. In co-infection assays on two-dimensional human lung organoids, prior infection with H3N2 influenza increased adherence of these serotype 3 isolates by 70%.

These results should be considered in the development of future vaccines.

## Forest diversity modulates differential species responses to disturbances in Iberian forests

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**Keywords:** Compositional shifts, Forest diversity, Aboveground productivity, Spanish Forest Inventory.

### Summary

Global change is altering forest dynamics through modification of disturbance regimes. However, the magnitude of the effects of disturbances strongly depends on the species-specific responses and the stand characteristics. Diverse forests have been shown to have complementary processes that make them stable against disturbances. However, the buffering effect of disturbances by structural and functional diversity and their implication in composition shifts are not well-known. To better understand the role of diversity modulating the effect of disturbances and compositional shifts, we modelled aboveground productivity at forest level and within functional groups (i. e., needle-leaved, broad-leaved deciduous and broad-leaved evergreen), testing this interaction while controlling by abiotic characteristics and forest structure. For that, we used data from 12,075 forest inventory plots. Overall, we found that total basal area is increasing over time, but the rate of increase is slowing down, especially in needle-leaved species. In addition, initial forest structure and climate underlaid aboveground productivity variations for the three functional groups. Finally, higher levels of structural diversity increased aboveground productivity in harvested plots regardless the functional group. Our results show that structural rather than functional diversification of the stands might be a key measure for the adaptation of Iberian forests to global change.

## Una evaluación de los principales mecanismos detrás de la relación entre biodiversidad y estabilidad a través de escalas (BIOSTAR: BIODiversidad STabilidad Relaciones)

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**Keywords:** biodiversity, stability, relationships, multifunctionality, functional traits.

### Summary

La estabilidad de las comunidades biológicas es vital para el mantenimiento de los servicios ecosistémicos, como la producción de alimento y forraje, la captación de carbono o la fertilidad del suelo. Previamente, se ha demostrado la importancia de la diversidad taxonómica para explicar la estabilidad temporal de la biomasa. Sin embargo, es posible enriquecer el debate sobre el posible efecto de la biodiversidad en la estabilidad de múltiples funciones y servicios ecosistémicos (multifuncionalidad) implementando un marco basado en los rasgos funcionales de las especies que coexisten en una comunidad. Por tanto, el objetivo de este proyecto es investigar, mediante un enfoque basado en los rasgos funcionales de las plantas, la relación entre biodiversidad y estabilidad, tanto en la misma escala como a escalas diferentes, y determinar los principales mecanismos de esta relación.

Este proyecto reunirá dos marcos de estudio recientes; el primero permite evaluar el efecto de la estabilidad a través de escalas y el segundo describe cómo utilizar un enfoque basado en rasgos funcionales para comprender cómo los efectos provocados por mecanismos de esta relación como el efecto de las especies dominantes, de las dinámicas compensatorias y de la redundancia afectan a la estabilidad de la multifuncionalidad.

## Application of artificial intelligence to improve the treatment of acute child malnutrition in emergency contexts

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**Keywords:** Undernutrition, Machine Learning, ENSEMBLE, weight gain, Niger.

### Summary

Acute child malnutrition is a global public health problem, affecting 45 million children under 5 years of age. The World Health Organization recommends monitoring weight gain weekly as an indicator of correct treatment. The present study aims to use machine learning techniques to predict weight gain during treatment in humanitarian contexts.

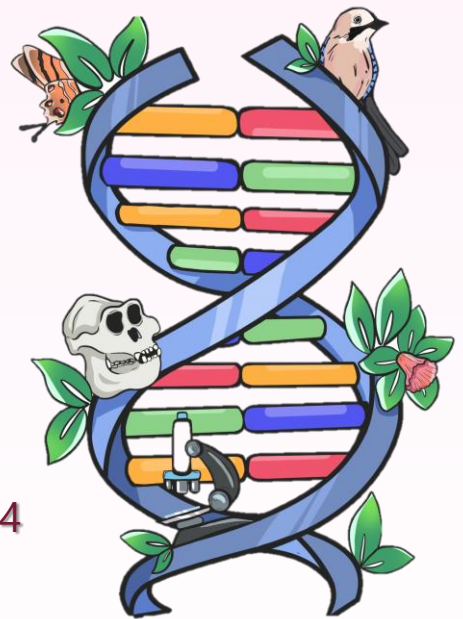
The sample consists of 455 children aged 6-59 months from Diffa Region (Niger) under treatment for acute malnutrition, from whom information on 51 socioeconomic variables was collected. After a variable selection procedure, an ensemble model was adjusted using 5 algorithms for prediction, combining them using a random forest meta-algorithm.

The fit of the final ensemble model ( $R^2=0.58$ ) improved the individual algorithms ( $R^2=0.12-0.25$ ). By constructing multiple ROC curves, an optimal cut-off point was identified with an Area Under the Curve (AUC) of 0.735 at the value of  $<5.5$  g/Kg/day to establish low weight gain. The ensemble model reached a success rate of 86.84% (66/76) among individuals below  $<5.5$  g/Kg/day in the test set. The results highlight the importance of adapting the cut-off points of international standards to each context, as well as its practical usefulness in optimizing the treatment of the most vulnerable groups.





# 8<sup>th</sup> PhDay Biología



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