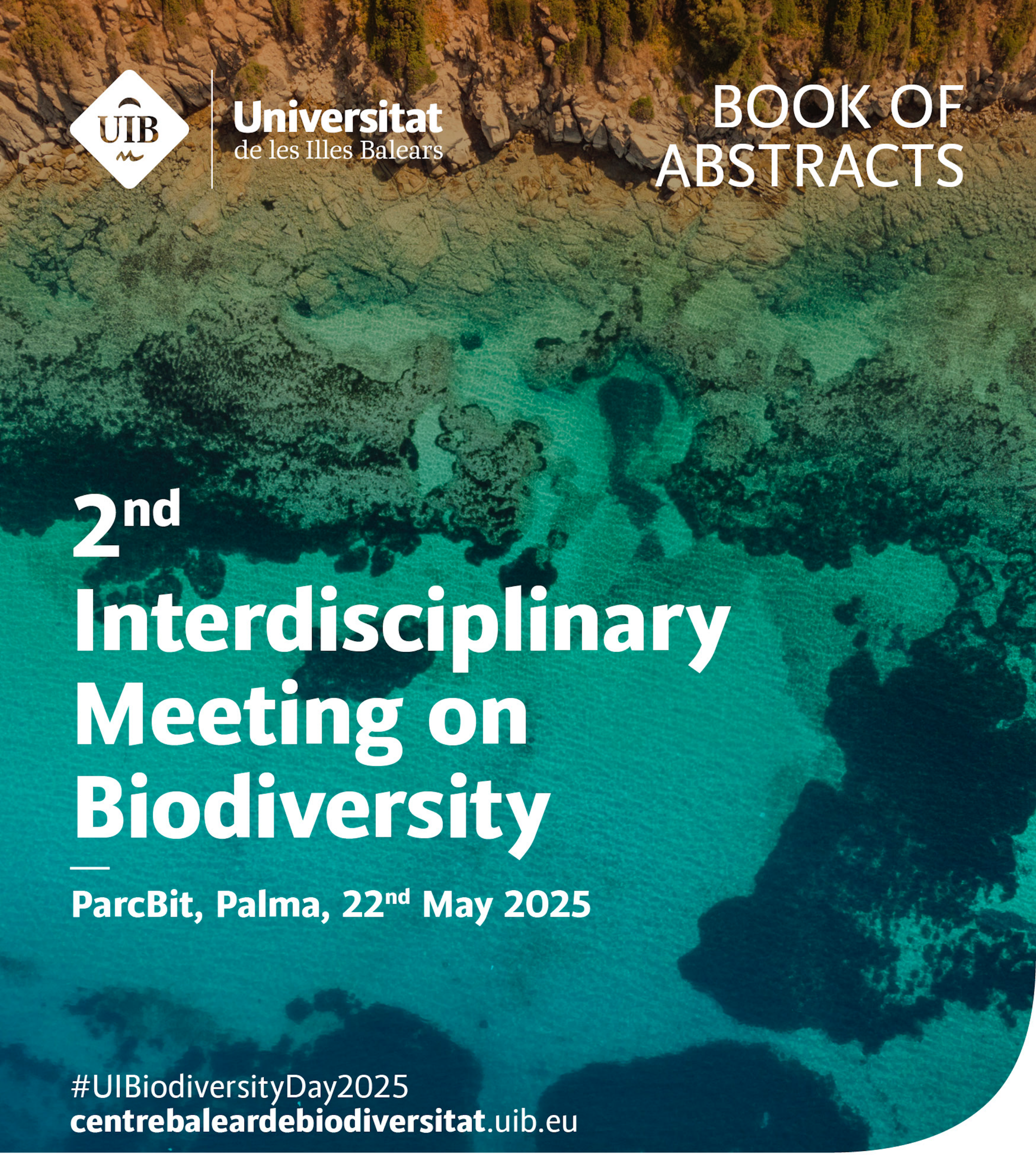

Universitat
de les Illes Balears

BOOK OF ABSTRACTS

2^{nd} Interdisciplinary Meeting on Biodiversity

ParcBit, Palma, 22^{nd} May 2025

#UIBiodiversityDay2025
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INFORMATION

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Disseny 2024-25: Servei d'Identitat i Cultura Institucional de la Universitat de les Illes Balears

Book of Abstracts

Biodiversity Day 2025

Palma de Mallorca - May 22, 2025

In celebration of the International Biodiversity Day, the Centre Balear de Biodiversitat (CBB-UIB) and the Institut de Biologia Evolutiva (IBE, CSIC-UPF) are proud to co-organise the second edition of the Biodiversity Interdisciplinary Meeting. This event is dedicated to fostering biodiversity research, promoting collaboration across scientific community, and sparking new connections.

This multidisciplinary forum welcomes researchers, students, and environmental managers across disciplines such as biology, evolution, ecology, conservation, and environmental science. Together, we will explore today's pressing challenges and opportunities in biodiversity, through a collective and innovative perspective.

Thematic areas

Throughout the day, experts will share the latest lines of research in our environment, highlighting topics such as:

– Strategies for the conservation and sustainable management of biodiversity.
– Acceleration in the discovery and characterisation of organisms.
– New tools for the study and analysis of biodiversity.
– Ecology, biological responses to environmental variables, and use of organisms as bioindicators.

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Session 1:

Invited Speaker: Josep Alós Crespí

Ecological and evolutionary implications of fish behavior in exploited species.

Josep Alós Crespí[1]
[1]Mediterranean Institute for Advanced Studies (IMEDEA, UIB-CSIC), Esporles, Spain

While much of the research on human-induced selection has focused on morphological traits such as body size, behavioral selectivity in fisheries is gaining recognition. Here we present evidence that harvesting of wild marine fish can rapidly induce strong selection on behavioral traits, with potentially far-reaching ecological and evolutionary consequences Using a combination of novel IA-based video surveys and electronic tracking of marine fish, we studied a coastal fishery and found that nearly 60% of the local adult population was harvested within just nine days of the fishing season opening. We observed that key behavioral traits—including home range size, center of activity, and total movement distance—were individually repeatable over time, consistent with the existence of behavioral types or personalities. Survival, a major component of fitness under exploitation, was negatively associated with both body size, spatial exploration and fish personality. Only individuals exhibiting restricted home ranges and low activity survived the fishing event, indicating strong selection against bold and exploratory phenotypes. No other measured traits explained variation in survival, reinforcing the primacy of behavior in determining vulnerability. These rapid shifts in behavioral composition may reduce ecosystem resilience and fishery yield, as evidenced by the observed decline in catch rates and early fishery abandonment. This talk highlights the urgent need to consider behavioral traits in fisheries management and underscores the importance of integrating genetic and epigenetic approaches to better understand the evolutionary implications of the emerging "timidity syndrome" in wild fish populations.

Invited Speaker: Aureliano Bombarely

Understanding Plant Biodiversity by Improving Genome Annotations.

Aureliano Bombarely[1]
[1] Polytechnic University of Valencia, Valencia, Spain

Thousands of plant genomes have been published in the last ten years. Although the quality of the genome assemblies has been greatly improved with the technological advances of the sequencing technologies, the methodologies to annotate genomes have important limitations. In this presentation, we will present our systematic study on the impact of transcript diversity, protein evolutionary divergence and tools on the quality of the genome annotations through the analysis of hundreds of plant genomes. Additionally, we will discuss the limitations of homology based functional annotations presenting other approaches based in Protein Language Models such as FANTASIA. Finally, we will present a case-study to highlight the utilities of applying machine learning such as Random Forest to the identification of gene families associated to the formation of arbuscular mycorrhizas.

Speed Talks:

Status of the Vespa velutina (Vespidae) Population in Mallorca in 2024.

Adrián Ventura[1], Cayetano Herrera[1], Gabriel Arbona[1], Mar Leza[1]
[1] Department of Biology (Zoology), University of the Balearic Islands, Palma, Balearic Islands, Spain
Presenter: Adrián Ventura (adrian.ventura@uib.cat)

The yellow-legged hornet (Vespa velutina) is an invasive predatory species and it was first detected in the Balearic Islands in 2015. The first report led to the implementation of an intensive control strategy and the species was officially eradicated in 2020 until mid-2021 when a new nest was detected and removed in the island. Genetic analysis showed two independent incursions in the island. Since then, no individuals were detected in the archipelago until last year 2024. This study aimed to assess the current status of V. velutina in Mallorca by analyzing nests detected in 2024. A total of 20 nests were located across diverse habitats, of which 18 were collected and analyzed. Variables measured included the number of individuals (males, workers, and potential queens), number of comb layers, nest dimensions, and geographic distribution. Findings reveal that V. velutina has established a breeding population in the central-western region of the island, showing ecological plasticity by nesting in both urban and natural environments. Most nests had reached the reproductive phase, with evidence of males and potential queens, indicating a population were able to expand. These results underscore the urgent need for early detection and targeted control strategies to mitigate the expected increase in nest numbers in 2025 and limit further ecological and agricultural impact. Moreover, the spatial and reproductive data from this analysis can help prioritize sampling areas for the next season, especially in regions where males were detected, thus improving management and control efforts. In 2025, monitoring efforts in Mallorca continue with numerous traps installed across the island, and any nests detected will be removed and studied as soon as possible.

Host-gut microbiota coevolution and its role in insular adaptation: A case study of the Balearic lizard Podarcis lilfordi.

Caterina Marquès Gomila*[1,2], Giacomo Tavecchia[3], Andreu Rotger[3], José Manuel Igual[3], Lodovico Sterzi[4], Joan Lluís Riera[1], Laura Baldo[1,2]

[1]Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain. [2]Institute for Research on Biodiversity (IRBio), Barcelona, Spain. [3]Animal Demography and Ecology Unit, IMEDEA, Consejo Superior de Investigaciones Científicas, Esporles, Spain. [4]Department of Biomedical and Clinical Sciences, Pediatric Clinical Research Center "Romeo and Enrica Invernizzi", Università Di Milano, 20157, Milan, Italy

*Presenter: Caterina Marquès Gomila, cmarques@ub.edu

Insular populations of terrestrial vertebrates often experience resource scarcity and seasonal fluctuations, requiring adaptations for a more efficient use of trophic resources and the ability to adjust to their availability. In this context, gut microbes are emerging as key players by modulating host metabolism and enhancing dietary flexibility. However, the specific contribution of gut microbiota to host adaptation and the evolutionary forces that shape their association remain poorly understood.

In this project, we investigate host–gut microbiota coevolution and its functional relevance in local adaptation by studying multiple populations of the endemic Balearic lizard Podarcis lilfordi. We combined lizard population genetic distances data (based on FST and single-nucleotide polymorphisms) with their gut microbial taxonomic profiles generated using full-length 16S rRNA sequences (Oxford Nanopore Technology). To characterize the microbial functional profile, we used newly generated shotgun metagenomic sequencing data.

Our results revealed a remarkably conserved core gut microbiota taxonomic profile across populations, suggesting ancestral inheritance and a strong resilience of these bacterial communities. Microbiota-based relative distances among populations closely mirrored those on host population genetics, pointing to an influence of the host phylogeographic history in shaping gut microbiota structure. Additionally, a set of bacterial genera was identified as responsible for this pattern, likely representing the "housekeeping" component of the lizard gut microbiota and emerging as important candidates for future studies aimed at better understanding host-microbe interactions.

Through the annotation of Clusters of Orthologous Groups (COG), categories, and metabolic pathways, we also provide preliminary insights into the main metabolic functions of the lizard gut microbes, and their patterns of variation across populations and in response to seasonal fluctuations. Our initial findings highlight the potential of gut microbial symbionts as key players in vertebrate insular adaptation and population persistence.

Tick-tock tune the clock: ongoing search for peracarida evolutionary timeline.

Chiara Zanoli [1,2*]
[1] University of Padua, Padua, Italy. [2] Mediterranean Institute for Advanced Studies (IMEDEA)
*Presenter: chiara.zanoli@studenti.unipd.it

Molecular clocks are essential for estimating the timing of evolutionary events, as they depend on precise calibration points to yield reliable divergence estimates. In previous studies, biogeographic events were used to calibrate molecular clocks for three Peracarida families (_Metacrangonyx_, _Pseudoniphargus_, and _Hyallela_), resulting in estimated divergence times for their most recent common ancestor (MRCA).
However, when these three lineages are combined in a single phylogeny under an uncorrelated log-normal clock and calibrated with two isopod fossils, significant discrepancies in the divergence times emerged. This raises a critical question: What is the source of this inconsistency? (1) Are the biogeographic calibrations from the previous studies flawed, or (2) is the molecular clock model applied inappropriately for this dataset?
This study aims to accurately estimate the true divergence times by identifying the most suitable molecular clock model. Specifically, we investigate two novel mixed clock models: (1) the Shrinkage-based Random Local Clock and (2) the Mixed Effects Clock. This study focuses on determining whether these models can resolve the incongruence between biogeographic and fossil-based calibrations, offering a more accurate understanding of Peracarida's evolutionary history.

Using environmental DNA metabarcoding to assess marine mammal biodiversity in the Western Mediterranean.

Chloé Fernandez[1]*; David March[1]; Carlos Barros-García[2]; Antonella Arcangeli[3]; Juan Antonio Raga[1]; Natalia Fraija-Fernández[1]
[1]Marine Zoology Unit, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain.[2] Biology Department, Avanqua-Oceanogràfic S.L., Valencia, Spain. [3] ISPRA National Institution for Environmental Research and Monitoring, Rome, Italy
* Presenter : chloe.fernandez@uv.es

Environmental DNA analysis has emerged as an effective biomonitoring technique in marine environments, demonstrating significant potential for assessing entire biological communities. This study presents data on marine mammal distribution in the Western Mediterranean gathered from more than two years of research. A total of 104 water samples, each ranging from 2 to 3 liters, were collected from various platforms, including commercial ferries, oceanographic vessels and tour boats between May 2021 and October 2023. Seventeen of these samples were taken from the Oceanogràfic aquarium, a controlled environment used for methodological validation, while the remaining samples were collected along the Cetacean Migratory Corridor, a Marine Protected Area (MPA) in the Western Mediterranean. Water was filtered using encapsulated Sterivex filters, and DNA was extracted and amplified using the previously designed marine vertebrate MarVer3 primers, targeting ~245 bp of the 16S rRNA gene. In the MPA, eDNA analysis identified resident cetacean species, including Tursiops truncatus, Delphinus delphis, Balaenoptera physalus, Grampus griseus, and unassigned Delphinidae variants. Using a phylogenetic framework, these last ones were taxonomically assigned to Stenella coeruleoalba, commonly occurring in the area, thus highlighting the challenges of differentiating closely related cetacean species. Additional sequencing data from other marine vertebrates facilitated the study of cetacean prey distribution through a trophic network exploration. In the aquarium, eDNA analysis successfully identified almost 60% of the known marine vertebrate diversity, and all marine mammal species: Delphinapterus leucas and Tursiops truncatus at species level and Phoca vitulina and Zalophus californianus at genus level. Interestingly, Stenella attenuata and Orcinus orca were also detected as false positives. These results are interpreted in light of the genetic similarity between closely delphinid species and the limitations in the completeness and accuracy of the reference database used. Study supported by Generalitat Valenciana through projects CETABIOENA (CISEJI/2022/5), IOS4DOM (CIDEGENT/2021/058), LIFE CONCEPTU MARIS (LIFE20 NAT/IT/001371).

On the Trail of Osmia Bees: Exploring Pollinator Diversity in Balearic Almond Orchards.

Gabriel Arbona[1], Adrián Ventura[1], Cayetano Herrera[1] and Mar Leza[1]
[1]Department of Biology (Zoology), University of the Balearic Islands, Palma, Balearic Islands, Spain
Presenter: Gabriel Arbona (gabriel.arbona@uib.cat)

Osmia rearing has emerged as a promising alternative for the pollination of crops such as almond, whose production is at risk due to the self-sterility of some varieties and the general decline in wild pollinator diversity and abundance. In most studies involving Osmia species, initial populations are sourced from local breeders. However, on Mallorca Island, no such breeders are available, and importing bees from other continental regions could lead to a genetic introgression in local populations. Therefore, we aimed to obtain a founder population from native wild Osmia individuals to establish an Osmia cocoons bank. To this end, we installed three types of trap-nests—commercial nests from BioDar® and handmade trap nests made from paper straws and natural reeds—in 15 almond orchards from contrasting landscape contexts. While surveying Osmia during almond bloom, we also assessed general pollinator diversity. Almond orchards were grouped into three clusters based on land-use cover. Although Osmia individuals were not observed during the flowering period, to date, a total of 30 nests were recovered, all from trap-nests made of natural reeds and from orchards belonging to different clusters. Pollinator diversity varied across clusters, but was generally higher in natural orchards, although considerable heterogeneity was observed. Although a phenological mismatch between almond bloom and Osmia nesting activity was recorded, and their abundance appeared to be low in agricultural areas, our findings confirm the presence of wild Osmia populations in these environments. This suggests that, with appropriate management and nesting resources, it is feasible to develop an Osmia cocoon bank based on wild individuals, offering a valuable native alternative for enhancing crop pollination. Nevertheless, further research is needed to identify the factors contributing to the low abundance of Osmia populations and to determine whether similar trends are occurring outside agricultural systems.

Low salinity seawater as a potential source of extremophilic halophiles.

Guillem Coll-García[1,2,3,4], Víctor Fernández-Juárez[4,5], Esteban Bustos-Caparros[1,2], Gerhard J. Herndl[3,6], Ramon Rossello Mora[2], Lasse Riemann4 & Rafael Bosch[1].

[1] Microbiology, Department of Biology, University of the Balearic Islands; Palma de Mallorca, Spain. [2] Marine Microbiology, Department of Animal and Microbial Diversity, IMEDEA (CSIC-UIB), Esporles, Illes Balears, Spain. [3] Microbial Oceanography, Department of Functional and Evolutionary Ecology, Bio-Oceanography and Marine Biology Unit, University of Vienna, Vienna, Austria. [4] Marine Biology Section, Department of Biology, University of Copenhagen, 3000 Helsingør, Denmark. [5] Hadal & Nordcee, Department of Biology, University of Southern Denmark, Odense, Denmark. [6] Dept. of Marine Microbiology and Biogeochemistry, Royal Netherlands Institute for Sea Research, Texel, The Netherlands.

Halophilic microorganisms thrive at high salinities, with some exhibiting optimal growth at concentrations close to salt saturation (~35%). It is also well known that above 20% salinity, the composition of microbial communities becomes convergent worldwide, with the bacterium Salinibacter ruber and the archaeon Haloquadratum walsbyi being the main representatives of the community (1,2). This convergence, along with genetic similarities among isolates from distant locations, may indicate that these systems are interconnected, allowing genetic fluxes among them. Thus, we propose that seawater could act as a reservoir of viable halophiles. To address this possibility, we incubated seawater from the Øresund Channel (Denmark), which has one of the lowest salinities (~1.4%) and experiences summer precipitation exceeding 70 mm/month, clearly limiting the development of halophilic habitats on its coast.

Two sets of 500 ml microcosms were prepared, with salinities adjusted using either NaCl or a mixture of salts mimicking the composition of a saltern, with salinity ranging between 5, 10, 15, 20, 25 to 30% in triplicates for each salinity. Microcosms were then incubated under a day-night cycle at room temperature (~21 °C) for 30 days to allow halophiles to proliferate.

Samples were taken to determine community composition via 16S rRNA amplicon sequencing, cell abundance, and recovery of cultivable microorganisms. Amplicon sequencing revealed clear shifts in community composition along the gradient with several of the identified genera being present in the HaloDom (3) database of halophiles. Their relative abundance increased after incubation, with moderate halophiles such as Marinobacter, Halomonas, and Idiomarina becoming dominant community members. This increase led to a marked reduction in α-diversity around 15% salinity, which was recovered above 20%. Cell abundances also increased significantly post-incubation, from 6.7 × 105 to 5.4 × 106 cells/ml on average, indicating the presence of viable halophiles across the salinity gradient. The recovery of nearly 400 isolates by cultivation, grouped into 140 clusters by MALDI-TOF for future taxonomic identification, further supports the finding of viable halophiles.

In summary, the brackish seawaters of the Øresund Channel harbour a diverse pool of viable halophilic taxa that proliferate along the salinity gradient. These results provide strong evidence that seawater can serve as a reservoir of halophiles. Further experiments are being conducted to elucidate its ecological significance.

Genomic Insights into Adaptation to Arid Environments in the Sun Spider Gluvia dorsalis.

Inés Galán-Luque[1,2]*, Marc Domènech[1,2], Javier Arañó-Ansola[1,2], Marta Olivé-Muñiz[1,2], Silvia García-Juan[1,2], Vadim Pisarenco[1,2], Julio Rozas[1,2], Mattia Giacomelli[1,2], Jesús Lozano-Fernández[1,2]
[1] Departament de Genètica, Microbiologia i Estadística, Universitat de Barcelona. [2] Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona
* inesgalanluque@gmail.com

Understanding the genomic basis of adaptation to extreme environments remains a major challenge in evolutionary biology and biodiversity research. Gluvia dorsalis, an endemic sun spider (Solifugae) of the Iberian Peninsula, inhabits arid ecosystems, representing an exceptional model to investigate the genetic innovations underlying adaptations to harsh environments. Despite its ecological importance, genomic resources for this species were absent until very recently. Here, we present the genome annotation of G. dorsalis, based on a high-quality chromosome-level assembly, which spans 787 Mb. After manual curation of the annotation results, a total of 15,217 protein-coding genes were identified, providing a robust foundation for downstream functional and evolutionary analyses.

In addition to its ecological value, the genome of G. dorsalis provides crucial insights into the evolutionary history of Chelicerata, one of the oldest and most morphologically diverse arthropod lineages. The phylogenetic relationships among arachnid orders remain among the most challenging to resolve due to ancient radiations, convergent evolution, and complex genomic events such as multiple independent whole-genome duplications. Solifuges, in particular, have historically been underrepresented in genomic studies, limiting our understanding of their placement within Arachnida. By providing a chromosome-level assembly and robust gene annotation for G. dorsalis, this study contributes significantly to filling this gap, allowing a more comprehensive reconstruction of chelicerate evolution and offering new opportunities to study genome evolution in arachnids adapted to extreme environments.

The genome of the smalles predator in the oceans.

Jordi Nonell Remedios [1]
[1] Institute of Evolutionary Biology (IBE), Barcelona, Spain
*Presenter Jordi Nonell Remedios: jordi.nonell@ibe.upf-csic.es

Minorisa minuta (del Campo, 2013) is a bacterivorous protist, almost abundant in many coastal ecosystems across the planet. Phylogenetically, up until recently, M. minuta was the sole and founder member of the genus Minorisa, placed inside the Chlorarachniophyceae class, mainly integrated by mixotrophic organisms that acquired the ability to feed themselves by photosynthesis after an event of secondary endosymbiosis with a green algae. Oddly enough, M. minuta is the only member of the Chlorarachniophytes that does not harbour chloroplasts, thus it is thought that it should be placed at the basal origins of the group, which makes it a really intresting species in order to study the acquisition of plasts in eukaryotes.
The main problem with Minorisa minuta is that it is a hard organism to reasearch on, since we quite still don’t grasp how to culture it in a laboratory, which is something it shares with many other marine protists. In order to bypass this hardship, protistology has adopted over the years technologies from other fields that allow the study of an organism with few to no cells as samples, such as single cell genomics or metagenomics.
These two research fields have been used combined in this project with the intention of assemblying a de novo genome powerful enough to represent the genomic diversity of Minorisa minuta. In turn, in this piece of work, there has been the effort to use this genome as the input of a pipeline that can compare up to 300 sequences of underresearched species in order the infer their position in the tree of life.

Microplastics Under Review: How Research Has Evolved, and What Comes Next.

Josef Thomas Greenhalgh[1]
[1] University of Barcelona, Barcelona, Spain

This speed talk presents a structured review of marine microplastic research, tracing its evolution over the past 40 years and analysing how scientific focus has shifted in response to public concern, technological advances, and institutional priorities. While no new data is presented, the talk synthesizes key trends in the literature, using quantitative publication data to map how marine microplastics have progressed from a fringe topic to a mainstream environmental concern with global relevance.

The first part of the talk briefly outlines the historical arc of the field: from early visual surveys of surface plastic in the 1980s, to the emergence of trophic transfer studies, and more recently to findings of microplastics in human tissues. A bibliometric analysis is used to highlight research surges—such as a 10-fold increase in annual publications between 2013 and 2019—and identify which subtopics (e.g. nanoplastics, deep-sea sedimentation, human health risks) have recently expanded most rapidly.

The second part explores how this evolving body of research has shaped, and sometimes distorted, public understanding. It asks whether the current scientific consensus aligns with media narratives, and whether human health risks from microplastic exposure are substantiated by evidence or still speculative. It also highlights areas where scientific interest may be lagging despite high ecological or societal relevance.

Finally, the talk proposes how these literature trends might justify new research projects. Gaps are identified in nanoplastics detection, how microplastics act as vectors for toxins in marine species, and chronic low-dose health exposure—each representing viable starting points for future work. Overall, this review aims to help non-specialist scientists situate themselves within the dynamic field of marine microplastics.

This speed talk will take attendees on a visually engaging journey through the milestones of marine microplastic research, outlining how our understanding of their sources, distribution, and impacts has matured and where the science is heading next.

The presentation begins by outlining the historical timeline of microplastic research, from early observations in the 1970s–80s to the development of major datasets in the North Pacific and Atlantic gyres during the 2000s. Landmark discoveries, like the identification of the Pacific Garbage Patch, served to raise public awareness about plastic pollution. More recent findings, such as the presence of microplastics in plant and animal tissues, everyday supermarket products, and even the human brain, reveal the far-reaching impacts of plastic waste. These discoveries highlight that plastic pollution is not just an eyesore but a potential threat to human health.

The presentation then transitions to the current focus of microplastic research. Key concerns include the role of microplastics as potential vectors for toxins and the critical question of whether their impact has been overexaggerated by sensationalist media or downplayed in scientific discourse. The presentation explores where the scientific consensus stands today, what uncertainties remain, and how these factors contrast with public perceptions.

In summary, microplastic pollution has become a significant topic over the past two decades, driven by rapid advancements in research. However, the combination of sensationalized headlines and misinformation may have left the public struggling with outdated or inaccurate information.

The goal of this talk is to provide a concise, well-organized overview of the marine microplastic research landscape—what we've learned, what's been misunderstood, and what challenges lie ahead. Attendees will leave with a clearer perspective on this environmental issue.

Session 2:

Invited Speaker: Pere Bover Arbós

Ancient DNA as a time machine for biodiversity research or lost and found: Rediscovering biodiversity with ancient DNA.

Pere Bover Arbós[1]
[1] University Institute of Research into Environmental Sciences of Aragon, University of Zaragosa, Zaragosa, Spain

In the face of the current accelerating biodiversity loss and environmental change, understanding the long-term dynamics of species and ecosystems has never been more crucial. In this sense, most biodiversity analyses and species managements plans are restricted to the parameters that can be observed and measured from living individuals, populations and ecosystems, commonly neglecting the past history of them. Ancient DNA (aDNA) analysis, the study of genomic data from fossil and sub-fossil samples, has emerged as a powerful tool to improve contemporary biodiversity studies and conservation strategies. By introducing temporal scales in such studies, ancient DNA can enrich our understanding of biodiversity and allows us to increase the number of perspectives to tackle modern conservation challenges. Additionally, data obtained from ancient genetic material are reshaping the way we assess, manage, and preserve species today and can also uncover evolutionary responses to past climate shifts and human impacts, offering valuable lessons for anticipating species' resilience or vulnerability in the Anthropocene.

In this talk we will shortly present three studies in which the Paleogenomic Laboratory of IUCA (Universidad de Zaragoza) has been involved, including the study of pre-European populations of Australian dingoes, the analysis of mitochondrial genomes of an unidentified extinct bird from Graciosa Island (Azores Archipelago, Atlantic Ocean), and the genomic characterization of the first introduced domestic goats in Mallorca (Balearic Islands, Mediterranean Sea). With these examples, we will highlight how aDNA reveals hidden population structures, presence or absence of past gene flow, and historical baselines of genetic diversity that are often obscured in modern datasets. These findings provide a critical context for interpreting current genetic patterns, detecting cryptic extinctions, addressing the practical implications of integrating ancient genetic data into species management policies and emphasizing the importance of interdisciplinary collaboration to increase the full potential of ancient DNA research.

Invited Speaker: Rosa Fernández

The genomic basis of animal terrestrialization.

Rosa Fernandez[1]
[1]Institute of Evolutionary Biology (IBE, CSIC-UPF), Barcelona, Spain

The transition of animals from aquatic to terrestrial environments—terrestrialization—represents one of the most consequential shifts in evolutionary history, having occurred independently across multiple lineages. While the ecological and morphological aspects of this transition have been widely studied, the underlying genomic mechanisms remain poorly understood. To investigate whether a conserved genetic program supports terrestrial adaptation, we combined large-scale comparative genomics, machine learning, and integrative multi-omics approaches across a broad sampling of aquatic and terrestrial invertebrates. Using experimentally induced stress responses that emulate key environmental challenges of terrestrial life, we examined gene expression and protein-level changes across diverse taxa. Our analyses provide new insights into how different lineages have navigated similar selective pressures through distinct molecular strategies. Rather than identifying a universal genomic toolkit for terrestrialization, our findings suggest a more nuanced picture of evolutionary innovation and convergence. This study sheds light on the complex and lineage-specific nature of terrestrial adaptation in animals and highlights the repurposing of ancient genetic elements in shaping modern biodiversity.

Invited Speaker: Josepa Gené Díaz

Unveiling species-by-species the culturable ascomycete diversity: from terrestrial substrates to aquatic sediments.

Josepa Gené[1]
[1]Pere Virgili Health Research Institute (IISPV) and University Research Institute for Sustainability, Climate Change and Energy Transition, Rovira i Virgili University, Reus, Spain

Fungi are a diverse group of eukaryotic organisms that remain highly enigmatic. While their role in decomposing organic matter and supporting ecosystems is well known, their full diversity is still far from understood. Found in nearly all environments—including terrestrial, aquatic, marine, and even extreme habitats—fungi are estimated to number around 3 million species worldwide. However, only about 150,000 have been formally described, and less than 1% have been cultured and preserved in fungal collections. This suggests that many fungal species remain undescribed, awaiting discovery and, if possible, being obtained in culture to explore their biological features.

To enhance our understanding of fungal diversity and address gaps in their taxonomy, we have spent more than three decades investigating filamentous ascomycetes from a variety of substrates —soil, dung, plant debris, human clinical specimens, etc.— originating from diverse regions around the world. Initially, identification was based on macro- and microscopic analyses of the fungal structures growing either on the natural substrate or in vitro. However, the use of molecular techniques for fungal identification revealed that the morphology alone was insufficient for their classification since species morphologically very similar could belong to distantly related fungal groups. This led to the reevaluation of known species, the redefinition of their classification, and even the definition of new lineages within the Fungal Kingdom, enabling a more precise analysis of fungal diversity.

Given that our country is considered one of the most important European reservoirs of biodiversity, we assumed that its fungal diversity would also be significant. In this context, over the past decade, supported by several national projects, we have focused on exploring the diversity and phylogeny of culturable filamentous ascomycetes from a range of terrestrial substrates—especially plant litter from natural habitats—as well as aquatic sediments from rivers and streams across the Iberian Peninsula. Between 2009 and 2014, surveys in natural and national parks led to the identification of over 500 species, including 47 new species, nine new genera, and seven new families of dematiaceous ascomycetes. Notably, Ordesa y Monte Perdido National Park showed the highest species diversity. Surveys conducted from 2018 to 2024 for investigating ascomycetes in fluvial sediments revealed 480 species across 115 genera, with 49 new species, seven new genera, and one new family. Interestingly, distinct fungal communities were found in different rivers and streams, likely reflecting variations in riparian environmental quality. Marine sediment surveys conducted between 2022 and 2024 revealed a marked reduction in diversity. Nevertheless, we recovered 190 species from depths of 6 to 27 m, including 20 novel ascomycetes and two new genera. Surprisingly, the greatest diversity and the most new species were found at depths of 20–27 m. Some of these marine strains are currently being investigated for their potential to produce bioactive compounds.

These findings underscore that our country is a reservoir of hidden fungal diversity, emphasising the need for continued research, particularly species-by-species identification through morphological and phylogenetic analyses, to uncover this diversity, enhance understanding of their evolution and ecological roles, and explore their potential for a wide range of applications.

Speed Talks

The genome sequence of Tethysbaena scabra (Pretus, 1991), the first known in the peracarid crustacean order Thermosbaenacea.

Joan Pons[1,†], Karen D. Schöninger-Almaraz[2,†,*], Laura Triginer-Llabrés[2,†], Carlos Juan[1,3], Damià Jaume[1], José A. Jurado-Rivera[3]
[1] Mediterranean Institute for Advanced Studies (IMEDEA, UIB-CSIC), Esporles, Balearic Islands, Spain. [2] Balearic Biodiversity Centre, University of the Balearic Islands (UIB), Palma, Balearic Islands, Spain. [3] University of the Balearic Islands (UIB), Palma, Balearic Islands, Spain
*Presenter: karen-daiana.schoninger@uib.cat

Tethysbaena scabra (Pretus, 1991) is a thermosbaenacean, a relict group of peracarid crustaceans characterized by the display in gravid females of a dorsal brood pouch formed by a posterior extension of the carapace. This species measures 2–3 mm in length, is eyeless and depigmented, inhabiting subterranean waters of raised salinity in caves and wells located near the marine coast. It is endemic to the Mediterranean islands of Mallorca and Menorca. There is no available information on genome size and chromosome number in thermosbaenaceans, therefore, here we present a chromosome-level genome assembly for T. scabra from Mallorca, which represents the first reference genome for the order Thermosbaenacea. To do this, a pool of 20 specimens were used for sequencing on Pacific Biosciences SEQUEL II (HiFi) instrument (Accession number: SAMEA113414145 qmTetScab1) and Hi-C data was generated from another pool of 20 individuals from the same collection site (Accession number: SAMEA118091338) using the library preparation Omni-C DNA and sequenced on the Illumina NovaSeq 6000 S4 instrument. The genome size was estimated using GenomeScope2 (Vurture et al., 2017) and diploidy was confirmed with Smudgeplot (Ranallo-Benavidez et al., 2020). Assembly was conducted using hifiasm (Cheng et al., 2021). Haplotypic duplications were withdrawn with purge_dups (Guan et al., 2020) and contig sequences from contaminant species were removed from assembly using Foreign Contamination Screen (Astashyn et al., 2022) and Whokaryote (Pronk et al., 2022). The scaffolding was performed with Hi-C data (Rao et al., 2014) using YaHS (Zhou et al., 2022) and the assembly obtained was checked for contamination with two rounds of Blobtools to ensure complete decontamination. Curation of contact map was performed using Pretext (Harry, 2022). The genome was analysed within the BlobToolKit environment and BUSCO scores were generated (Challis et al., 2020). To assess the assembly metrics, the k-mer completeness and QV consensus quality values were calculated using Meryl and Merqury (Rhie et al., 2020). To obtain the mitochondrial genome, sequence contigs were compared with a relaxed BLASTn algorithm against a database built with mitogenome sequences of several peracarid species. The sequence of 30 kb with a positive match was circularized in MitoMaker (Schomaker-Bastos and Prosdocimi, 2018) and annotated in Mitos2 (Donath et al., 2019). Repetitive annotation was performed using RepeatMasker and RepeatOBserver (Elphinstone, C., Elphinstone, R., Todesco, M., & Rieseberg, L., 2023). An assembly spanning 1.18 Gb across 23 scaffolds was obtained, with a scaffold N50 of 74.6 Mb. The final assembly sequence, confirmed by Hi-C data, was assigned to 17 scaffolds at the chromosome level, with a value of BUSCO (Manni et al., 2021; Simão FA et al., 2015) completeness obtained is 94.7%, using the arthropods_odb10 reference set.

Antimicrobial resistance of the endemic Balearic lizard Podarcis lilfordi and implications for population resilience.

Katherin Otalora[1,2], Jessica Gomez-Garrido[3,4], Laura Baldo[1,5]*

[1] Department of Evolutionary Biology, Ecology and Environmental Sciences, Biology Faculty, University of Barcelona (UB), Barcelona, Spain. [2] Fundación FUNMAJO, EBA, RAIEC, Biodiversity Branch, Cucaita, Boyacá, Colombia. [3] Centro Nacional de Análisis Genómico (CNAG), Baldiri Reixac 4, 08028 Barcelona, Spain. [4] Universitat de Barcelona (UB), Barcelona, Spain. [5] Institute for Research on Biodiversity (IRBio), University of Barcelona (UB), Barcelona, Spain.

* Presenter: baldo.laura@ub.edu

Reptiles are known for their remarkable resistance to infections, making them a critical model for studying the molecular basis of innate immunity. Key components of their innate immune response are the antimicrobial peptides (AMPs) — small, rapidly evolving molecules with a broad spectrum of antimicrobial activity that serve as the first line of defense against pathogens, while also acting as critical modulators of the host-microbe interactions.

The Balearic lizard Podarcis lilfordi offers a particularly interesting system to address the evolution of antimicrobial peptides and their role in population resilience. Due to the insularity of this species and the long-term monitoring of several populations, this endemic species is a growing natural model for integrative studies on host-gut microbiota and pathogen resistance in a context of a rapidly changing environment.

Here we present the first and comprehensive identification of major classes of AMPs (defensins and cathelicidins) in the P. lilfordi genome by means of extensive genomic screening and comparative analysis with closely related lizards. The identification of key players in lizard innate immunity sets now the basis for future research into the ecoimmunology aspects of these endangered populations and their capacity to respond to rising infection threats associated with increasing human impacts on these islands.

Using Nanopore's Adaptive Sampling to enrich metabarcoding reads to analyse diet composition in Parapenaeus longirostris.

Carolina de Oliveira Magalhães[1,2], Laura Triginer-Llabrés[1,2], Karen D. Schöninger-Almaraz[1,2], Sergio Ramirez-Amaro[2,3], Imene Benali[1,2], Ramon Gallego[4], Lluís Moragues-Solanas[1,2],*,#.

[1] Balearic Biodiversity Centre (CBB), Department of Biology, University of the Balearic Islands, Palma, Spain. [2] Department of Biology, University of the Balearic Islands, Palma, Spain. [3] Spanish Institute of Oceanography, Balearic Oceanographic Centre (IEO-CSIC), Palma, Spain. [4] Department of Biology, Faculty of Science, Autonomous University of Madrid, Madrid, Spain.

* Corresponding author – lluis.moragues@uib.cat

Presenting author - lluis.moragues@uib.cat

Accurate characterization of diet composition is critical for trophic-web modelling and ecosystem-based management, particularly for ecologically and commercially valuable benthic species such as the deep-water white shrimp (Parapenaeus longirostris). Conventional approaches, direct observation or morphological identification of stomach contents, are complex tasks since prey tissues are digested rapidly, making correct identification difficult. High-throughput metabarcoding can overcome these limitations, yet its efficiency is often hampered by the overwhelming co-sequencing of host DNA, which reduces recovery of informative dietary reads. Nanopore Adaptive Sampling (NAS), Oxford Nanopore's real-time, on-device read-ejection system, addresses this issue by live base-calling DNA strands as they enter the pore, comparing them to a user-defined reference, and reversing pore voltage to eject sequences matching unwanted (host) DNA. In this study, we tested whether NAS could effectively deplete host DNA and enrich prey DNA in P. longirostris gut content libraries. To do this, we used three gut samples of P. longirostris, which were collected during the oceanographic survey MEDITS in 2024. DNA was extracted from three gut samples (biological replicates) and was PCR-amplified using universal cytochrome c oxidase subunit I (COI) primers and sequenced on PromethION flow cells in separate runs with and without NAS. Adaptive sampling was configured to reject P. longirostris reference sequences. Between 6 and 12 Gb per sample were processed, including filtering and taxonomic assignment to the species level. When applying NAS, 30.7±0.8% (mean ± SEM, n = 3) of total sequenced bases were assigned to non-Parapenaeus sequences (presumptive dietary material), compared to 19.6±0.7% in the non-NAS dataset. This corresponds to a 11.1% increase in non-host sequence yield, demonstrating that NAS significantly enhances ($p < 0.005$) recovery of dietary information from gut content sequencing.

These results demonstrate that coupling Nanopore Adaptive Sampling with metabarcoding significantly enhances dietary signal recovery from host-dominated samples, offering a scalable and cost-effective strategy for researchers investigating trophic interactions, gut content analysis, or biodiversity assessment across a range of ecological and taxonomic contexts.

Inhibition of sexual reproduction in rotifer populations: A transgenerational effect in relation to environmental predictability.

Noemi Colinas[1]*, María J. Carmona[1], Manuel Serra[1] and Eduardo M. García-Roger
[1]Evolutionary Ecology Lab, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain.
*Presenter: noemi.colinas@uv.es

Understanding how organisms adapt to time-varying environments is a central question in evolutionary ecology. A way to cope with environmental fluctuations where predictable conditions affect several generations of individuals is through nongenetic transgenerational effects. These effects allow the phenotype of ancestors to affect the phenotype of their descendants, matching it with the environmental conditions expected in future generations. Facultatively sexual rotifers inhabiting water bodies that cover a wide gradient of environmental predictability in Eastern Spain are a good study model for this topic. In their life cycle, sex is linked to diapausing-egg production that enables survival between growing seasons. In several rotifer species, sexual reproduction is inhibited in several generations after diapausing-egg hatching. According to theorical predictions, organisms may cope with predictable environmental fluctuations that affect several generations through these nongenetic transgenerational inhibitory effects on sexual reproduction. By contrast, these effects may be harmful in unpredictable fluctuations if diapausing eggs are not produced before the end of the growing season. This research hypothesizes that in ponds where the growing season length is predictable, rotifer clones would reproduce asexually for more generations, allowing a fuller exploitation of the growing season and maximizing the production of diapausing eggs at the end of the season. This prediction was tested by estimating the proportion of sexual females (i.e., the proportion of sexual reproduction) produced by several clones of the rotifer Brachionus plicatilis inhabiting ponds that vary in the predictability of the length of their growing season. Specifically, the sexual response of several clones from eight ponds was studied across ten generations by means of self-induction sex bioassays. A total of 1,860 bioassays were conducted (8 populations × 6–8 clones/population × 3 lineages/clone × 10 generations). Rotifer clones from the more predictable ponds showed a lower proportion of sexual reproduction from the earliest generations, with an increase in the later generations. In contrast, clones from the more unpredictable ponds displayed an early onset of sexual reproduction, responding to population density immediately after hatching from the diapausing egg. These results provide the first empirical evidence of the adaptive value of the transgenerational effect in relation to the degree of growing-season length predictability experienced by Brachionus plicatilis populations.

Isolation and culture of symbiotic bacteria from Mediterranean corals.

Rocio Mozo[1]*, Andrea Illa-Oviedo[1,2], Javier del Campo[1]
[1] Institute of Evolutionary Biology (CSIC–Pompeu Fabra University), Barcelona, Spain. [2] Institute of Marine Sciences (CSIC), Barcelona, Spain
*Presenter: rocio.mozo@ibe.upf-csic.es

Corals harbor a diverse bacterial community that facilitates adaptation and sustains their health. In coral holobiont research, culture-independent approaches transformed the previously existing paradigm. Molecular techniques such as metabarcoding unveiled a great diversity of previously unnoticed bacterial symbionts. Coral microbiome characterization has been based on these techniques during the last decade, but relying solely on them does not allow a detailed understanding of coral holobiont complex dynamics. Returning to traditional microbiological techniques and in-vitro experimentation can provide innovative insights into symbiont roles, their physiology and interactions within the holobiont. Under this premise, this project aims to isolate and culture bacteria from 4 Mediterranean corals (Cladocora caespitosa, Paramuricea clavata, Eunicella sp., Leptogorgia sarmentosa). The retrieval of 91 pure bacterial isolates and their initial classification based on the 16S rRNA gene reveals a great diversity of symbionts amenable to culture. Several isolates represent novel species from relevant genera, such as Vibrio, reinforcing the benefits of culture-based studies. All cultures were stored in a cryobank to easily access strains for future projects. The long-term availability of cultured coral-associated bacteria will allow the generation of genomes or their use in experimental ecology studies, among other uses.

Unleashing The Secrets Of Iberian Snakes: Exploring Their Venom Evolution Through Multi-Omics.

Sergi Tulloch Jiménez[1]*, Maria Estarellas[1], Bernat Burriel[2], Gabriel Mochales[3], Daniel Fernández-Guiberteau[4], Laura Blasón[4], Andrea Jhulyana López-Caro[4], Davinia Pla[5], Tyler Alioto[6,7], Juan José Calvete[5], Salvador Carranza[1]

[1]Institute of Evolutionary Biology (CSIC–Pompeu Fabra University), Barcelona, Spain. [2] Natural Sciences Museum of Barcelona, Barcelona, Spain. [3] New York University (NYU), Abu Dhabi, United Arab Emirates. [4] Calafell Research and Environmental Education Centre (CREAC–GRENP–Calafell City Council), Spain. [5] Institute of Biomedicine of Valencia (CSIC), Valencia, Spain. [6] National Center for Genomic Analysis (CNAG), Barcelona, Spain. [7]University of Barcelona (UB), Barcelona, Spain.

*Presenter: sergi.tulloch@ibe.upf-csic.es

Venom is a remarkable evolutionary innovation that has independently evolved many times across the animal kingdom, serving various purposes such as hunting and self-defence. Due to their diverse evolutionary histories and resulting variability, animal venoms offer fascinating models for studying key biological processes, including gene duplication, convergent evolution, genotype-phenotype mapping, and tissue development. Additionally, the bioactivity of many toxins makes them promising leads for novel human therapeutics. In snakes, venom is produced by specialized exocrine glands and is highly species-specific, making it essential to understand their systematics and phylogeny to advance toxicology and improve snakebite treatment.

Although snake venom gene evolution has been studied extensively for decades, earlier work often lacked access to complete genomes and broad tissue gene expression data—leading to contested conclusions, such as the legitimacy of the Toxicofera clade and a single origin of venom in reptiles. Now, the use of high-quality genomes from venomous snakes, integrated with transcriptomic and proteomic data, enables the generation of a comprehensive catalogue of venom-gland-specific toxin genes -known as “venom-ome-specific toxins”- which show venom-gland-specific expression and likely encode the core venom effector proteins.

In this presentation, I will introduce my PhD research project aimed at generating and comparing high-quality genomic, transcriptomic, and proteomic data for all snake genera present in the Iberian Peninsula, with a particular focus on all venomous snake species native to the region. The ultimate goal is to create a comprehensive catalogue of “venom-ome-specific toxins,” which will serve as a valuable resource for understanding the evolution of snake venom arsenals. In parallel, the project will use whole-genome sequencing data to carry out an in-depth analysis of population dynamics, as well as intra- and interspecific phylogenies within each studied genus. These analyses are expected to resolve key, and sometimes conflicting, phylogenetic hypotheses, while providing novel insights into the speciation, hybridization, demography, and evolutionary history of Iberian snakes.

Specifind: Automating Species' Occurrence Discovery in Scientific Literature through NLP.

Golomb Durán T.[1], Díaz A.[1], Barroso M.[1], Cancellario T.[1]
[1]Balearic Biodiversity Centre (CBB), Department of Biology, University of the Balearic Islands, Palma, Spain.

A vast amount of valuable information on species' occurrences is embedded within the unstructured and continuously expanding body of ecological literature written in natural language. This dispersed knowledge, if effectively extracted, can significantly enhance our understanding of species distribution and ecology, ultimately enabling more targeted and informed conservation efforts. We introduce Specifind, a Python package designed to facilitate the extraction of species occurrence data by identifying scientific species names and geographic locations, and uncovering relationships between them. At the heart of Specifind is a newly developed and expertly annotated dataset comprising over one thousand open-access abstracts drawn from five key domains: biogeography, botany, entomology, mycology, and zoology. The tool leverages a suite of natural language processing (NLP) components, including Sentence and Clause Segmentation, Named Entity Recognition (NER), Relation Extraction (RE), Coreference Resolution, and a specialized Optical Character Recognition (OCR) system tailored for scientific papers. These components, implemented using SpaCy's NLP framework with transformer-based architectures and contextual embeddings, combining our custom-trained models with other state-of-the-art (SOTA) models, enable accurate identification of species and locations, as well as their contextual linking—even when referenced across sentence boundaries. Specifind serves as a valuable resource for bridging the distribution knowledge gap, reducing the high costs associated with manual bibliographic tasks, and thereby advancing biodiversity research, informing conservation strategies, and deepening our understanding of species distribution and ecological analyses.

Approaching T2T genome assembly at scale for the Earth Biogenome Project.

Tyler Alioto[1,2]
[1] National Center for Genomic Analysis (CNAG), Barcelona, Spain. [2] University of Barcelona (UB), Barcelona, Spain.
*Presenter: tyler.alioto@cnag.eu

The CNAG Genome Assembly and Annotation Team contributes to several projects under the Earth BioGenome Project including the European Reference Genome Atlas (ERGA) and the Catalan Initiative for the Earth BioGenome Project (CBP). Using long read sequencing technologies (Oxford Nanopore Technologies and/or Pacific Biosciences) combined with proximity ligation data (Hi-C), our automated genome assembly workflow is now routinely generating phased diploid (or haploid, tetraploid) assemblies at chromosome level with few scaffold gaps. For many clades, we can assemble the majority of chromosomes from telomere-to-telomere with zero gaps with only minimal manual curation required. We are finding that ONT has "closed the gap" on PacBio's perceived lead, producing more contiguous assemblies at nearly the same consensus quality. In cases with limited sample availability, PacBio still holds an advantage over ONT. We are currently re-formulating our sequencing strategies to optimize results, reduce costs, scale up, and free up time to focus our sights on remaining assembly challenges such as complex centromeres, rDNA clusters and metagenomic samples.

Catalan Initiative for the Earth Biogenome Project: Building bridges in biodiversity genomics

The Catalan Initiative for the Earth BioGenome Project: Building Bridges in Biodiversity Genomics.

Javier del Campo[1], Marta Riutort[2]
[1] Institute of Evolutionary Biology (IBE, CSIC-UPF), [2]University of Barcelona, Barcelona, Spain.

The Catalan Initiative for the Earth BioGenome Project (CBP) is a collaborative platform that brings together a broad community of expertise to advance biodiversity genomics across the Catalan-speaking territories. Launched by the Societat Catalana de Biologia (SCB) in partnership with the Institució Catalana d'Història Natural (ICHN), both part of the Institut d'Estudis Catalans (IEC), the initiative aims to bridge traditional biodiversity knowledge with cutting-edge genomic science.

The CBP unites more than 20 institutions, including research centres, museums, zoos, botanical gardens, universities, and scientific societies, alongside advanced infrastructures for genome sequencing and computational biology. Together, these partners form a robust network dedicated to documenting and understanding the genetic diversity of regional eukaryotic species.

Affiliated with the global Earth BioGenome Project (EBP) and the European Reference Genome Atlas (ERGA), the CBP contributes to the ambitious goal of sequencing the genomes of all eukaryotic life on Earth. It collaborates closely with national and regional ERGA nodes, particularly ERGA-Spain, ERGA-France, and ERGA-Andorra. By fostering connections across disciplines, sectors, and borders, the CBP exemplifies how regional initiatives can play a central role in global biodiversity efforts, laying the groundwork for future discoveries and conservation strategies.

Session 3:

Invited Speaker: Tommaso Cancellario

Balearica: A new platform for balearic biodiversity data integration and research

Cancellario T.[1]
[1]Balearic Centre for Biodiversity, University of the Balearic Islands, Palma de Mallorca, Spain.

In a world of rapid environmental change, expanding our understanding of biodiversity and strengthening conservation efforts is crucial. While biodiversity conservation is a global priority, protecting fragile ecosystems, especially those found on small islands, requires urgent attention. These ecosystems often host unique endemic species with specialized ecological functions, high levels of genetic diversity, and distinct adaptations. However, they are also highly vulnerable to threats such as habitat loss, invasive species, and the impacts of climate change. To tackle these challenges and promote biodiversity research in the Balearic Archipelago, the Centre Balear de Biodiversitat has developed Balearica, a cutting-edge and publicly accessible biodiversity platform. Balearica is a comprehensive system designed to collect, manage, analyze, and share biodiversity data. It operates by integrating diverse data sources, including field observations, museum collections, genetic information, and species distribution records. These datasets are gathered from scientific studies, public databases, and grey literature, creating a robust and comprehensive repository of biodiversity knowledge. By bringing together these varied resources, Balearica offers a powerful tool for researchers, conservationists, policymakers, and the public. It aids in informed decision-making, enhances ecological studies, and facilitate conservation strategies, all geared towards preserving the Balearic biodiversity. The platform is characterized by an user-friendly interface fosters collaboration, knowledge exchange, and broad participation in conservation efforts, making it a vital resource for anyone invested in the region’s natural heritage.

Invited Speaker: Ramon Massana

Exploring the hidden diversity of the smallest marine protists.

Ramon Massana[1]
Institute of Marine Sciences (ICM), Spanish National Research Council (CSIC), Barcelona, Spain.

Small protists (up to 3 μm in size) are integral members of marine ecosystems in terms of cell abundance and biomass, and play crucial roles in food webs and biogeochemical cycles. Their diversity can hardly be investigated by standard microscopy, and instead a variety of molecular tools have been applied, unveiling a large phylogenetic diversity and the presence of novel lineages within the assemblage. In this talk I will present a general overview of the taxonomic groups forming these tiny eukaryotic assemblages, with a particular focus on the extent, diversity and functional roles of the unveiled novelty. The combination of large marine datasets and new sequencing capabilities allows a detailed study of their temporal and spatial dynamics in the ocean.

Invited Speaker: Naiara Rodriguez-Ezpeleta

Shedding light on ocean DNA: Exploring marine biodiversity across ecosystems and biological dimensions for enhanced conservation.

Naiara Rodriguez-Ezpeleta[1]
[1] AZTI – Marine and Food Research Center, Marine Research Division, Sukarrieta, Bizkaia, Spain.

Understanding and conserving marine biodiversity requires exploring its complexity across multiple dimensions, from genes to ecosystems, from microscopic plankton to large marine mammals, and from coastal waters to the deep ocean. However, the limitations of traditional monitoring methods, especially in remote, deep, or highly diverse environments, often hinder our ability to detect and track this biodiversity effectively. In this talk, I will use case studies spanning different oceanic regions, habitats, and taxonomic groups to illustrate how DNA-based methods are transforming our ability to inform more effective, evidence-based conservation strategies in the face of accelerating environmental change. By combining genetic tools with ecological knowledge, we can better understand how marine biodiversity is structured and connected—and make more informed decisions to protect it.

Invited Speaker: Maite Vázquez Luis

Challenges in the conservation of marine biodiversity: the case of Pinna nobilis.

Maite Vázquez-Luis[1]
[1] Spanish Institute of Oceanography – Balearic Oceanographic Centre (IEO, CSIC), Palma de Mallorca, Spain.
*maite.vazquez@ieo.csic.es

Abstract: Marine biodiversity faces a series of threats producing a variety of impacts, among which species extinction is one of the most dramatic scenarios. In this situation is the largest and endemic bivalve to the Mediterranean Sea, the critically endangered species Pinna nobilis. At the present times, the species faces an unprecedented challenge after the Mass Mortality Event (MME) that has affected its populations since autumn 2016. Since that moment, different actions have been performed in our group, in collaboration with researchers from national and international institutions, together with volunteers and managers, aiming to improve the knowledge and conservation status of Pinna nobilis.

Monitoring of survivors in open sea in the Spanish Mediterranean coast indicate that, throughout a 8-year period after the start of the MME (2017-2024), the geographical distribution of the survivors is currently concentrated in the Autonomous Regions of Catalonia, the Balearic Islands and, to a lesser extent, the Valencian Community, with focal points of density of specimens in Cap de Creus (Catalonia) and Menorca (Balearic Islands). During the exhaustive monitoring of individuals of Pinna nobilis, the active participation of citizen science became decisive, locating almost half of the survivors. Most individuals were found in marine protected areas, mainly in Posidonia oceanica meadows at a depth of 1-10 m. Taxonomic analyses, both morphological and molecular, allowed the identification of some hybrids among the survivors. These hybrids seem to be resistant to the MME and have been found scattered during the census of individuals. On the other hand, several survivors were translocated to safer areas and the impact of the translocation was evaluated without finding significant negative effects.

In addition, few populations remain unaffected in “sanctuary areas”, where a natural barrier prevents the pathogen´s spread to the non-resistant population. Only two populations remain in Spanish waters, the Mar Menor lagoon and Ebro Delta, both of which are additionally subject to anthropogenic pressures (fishing, anchoring, water sports, agricultural discharges, etc...). Monitoring key demographic processes, population fitness and vital rates is crucial for the effective conservation of this threatened species, which may provide the scientific basis of its population dynamics needed to implement successful recovery programmes. Population dynamics in both sanctuary areas provide similar results, showing negative trends with high mortality rates that have led to the loss of more than a third of the specimens in few years.

Moreover, other research and conservation actions are being performed, such as evaluation of natural recruitment, captive breeding, search of new optimal sites, genetic studies among others. The knowledge acquired during these years emphasized the necessity for collaborative monitoring, especially to understand the current critical situation of P. nobilis and to implement effective conservation measures of these emblematic species

Poster Session:

Biodumpy: A Python package for downloading comprehensive biological datasets.

Cancellario T.[1], Golomb Durán T.[1], Far A.[1], Roldán A.[1], Capa M.[1]
Balearic Centre for Biodiversity, University of the Balearic Islands, Palma de Mallorca, Spain.

In recent years, the scientific community has experienced a rapid expansion of public biodiversity platforms and associated datasets. Advances in research, institutional initiatives, increasing data storage capacities and powerful computational resources have greatly enhanced access to ecological and biological data, spanning vast geographic areas, extended time frames, and diverse taxonomic groups. These datasets have become essential for ecological research, enabling more comprehensive analyses and the facilitate the exploration of hypotheses that were previously constrained by limited data availability, quality concerns, and inconsistent sources.

As a result, a growing number of programming packages have emerged to facilitate data retrieval. However, most are limited to single databases, posing challenges for researchers seeking to integrate information across multiple platforms.

To address this gap, we developped biodumpy, a Python package designed to streamline the retrieval, management, and integration of biological data from various public databases. biodumpy provides access to 10 specialized modules, unifying the retrieval of up-to-date datasets across genetic (e.g., NCBI, BOLD), distributional (e.g., GBIF, OBIS), taxonomic (e.g., Catalogue of Life), and bibliographic (e.g., Crossref) sources. With just a few command-line inputs, users can interact with dedicated modules designed for efficient data retrieval by taxon, with support for processing multiple modules simultaneously. We believe biodumpy will significantly enhance biological data acquisition, enable more comprehensive analyses, and advance ecological research in tackling complex environmental challenges.

Workflow for using Nanopore technology to enhance dietary composition studies: the deep-water rose shrimp Parapenaeus longirostris as a case of study.

Carolina de Oliveira Magalhães[1,2]*, Karen D. Schöninger-Almaraz[1,2], Laura Triginer-Llabrés[1,2], Sergio Ramirez-Amaro[2,3], Lluís Moragues-Solanas[1,2]#.

[1] Balearic Biodiversity Centre (CBB), Department of Biology, University of the Balearic Islands, Palma, Spain. [2] University of the Balearic Islands, Department of Biology, Palma, Spain. [3] Spanish Institute of Oceanography, Balearic Oceanographic Centre (IEO-CSIC), Palma, Spain.

* Presenting autor: carolina.oliveira@uib.es

Corresponding autor: lluis.moragues@uib.cat

The study of marine organisms' diets provides valuable insights into their trophic ecology and the roles they play within complex marine ecosystems. Understanding dietary patterns helps clarify species interactions and ecosystem functioning. In this work, we employed long-read sequencing using the Oxford Nanopore platform to investigate the diet composition of Parapenaeus longirostris, a deep-sea shrimp with broad distribution in the Mediterranean Sea and recognized ecological and economical relevance. Although short-read sequencing platforms have traditionally dominated metabarcoding diet studies, they are often limited in resolving closely related taxa due to the short length of amplicons. In contrast, Nanopore sequencing offers substantial advantages through its capacity to generate long reads, enabling higher taxonomic resolution, better haplotype discrimination, and more accurate identification of closely related or cryptic species. Despite these benefits, the use of Nanopore technology in dietary metabarcoding remains limited. In this study, we aim to explore and establish a dedicated workflow leveraging Nanopore sequencing for diet analysis, highlighting its potential as a flexible, real-time, and scalable alternative to conventional platforms. To characterize the diet of these organisms with high taxonomic resolution, we analyzed two male individuals collected from their natural habitat—one with a full stomach and the other with an empty one. The stomach contents were carefully extracted and subjected to DNA extraction, followed by PCR amplification of the mitochondrial COI gene (Cytochrome C Oxidase subunit I) using universal primers suitable for metabarcoding studies. The raw sequencing reads displayed high quality (>10QC), with read counts ranging from 15 to 30 million per sample and average read lengths between 594 and 618 base pairs. Although taxonomic data analysis is ongoing, preliminary results prove the technical feasibility and potential of Nanopore sequencing for trophic ecology studies in marine invertebrates, demonstrating that this protocol can generate large amounts of long-fragment reads per sample. The observed differences in stomach content may also reflect behavioural or ecological influences, including feeding selectivity, temporal feeding patterns, or individual variability. Ultimately, the application of DNA metabarcoding to uncover the dietary composition of marine species represents a powerful and increasingly accessible tool. It helps overcome limitations associated with traditional morphological gut content analysis and contributes meaningfully to the understanding of marine food webs, biodiversity monitoring, and the assessment of anthropogenic impacts on ocean ecosystems.

Host-gut microbiota coevolution and its role in insular adaptation: A case study of the Balearic lizard Podarcis lilfordi.

Caterina Marquès Gomila[*1,2], Giacomo Tavecchia[3], Andreu Rotger[3], José Manuel Igual[3], Lodovico Sterzi[4], Joan Lluís Riera[1], Laura Baldo[1,2]
[1]Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain. [2]Institute for Research on Biodiversity (IRBio), Barcelona, Spain. [3]Animal Demography and Ecology Unit, IMEDEA, Consejo Superior de Investigaciones Científicas, Esporles, Spain. [4]Department of Biomedical and Clinical Sciences, Pediatric Clinical Research Center "Romeo and Enrica Invernizzi", Università Di Milano, 20157, Milan, Italy.
*Presenter: Caterina Marquès Gomila, cmarques@ub.edu

Insular populations of terrestrial vertebrates often experience resource scarcity and seasonal fluctuations, requiring adaptations for a more efficient use of trophic resources and the ability to adjust to their availability. In this context, gut microbes are emerging as key players by modulating host metabolism and enhancing dietary flexibility. However, the specific contribution of gut microbiota to host adaptation and the evolutionary forces that shape their association remain poorly understood.

In this project, we investigate host–gut microbiota coevolution and its functional relevance in local adaptation by studying multiple populations of the endemic Balearic lizard Podarcis lilfordi. We combined lizard population genetic distances data (based on FST and single-nucleotide polymorphisms) with their gut microbial taxonomic profiles generated using full-length 16S rRNA sequences (Oxford Nanopore Technology). To characterize the microbial functional profile, we used newly generated shotgun metagenomic sequencing data.

Our results revealed a remarkably conserved core gut microbiota taxonomic profile across populations, suggesting ancestral inheritance and a strong resilience of these bacterial communities. Microbiota-based relative distances among populations closely mirrored those on host population genetics, pointing to an influence of the host phylogeographic history in shaping gut microbiota structure. Additionally, a set of bacterial genera was identified as responsible for this pattern, likely representing the "housekeeping" component of the lizard gut microbiota and emerging as important candidates for future studies aimed at better understanding host-microbe interactions.

Through the annotation of Clusters of Orthologous Groups (COG), categories, and metabolic pathways, we also provide preliminary insights into the main metabolic functions of the lizard gut microbes, and their patterns of variation across populations and in response to seasonal fluctuations. Our initial findings highlight the potential of gut microbial symbionts as key players in vertebrate insular adaptation and population persistence.

Using environmental DNA metabarcoding to assess marine mammal biodiversity in the Western Mediterranean.

Chloé Fernandez[1]*; David March[1]; Carlos Barros-García[2]; Antonella Arcangeli[3]; Juan Antonio Raga[1]; Natalia Fraija-Fernández[1]
[1] Marine Zoology Unit, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain. [2]Biology Department, Avanqua-Oceanogràfic S.L., Valencia, Spain. [3] ISPRA National Institution for Environmental Research and Monitoring, Rome, Italy.
* Presenter : chloe.fernandez@uv.es

Environmental DNA analysis has emerged as an effective biomonitoring technique in marine environments, demonstrating significant potential for assessing entire biological communities. This study presents data on marine mammal distribution in the Western Mediterranean gathered from more than two years of research. A total of 104 water samples, each ranging from 2 to 3 liters, were collected from various platforms, including commercial ferries, oceanographic vessels and tour boats between May 2021 and October 2023. Seventeen of these samples were taken from the Oceanogràfic aquarium, a controlled environment used for methodological validation, while the remaining samples were collected along the Cetacean Migratory Corridor, a Marine Protected Area (MPA) in the Western Mediterranean. Water was filtered using encapsulated Sterivex filters, and DNA was extracted and amplified using the previously designed marine vertebrate MarVer3 primers, targeting ~245 bp of the 16S rRNA gene. In the MPA, eDNA analysis identified resident cetacean species, including Tursiops truncatus, Delphinus delphis, Balaenoptera physalus, Grampus griseus, and unassigned Delphinidae variants. Using a phylogenetic framework, these last ones were taxonomically assigned to Stenella coeruleoalba, commonly occurring in the area, thus highlighting the challenges of differentiating closely related cetacean species. Additional sequencing data from other marine vertebrates facilitated the study of cetacean prey distribution through a trophic network exploration. In the aquarium, eDNA analysis successfully identified almost 60% of the known marine vertebrate diversity, and all marine mammal species: Delphinapterus leucas and Tursiops truncatus at species level and Phoca vitulina and Zalophus californianus at genus level. Interestingly, Stenella attenuata and Orcinus orca were also detected as false positives. These results are interpreted in light of the genetic similarity between closely delphinid species and the limitations in the completeness and accuracy of the reference database used. Study supported by Generalitat Valenciana through projects CETABIOENA (CISEJI/2022/5), IOS4DOM (CIDEGENT/2021/058), LIFE CONCEPTU MARIS (LIFE20 NAT/IT/001371).

Biases in conservation efforts and limited genetic data hinder protection of Mediterranean marine invertebrates.

Claudio Padua[1], Tommaso Cancellario[1], Maria Capa[1]
[1]Balearic Biodiversity Centre (CBB-CMB), University of the Balearic Islands, Palma, Spain.
*Presenter: claudio.padua@uib.es

Genetic diversity is a valuable indicator for assessing the conservation status of species, making the availability of high-quality DNA data essential for designing effective biodiversity conservation strategies. However, despite the rapid and cost-effective advances in genomic technologies, substantial knowledge gaps remain for many emblematic and potentially vulnerable species. The limited representation of reference DNA sequences in public databases reflects the overall scarcity of available genetic data, posing a major constraint for population genetic studies.

In the Mediterranean Sea, benthic invertebrate communities are threatened by multiple stressors, which affect species from shallow to deep habitats. In recent decades, several International Conservation Agreements (ICAs) have provided legal frameworks for the protection of vulnerable or overexploited invertebrates, with the conservation status of many species assessed by the International Union for Conservation of Nature (IUCN) Red List. Despite their ecological importance and vulnerability, most Mediterranean marine invertebrates remain poorly studied. A key limitation is the widespread lack of genetic data, which hampers accurate species identification and assessment—an essential step toward improving marine conservation strategies.

This study aims to: 1) provide an overview of the current protection status of Mediterranean marine invertebrates across different ICAs and identify gaps across taxonomic groups and, 2) evaluate the availability of genetic data in public repositories to highlight potential biases in the taxonomic representation of DNA sequence across different phyla. A comprehensive taxonomy checklist of Mediterranean invertebrates included in ICAs was compiled, and genetic data were subsequently retrieved. The most frequently used short molecular markers were identified and compared across taxonomic groups.

The results reveal a clear inequity in conservation efforts across Mediterranean invertebrate biodiversity, with abundant groups like Annelida and Platyhelminthes entirely unrepresented, while conservation measures disproportionately focus on phyla like Cnidaria and Echinodermata—only the fifth and eighth most speciose in the region, respectively. Strikingly, the majority of species assessed by the IUCN Red List are classified as Data Deficient, reflecting a lack of information, especially concerning potentially vulnerable taxa. Analysis of available genetic data confirms that efforts focus on a few charismatic taxa, with the mitochondrial Cytochrome c oxidase subunit I (COI) being the most predominant molecular marker in use. These findings underscore the urgent need to enhance genetic studies on vulnerable invertebrates to support conservation assessments, while also highlighting the underrepresentation of Mediterranean invertebrate biodiversity within current protection frameworks.

Genetic study of the genera Colwellia, Cognaticolwellia, and Polaribacter from two marine sediment samples from Svalbard, Norway.

Eva Mangado Mier[1]*, Katrin Knittel[2], Jens Harder[2], Rudolf Amann[2], Tomeu Viver[1]
[1] Marine Microbiology Group, Department of Animal and Microbial Biodiversity, Mediterranean Institute for Advanced Studies (IMEDEA, CSIC-UIB), Esporles, Spain. [2] Department of Molecular Ecology, Max Planck Institute for Marine Microbiology, Bremen, Germany.
*evamangadomier@gmail.com

Based on extensive genome comparisons at the intraspecies level, using average nucleotide identity (ANI) and the percentage of genome shared (i.e., genes) between pairs of genomes, we observed that species are composed of discrete groups of genomes, each defined by ANI values greater than 99.8%, revealing natural genomic "gaps" within species. Those genome units were proposed to be called "genomovars", representing the smallest evolving units within a species (Viver et al., 2024; Rodriguez et al., 2023). As a proof of concept, in this study we conducted a sampling expedition in the Svalbard archipelago in December 2021 and 2023, collecting sandy sediments from the coast of Isfjorden (Svalbard), where temperatures permanently remain <4°C. From these samples, over 1,000 aerobic, heterotrophic, psychrophilic strains were isolated in pure culture, and subsequently analyzed using MALDI-TOF mass spectrometry in tandem with 16S rRNA gene analysis. Members of the genera Colwellia, Cognaticolwellia, and Polaribacter were the most represented in our strain collection, and we randomly selected 12, 57, and 58 isolates, respectively, for genome sequencing. Phylogenetic analyses based on core-genome alignments, along with pairwise ANI calculations, were conducted to assess boundaries at both inter- and intraspecies levels. By comparing the ANI values of the new isolates with genomes of previously characterized species, we identified 5 Colwellia, 6 Cognaticolwellia, and 13 Polaribacter novel species, based on an ANI threshold of ≥ 97.6%. Moreover, at the intraspecies level, we observed a lower occurrence of ANI values in between 99.2 and 99.8%, revealing the consistent observation of the genomovar-level ANI gap, highlighting its potential for studying intraspecific genomic discontinuities and provides a robust approach for studing microbial diversity at intraspecies level.

Biomonitoring the potential risk of rivers submitted to anthropic pressure using the snails (Lymnaea stagnalis) as a sentinel speceies.

Benali[1,2] I., Boualit[3] L., Monbaron[3] L., Tisserand[3] F., Bouderbala[2] M., Chèvre[3] N.
[1]Balearic Biodiversity Centre (CBB), University of the Balearic Islands, Palma, Spain. [2]Laboratory Network for Environmental Monitoring (LRSE), University of Oran 1 Ahmed Ben Bella. [3]Faculty of Geosciences and Environment, University of Lausanne, 1015 Lausanne, Switzerland.

Most rivers in the North-West of Algeria have a catchment considerably influenced by localities and agricultural activities, which can generate discharges of various pollutants and weaken biodiversity. This study aims to assess the risk of two rivers submitted to anthropic pressure: El Malah river (EM), and Sidi Djelloul river (SD), using a gastropod species Lymnaea stagnalis as a bioindicator. To reach this goal, we selected 09 sites along both rivers, and we analyzed the abundance of the population, and the biomarkers activities (Acetylcholinesterase (AChE), Glutathione S-Transferase (GST), Lipid Peroxidation (LPO)). Sampling was done for four seasons during 2020/2021. The ecological distribution study demonstrated a longitudinal decrease in the abundance of the population along both rivers from upstream to downstream. Moreover, no specimen was recorded in the areas submitted to wastewater discharges, to discontinuous drying out due to the lack of rain, or to a high irrigation rate. The results also showed a significant increase in GST activity and a significant decrease in AChE activity in the snail from SD river, suggesting greater exposure to insecticides at this site. Indeed, many insecticides are cholinesterase inhibitors. An increase in GST activity could indicate general oxidative stress. However, no statistically significant variation was observed in LPO activity. This study represents a first step in the risk assessment of rivers highly influenced by anthropic pressure in Algeria. It allowed to demonstrate that there is a high and chronic risk for invertebrate communities and the fluvial ecosystems in general. Measures must be implemented, such as urban wastewater treatment and the promotion of extensive agriculture.

DNA Metabarcoding the Trophic Ecology of the red shrimp Aristeus antennatus in the Western Mediterranean.

Iris Alemany [1]*, Sergio Ramírez-Amaro[1, 2], María Valls[2], Beatriz Guijarro[2], José A. Jurado-Rivera[1]
[1] Department of Biology, Genetics Area, University of the Balearic Islands, Palma de Mallorca, Balearic Islands, Spain. [2]Balearic Oceanographic Centre (COB-IEO), Spanish Institute of Oceanography (CSIC), Palma de Mallorca, Balearic Islands, Spain. Presenter: iris.alemany@uib.es

The red shrimp, Aristeus antennatus, is a key species within deep-sea ecosystems and represents a valuable fishery resource in the Mediterranean. Despite its ecological relevance, the trophic ecology of A. antennatus remains poorly characterized, primarily due to the inherent limitations of traditional gut content analysis, which often fails to detect soft-bodied or highly digested prey. In this study, we employed an alternative method based on high-throughput DNA metabarcoding to comprehensively assess the diet of A. antennatus across multiple locations in the Balearic Islands. A total of 285 gut content samples were collected from both males and females from 15 stations during the MEDITS bottom trawl scientific surveys in 2023. The DNA from the samples was extracted and subjected to metabarcoding based on the mitochondrial cytochrome c oxidase subunit I gene. To prevent the amplification of the predator's own DNA, specific blocking primers were designed.

A total of 246 operational taxonomic units (OTUs) were detected from all the samples. Taxonomic assignment revealed high resolution, with all of them classified at both the kingdom and the phylum levels, 244 OTUs were further classified at class, 172 at order, 140 at family, 125 at genus level and 101 at species level. Prey richness per sample exhibited considerable variability, ranging from 1 to a maximum of 30 OTUs, with an average of 12 consumed OTUs per individual. The analysis of prey composition revealed a marked predominance of five phyla: Arthropoda (31.3% of total OTUs), Annelida (18.6%), Chordata (15.9%), Mollusca (12.2%), and Cnidaria (6.5%), which represent around 85% of the prey OTUs. Further taxonomic resolution at the class level identified Malacostraca (23.4%), Polychaeta (17.2%) and Actinopterygii (11.9%) as primary prey groups, followed by, Hydrozoa (6.2%), Cephalopoda (5.3%) and Gastropoda (5.3%). The significant representation of both benthic-associated (Annelida, benthic Arthropoda) and pelagic-derived (Scyphozoa, Oegopsida, Euphausiacea) prey items confirms that A. antennatus exhibits a benthopelagic feeding behavior, efficiently exploiting multiple vertical habitat strata. This multilevel trophic analysis substantiates the ecological classification of A. antennatus as a euryphagous predator with considerable trophic plasticity, occupying a complex ecological niche within deep sea ecosystems in the Mediterranean.

Our findings highlight the effectiveness of DNA metabarcoding in elucidating complex trophic interactions within deep-sea ecosystems, offering an unprecedentedly detailed dietary profile for A. antennatus in the Balearic Islands. This comprehensive approach enhances our understanding of food web structure and ecosystem connectivity, and provides valuable insights for the sustainable management and conservation of deep-sea fisheries resources.

CNAG's Long-read Assembly Workflow in Snkemake (CLAWS).

Jèssica Gómez-Garrido [1,2]*, Francisco Câmara [1,2], Fernando Cruz [1,2] and Tyler Alioto [1,2]
[1] National Center for Genomic Analysis (CNAG), Barcelona, Spain. [2] University of Barcelona (UB), 08028 Barcelona, Spain.
*Presenter: jessica.gomez@cnag.eu

Thanks to the recent improvements in sequencing technologies and computational capacities, it is now possible to consider sequencing all life on earth. However, this ambitious objective set by the Earth Biogenome Project (EBP) still requires the participation of many scientists and computational resources. Hence, there is a big need for developing and optimizing computational tools that can take the sequencing data and produce genome assemblies reducing the amount of necessary human or computational resources.

In this poster we present CLAWS, which is a Snakemake-based pipeline that assembles long-reads of any eukaryotic species into high-quality reference genomes. It takes as input ONT or PacBio HiFi long-reads and assembles them with Flye, Hifiasm and/or Nextdenovo. Additionally, it can also take Illumina reads that will be used for polishing ONT-based genome assemblies. Finally, it runs purge-dups to remove any artificial duplications and produces chromosome-level assemblies by scaffolding with 10X-linked and/or Hi-C reads. To aid comparison and evaluation of the different assemblies obtained along the pipeline, it computes several statistics (gfastastats, Busco, Merqury) and summarizes them into a final table.

It is implemented as a modular pipeline, with five different subworkflows: 1) read preprocessing, 2) assembly, 3) polishing, 4) post-polishing (e.g. purging and scaffolding), and 5) assembly evaluation. This modular division makes it very flexible. It can either run from start to end (e.g., starting from preprocessing and evaluating input reads to producing pretext files from scaffolded assemblies) or it can start and end at any step. Its only argument is a configuration file that will detail which steps should be run as well as the specific parameters for each of these steps. This configuration file is produced by the "create_config_file.py" embedded script and enables the modification of all the options of the different used tools.

CLAWS, which to-date has successfully assembled a huge variety of organisms such as vertebrates, arthropods, corals, worms, shellfishes and plants, is open-source and can be freely downloaded.

Using flower eDNA metabarcoding to identify the effects of forest structure and microclimate on flower-visiting arthropods.

Joan Díaz-Calafat[1]*, Donnie Lee Peterson[1], Pieter De Frenne[2], Adam Felton[1], Erik Öckinger[3], Sara A. O. Cousins[4], Fabian Roger[5], Michelle Cleary[1], Per-Ola Hedwall[1]

[1] Southern Swedish Forest Research Centre, Swedish University of Agricultural Sciences, Lomma, Sweden. [2] Forest & Nature Lab, Department of Environment, Ghent University, Melle-Gontrode, Belgium. [3] Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden. [4] Department of Physical Geography, Stockholm University, Stockholm, Sweden. [5] Department of Environmental Systems Science, ETH Zürich

*Presenter: joandiazcalafat@gmail.com

Recoding pollinators can be challenging in contexts where plant-pollinator interactions are limited, thereby constraining the assessment of their ecological responses. For example, forests usually offer fewer floral resources for pollinators compared to ecosystems like grasslands. In addition, forest understory microclimates affect the spatial and temporal patterns of pollinator activity, making their detection even more challenging. In this study, we use environmental DNA (eDNA) to address these challenges and investigate the influence of forest microclimate, density and tree composition on the diversity of flower-visiting arthropods in a Swedish forest. We used two flowering plant species, Fragaria vesca and Trifolium pratense, as sentinel plants, placing them across 40 plots within a mixed forest that varied in forest density and broadleaf dominance. The metabarcoding of flower eDNA documented a high diversity of arthropods with very specific communities in different forest plots. This high species turnover suggests either short eDNA persistence on flowers or unmeasured ecological factors structuring these communities. We found that forest structure, particularly light availability in broadleaf-dominated open plots, positively influenced species richness of arthropods, while microclimate had a small impact. These effects varied between plant species, likely due to differences in flower visitor communities. Our study also offers significant methodological insights into using flower eDNA for detecting flower-visiting taxa. We show that the number of flowers pooled in the same DNA extraction positively influences the number of taxa detected, and that flower shape probably affects eDNA persistence. By improving methods in flower eDNA sampling and analysis, future studies will enhance our ability to assess ecological interactions and conservation needs in forest environments and other ecosystems.

Presence of cryptic species of the genus Ophiothrix in the Balearic Islands.

Joan Riera[1]*, Joana F. Ferragut[1], Marta Bassitta[1], Enric Massuti[2], Belén Calero[2], Xisco Ordines[2], Sergio Ramírez-Amaro[1,2]
[1] Genetics Area (HEGEN-UNICS Group), University of the Balearic Islands, Palma, Spain. [2] Spanish Institute of Oceanography, Balearic Oceanographic Centre, Palma, Spain.
*Presenter: joan.riera.fabre.98@gmail.com

Ophiothrix is a genus of brittle starts that includes species complex and cryptic species. This genus is widely distributed and ecologically relevant, often found in association with sponges and corals, where they play an essential role in benthic food webs. Ophiothrix fragilis (Abuldgaard in O.F. Müller) is one of the most common and well-known ophiuroids in the Atlantic and Mediterranean, with a wide geographic and bathymetric range. The taxonomy of this species has been controversial because of its morphological variability. Different studies have indicated that O. fragilis is a complex species suggesting the presence of multiple cryptic species. In this context, in addition to the presence of O. fragilis, two closely related lineages have also been found, referred to as Ophiothrix sp. II and Ophiothrix sp. III.

The goal of this study was to characterize genetically up to 7 different phenotypes of Ophiothrix specimens collected from the Balearic Islands. The specimens were sorted into these phenotypes after a detailed external morphological analysis based on usual characters used to classify the species of this genus. The specimens were collected from different locations around the Archipelago during three oceanographic surveys: MEDITS_2019, 2022, INTEMARES_A4, A22B, and CIRCALEBA_21, 22. Genetic characterization was based on the cytochrome c oxidase subunit I and the 16S rRNA, (hereafter COI and 16S) mitochondrial markers. The analyses included haplotype networks, phylogenetic analysis, species delimitation and genetic distances. Furthermore, we included into these analyses sequences of COI and 16S from other Ophiothrix species found in GenBank database.

The resulting haplotype networks showed three distinct genetic groups for both fragments. These groups were also supported by phylogenetic and species delimitations analyses, with high values of genetic distances between them for both fragments. Our results clearly revealed the presence of three distinct genetic lineages within the Ophiothrix complex in the Balearic Islands. Genetic distance analyses among various Ophiothrix species suggest that these lineages may represent separate species, as the observed divergence values are comparable to those typically found between valid species.

These findings highlight the need for a proper taxonomic description of these putative new species. Further analyses should be conducted to clarify their morphological traits, genetic divergence and spatial distributions. The identification of cryptic species within Ophiuroidea is essential for understanding marine biodiversity, as many distinct evolutionary lineages remain hidden due to morphological convergence.

Describing the Diversity and Global Distribution of Plastid-Bearing Coral Symbionts Re-Using Published Microbiome Data.

Joana Krause-Massaguer[1]*, Bradley A. Weiler[2], Javier del Campo[1,2]

[1] Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Barcelona, Spain. [2] Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami, Miami, USA.

*Joana Krause-Massaguer: joana.krause@ibe.upf-csic.es .

Corals form intricate symbiotic relationships with a diverse microbial community that influences their physiology, evolution, and ecological function. The study of coral microbiomes has largely focused on bacteria and Symbiodiniaceae protists, leaving the vast majority of the broader protist community overlooked. In this work, we performed a meta-analysis of publicly available 16S rRNA gene datasets to examine the diversity and global distribution of plastid-bearing microeukaryotic symbionts in corals. Sequences of plastid origin are often discarded as noise in microbiome analyses, but they carry valuable ecological information and should be actively retained and analyzed. We reprocessed 3,735 samples from 48 studies, generating a unified dataset of 17,732 Amplicon Sequence Variants (ASVs) and over 13 million reads. To minimize methodological bias, analyses were limited to the V3-V4 region of the 16S rRNA gene. We assessed Shannon diversity in relation to coral health status (healthy, bleached, diseased), host taxonomy, and geographic location. Compositional analyses revealed shifts in microeukaryotic community composition across coral health conditions, host taxa, and geographic location. Apicomplexans and Chlorophyta (green algae) consistently emerged as the most relatively abundant plastid-bearing symbionts across all locations. We examined apicomplexan sequences in greater detail by placing reads into a reference phylogeny, which confirmed that most reads belonged to the Corallicolidae, a family of abundant and wide-spread coral microeukaryotic symbionts. Through heatmaps, we identified that the most abundant ASVs belonged to Corallicola and Ostreobium, a genus of green algae. Prevalence plots were built to asses whether the identified ASVs were specific to certain samples or widespread across the dataset. This large- scale meta-analysis provides a comprehensive overview of plastid-bearing symbiont diversity across a wide ecological and geographic range. It highlights the large diversity of coral-associated protists and demonstrates the potential of reusing existing microbiome data to develop novel findings

Parasitism in the endemic Balearic lizard Podarcis lilfordi: updated insights from helminth distribution and prevalence.

José Antonio de los Ríos-Solera[1]*, Alexis Ribas[2], Giacomo Tavecchia[3], Ines Delgado-Pizzo[1], Laura Baldo[1]
[1]Department of evolutionary biology, ecology and environmental sciences. Faculty of Biology. University of Barcelona (UB). Barcelona. Spain. [2] Department of Biology, Health, and Environmental Science, Parasitology Laboratory. Faculty of Pharmacy. University of Barcelona (UB). Barcelona. Spain. [3]Animal Demography and Ecology Unit, IMEDEA, Consejo Superior de Investigaciones Científicas, Esporles, Spain.
*Corresponding author: josedelosrios@ub.edu

Studying parasitism on islands highlights how isolation and limited biodiversity shape host-parasite coevolution and ecosystem stability. This study aims to explore the diversity and prevalence of intestinal helminth parasites in the Balearic lizard, an endemic and endangered species that is distributed in several islets within the Balearic archipelagos. To this purpose, nearly 200 fecal samples were collected on six islets around Mallorca and in the Cabrera Archipelago. For the detection of parasites, coprological analyses were carried out to identify the presence of eggs and adult stages. In addition, male and female adult nematodes were collected and their body structures were analysed and differentiated under microscopy. The results show the presence of two endemic nematode species, Spauligodon cabrerae and Parapharyngodon lilfordii (Nematoda, Oxyuroidea), formerly described in the late 1980's. While S. cabrerae was found exclusively on the two main islands Cabrera and Dragonera, P. lilfordii is present in all locations under study. For both parasites, the lizard is the only direct vector of transmission. The overall proportion of infected individuals per population/island (i.e., prevalence) ranged from 21% to 75%, indicating that gut helminths are a common companion of the Balearic lizard and have persisted within the host populations during last 45 years. Our findings set the basis to explore the ecology of parasites in island ecosystems and their role on persistence of these endangered populations.

Gut microbiota community is associated with trophic spectrum in the invasive species Vespa velutina.

Cayetano Herrera [1], Iris Alemany [2], Mar Leza [1], Gabriel Arbona [1], and José A. Jurado-Rivera [2]*
[1] Department of Biology (Zoology), University of the Balearic Islands, Ctra. Valldemossa km 7.5, Palma, Balearic Islands, Spain. [2] Department of Biology (Genetics), University of the Balearic Islands, Ctra. Valldemossa km 7.5, Palma, Balearic Islands, Spain.
*Presenter: José A. Jurado-Rivera

Diet is a key factor shaping the gut microbiota in insects, influencing digestion, metabolism, and potential adaptation to new environments. In invasive species like Vespa velutina nigrithorax, dietary flexibility may be linked to microbial composition, potentially facilitating its ecological success. However, the diet and gut microbiota in this species remains poorly understood. In this study, we analysed both the diet and the gut microbiota of V. velutina larvae in Mallorca under a metabarcoding framework based on coxI DNA and 16S rRNA sequences, respectively. Results showed dietary variation between nests, with a preference for hymenopteran and dipteran insects, highlighting its impact on local insect populations with different functional roles (i.e. pollinators, detritivores). Moreover, our results show a highly significant positive correlation between diet richness and microbial diversity, indicating that dietary variation influences gut microbial composition. Firmicutes (49.42%) and Actinobacteriota (31.75%) were the dominant bacterial phyla, with specific microbial taxa associated with certain insect prey families. These findings suggest that microbial communities in V. velutina adjust to different dietary inputs, potentially enhancing digestive efficiency and adaptability to novel environments. This research enhances our understanding of predator-prey interactions in invaded ecosystems and underscores the importance of DNA metabarcoding tools for studying the foraging behaviour of invasive species, while also highlighting the role of gut microbiota and its potential adaptation to diet in V. velutina, providing insights into the microbial mechanisms that may contribute to its invasive success.

The genome sequence of Tethysbaena scabra (Pretus, 1991), the first known in the peracarid crustacean order Thermosbaenacea.

Joan Pons[1,†], Karen D. Schöninger-Almaraz[2,†,*], Laura Triginer-Llabrés[2,†], Carlos Juan[1,3], Damià Jaume[1], José A. Jurado-Rivera[3] [1] Mediterranean Institute for Advanced Studies (IMEDEA, UIB-CSIC), Esporles, Balearic Islands, Spain. [2] Balearic Biodiversity Centre, University of the Balearic Islands (UIB), Palma, Balearic Islands, Spain. [3] University of the Balearic Islands (UIB), Palma, Balearic Islands, Spain.
*Presenter: karen-daiana.schoninger@uib.cat

Tethysbaena scabra (Pretus, 1991) is a thermosbaenacean, a relict group of peracarid crustaceans characterized by the display in gravid females of a dorsal brood pouch formed by a posterior extension of the carapace. This species measures 2–3 mm in length, is eyeless and depigmented, inhabiting subterranean waters of raised salinity in caves and wells located near the marine coast. It is endemic to the Mediterranean islands of Mallorca and Menorca. There is no available information on genome size and chromosome number in thermosbaenaceans, therefore, here we present a chromosome-level genome assembly for T. scabra from Mallorca, which represents the first reference genome for the order Thermosbaenacea. To do this, a pool of 20 specimens were used for sequencing on Pacific Biosciences SEQUEL II (HiFi) instrument (Accession number: SAMEA113414145 qmTetScab1) and Hi-C data was generated from another pool of 20 individuals from the same collection site (Accession number: SAMEA118091338) using the library preparation Omni-C DNA and sequenced on the Illumina NovaSeq 6000 S4 instrument. The genome size was estimated using GenomeScope2 (Vurture et al., 2017) and diploidy was confirmed with Smudgeplot (Ranallo-Benavidez et al., 2020). Assembly was conducted using hifiasm (Cheng et al., 2021). Haplotypic duplications were withdrawn with purge_dups (Guan et al., 2020) and contig sequences from contaminant species were removed from assembly using Foreign Contamination Screen (Astashyn et al., 2022) and Whokaryote (Pronk et al., 2022). The scaffolding was performed with Hi-C data (Rao et al., 2014) using YaHS (Zhou et al., 2022) and the assembly obtained was checked for contamination with two rounds of Blobtools to ensure complete decontamination. Curation of contact map was performed using Pretext (Harry, 2022). The genome was analysed within the BlobToolKit environment and BUSCO scores were generated (Challis et al., 2020). To assess the assembly metrics, the k-mer completeness and QV consensus quality values were calculated using Meryl and Merqury (Rhie et al., 2020). To obtain the mitochondrial genome, sequence contigs were compared with a relaxed BLASTn algorithm against a database built with mitogenome sequences of several peracarid species. The sequence of 30 kb with a positive match was circularized in MitoMaker (Schomaker-Bastos and Prosdocimi, 2018) and annotated in Mitos2 (Donath et al., 2019). Repetitive annotation was performed using RepeatMasker and RepeatOBserver (Elphinstone, C., Elphinstone, R., Todesco, M., & Rieseberg, L., 2023). An assembly spanning 1.18 Gb across 23 scaffolds was obtained, with a scaffold N50 of 74.6 Mb. The final assembly sequence, confirmed by Hi-C data, was assigned to 17 scaffolds at the chromosome level, with a value of BUSCO (Manni et al., 2021; Simão FA et al., 2015) completeness obtained is 94.7%, using the arthropods_odb10 reference set.

Genome of Naufraga balearica, an endemic and monospecific plant of Mallorca.

Laura Triginer-Llabrés[1]*, Bartomeu Oliver-Riera[1], Carolina de Oliveira Magalhães[1], Lluís Moragues-Solanas[1], Joana Cursach Seguí[2] and Enrique Arboleda[1]
[1] Balearic Biodiversity Centre, University of the Balearic Islands, Palma, Spain. [2] University of the Balearic Islands, Palma, Spain.
*Presenter: laura.triginer@uib.eu

Naufraga balearica (Constance & Canno, 1967) is a small, diploid and perennial herb endemic to Mallorca, found only in a few isolated pockets at the northern end of the Tramuntana mountain range. Its limited distribution, low abundance, short mobility range of its pollinating ants, monospecific nature, and exposure to habitat alteration, grazing and trampling by herbivorous fauna has favored its inclusion in the IUCN Red List under the Critically Endangered Status level. The current project aims to generate the reference genome of Naufraga balearica at the chromosomal level. This assembly will follow the ERGA standards, and it is conducted under the umbrella of the Catalan Biogenome Project (an EBP-affiliated project network with the objective of sequencing the genome of more than 40000 eukaryotic species living in the Catalan Linguistic Area). This will represent the first chromosomal-level genome assembly for a plant species endemic to Balearic Islands. Furthermore, a repetitive, structural and functional gene annotation, via transcriptomics, will be provided in the near future once RNA sequencing is completed.

Individuals collected from a single population at Cap de Formentor (northern tip of the Serra de Tramuntana) were flash-frozen in liquid nitrogen before High Molecular Weight DNA extraction. Long-reads were sequenced with ONT (P2-Solo, 40x coverage) and short-readswith Illumina Illumina (NovaSeq 6000). Preliminary results have produced a draft genome version of 1,8Gb in size, a slightly low GC content (33%), and high homozygosity values for natural and unmanipulated wild species. A comparison of these values with those of closely related species, for which their complete genome is available, is presented. The finalized assembled version, together with the chromosomal mapping, will provide a valuable resource for the management and evolutionary understanding of this paleoendemic species, while also aiming for a rise in its cultural appropriation as an emblematic representative of the Balearic Islands.

Endophytic microbial diverstiy in wild Mediterranean plants: Implications for biocontrol of Xylella fastidiosa in the Balearic Islands.

Marc Crespo [1]*, Maria Cañellas [1], Juan Rita [2], Antonio Busquets [3], Catalina Cabot [1], Margarita Gomila [1]
[1] Microbiology, Department of Biology, University of the Balearic Islands, Palma de Mallorca, Spain. [2] Botany, Department of Biology, University of the Balearic Islands, Palma de Mallorca, Spain. [3]Scientific and Technical Services, University of the Balearic Islands, Palma de Mallorca, Spain.
*Presenter: marc.crespo@uib.cat

Since its detection in the Balearic Islands in 2016, Xylella fastidiosa, a quarantine phytopathogen in the European Union, has posed an increasing threat to agriculture and local biodiversity. With more than 700 known host species, its presence represents a significant ecological risk, particularly for the endemic flora of the Balearic Islands. Although its impact on cultivated species has been extensively studied, its effects on wild flora remain poorly understood. In this study, we evaluated the endophytic microbial diversity in Cistus albidus, Rosmarinus officinalis, and Santolina magonica, aiming to identify potential natural reservoirs, bioindicators, and biocontrol agents against X. fastidiosa.

The endophytic microbiota of these three plant species was characterized using culture-dependent methods. Seasonal sampling was conducted over the course of one year, analyzing the same six plants per species and season (some of them positive for X. fastidiosa, as determined by qPCR). Endophytic isolates obtained from different culture media (BCYE, cetrimide, R2A, and nutrient agar) were characterized and identified by MALDI-TOF MS and 16S rRNA gene sequencing.

The results revealed high bacterial diversity, that varied seasonally, with no clear correlation between the microbial composition of X. fastidiosa-infected and non-infected plants. Among the isolates, several species with potential biocontrol activity were identified, such as Curtobacterium flaccumfaciens, Methylobacterium mesophilicum, Micrococcus luteus, Pantoea agglomerans, Pseudomonas syringae, and Pseudomonas graminis. This study highlights the role of wild plant species as reservoirs of specific microbiota and their potential application in the development of biological control strategies against X. fastidiosa.

OSSOMICS: Tracing genetic and morphological diversity in Balearic Islands endemic species.

Margarida Barcelo-Serra[1]*, Pere Bover[2], Joan Pons[1] & Alejandro Valenzuela[1]
[1] Mediterranean Institute for Advanced Studies (IMEDEA, UIB-CSIC), Esporles, Balearic Islands, Spain. [2] University Institute for Research in Environmental Sciences (IUCA), Zaragoza, Spain
*Presenter: mbarcelo@imedea.uib-csic.es

Biodiversity is the variability of ecosystems, species and their underlying genetics found on Earth. When pursuing biodiversity studies, endemic species are of particular interest due to their unique morphological and genomic traits and their pivotal ecological roles within their restricted geographical ranges. Consequently, endemic species often require targeted conservation strategies. Islands, as biodiversity hot-spots, are characterized by a high number of endemic species and are particularly sensitive to environmental disturbances. Most biodiversity studies typically focus on present-day patterns; however, understanding long-term dynamics is essential to assess species' adaptive capacities and resilience. Technological advances now allow the study of morphological and genetic diversity in ancient populations, enabling the reconstruction of past population sizes, evolutionary trajectories and the detection of impacts of human activities. This broader perspective enhances our understanding of anthropogenic effects on vulnerable endemic species. In this work, we aim to integrate present-day genomics, paleogenomics and morphological analyses to build a more comprehensive picture of how endemic species respond to environmental changes over time. We present an integrative study of four endemic vertebrate taxa from the Balearic Islands: the reptile Podarcis lilfordi, the amphibian Alytes muletensis, the bird Gulosus aristotelis and the mammal Martes martes. These taxa represent major vertebrate classes and serve as bioindicators of terrestrial, freshwater and coastal marine environments. By comparing ancient and modern mitochondrial genomes and morphological traits, we aim to quantify genetic erosion as a proxy for episodes of environmental stress, particularly during periods comprising human colonization. This approach will help assess the impact of environmental changes on local biota and provide important insights into the historical resilience and vulnerability of insular endemic species in the face of ongoing anthropogenic pressures.

Genetic and agronomic characterization of almond (Prunus dulcis) cultivars from the island of Majorca.

M. Carme Garau[1]*, Jeroni Pou[2], Llorenç Tortella[2], Jaume Miquel[2], Biel Pisà, and Aina M. Leza[1]
[1] Institute for Agri-food and Fisheries Research and Training of the Balearic Islands (IRFAP), Government of the Balearic Islands, Palma, Spain. [2] Empresa de Transformación Agraria S.A. (TRAGSA), Palma, Spain.
*presenter: mcgarau@irfap.es

Conserving crop biodiversity is essential for ensuring future agricultural resilience, particularly in the face of emerging challenges such as climate change and phytosanitary threats. Germplasm banks act as critical repositories of genetic diversity and serve as indispensable tools for breeding and adaptation strategies. Changes in chilling requirements, along with the emergence of Xylella fastidiosa in the Balearic Islands in 2016, highlight the urgency of identifying promising local genotypes for breeding programs. This study evaluates the genetic diversity, flowering phenology, disease incidence, and physical traits of almond cultivars from the Majorca almond (Prunus dulcis) collection. Characterization was carried out at the almond germplasm bank of Son Real (Mallorca, Spain), established in 2014. The dataset includes 37 local landraces and five commercial cultivars. Genetic diversity was assessed using nine polymorphic SSR markers, following ECPGR guidelines. Agronomic traits, including seed yield and flowering phenology (based on Baglioni's scale), were recorded, along with the incidence of Xylella fastidiosa after nine years of known infection. Additionally, physical characteristics of fruit pods and seeds were evaluated. Seven genetic clusters were identified, with the 'Jordi' cultivar showing the lowest genetic similarity (<19%) to the rest. Two cases of synonymy were also detected. Flowering was generally earlier among local genotypes, notably in the 'Caragola' cultivar. The lowest Xylella fastidiosa incidence was observed in 'Capirons', 'Pere Xina', and 'Mare de Déu', while most other cultivars were severely affected. Principal Component Analysis (PCA) explained more than 50% of the observed variability among cultivars and helped distinguish cultivar patterns. This comprehensive evaluation highlights the underexplored phenological diversity and resilience traits present in local almond germplasm. These cultivars, conserved in germplasm banks, may play a crucial role in future breeding programs to address climate change and emerging plant diseases.

The genetic maps of European ants: a roadmap for phylogeography and species discovery.

Mattia Menchetti[1]*, Bonnie Blaimer[2], Lech Borowiec[3], Cecilia Corbella[1], Fede García[4], Kiko Gómez[5], José María Gómez Durán[6], Albena Lapeva-Gjonova[7], Alberto Tinaut[8], Francisca Ruano[8], Sebastian Salata[3], Elisabetta Sbrega[1], Maria Serracanta[1,9], Sämi Schär[10], Enrico Schifani[1,11], Tomash Suchan[12] , Paul D. N. Hebert[13], Leonardo Dapporto[14], Roger Vila[1]

[1] Institut de Biologia Evolutiva (CSIC-UPF), Barcelona, Spain. [2] Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Center for Integrative Biodiversity Discovery, Berlin, Germany. [3] Department of Biodiversity and Evolutionary Taxonomy, Myrmecological Laboratory, University of Wroclaw, Wroclaw, Poland. [4] Barcelona, Spain. [5] Garraf, Barcelona, Spain. [6] Madrid, Spain. [7] Department of Zoology and Anthropology, Faculty of Biology, Sofia University, Sofia, Bulgaria. [8] Department of Zoology, University of Granada, Campus de Fuentenueva s/n, Granada, Spain. [9] Facultat de Biociències, Universitat Autònoma de Barcelona, Barcelona, Spain. [10] Dietikon, Zürich, Switzerland. [11] Department of Chemistry, Life Sciences, and Environmental Sustainability, University of Parma, Parma, Italy. [12] W. Szafer Institute of Botany, Polish Academy 1057 of Sciences, Kraków, Poland. [13] Centre for Biodiversity Genomics, University of Guelph, Guelph, Canada. [14] ZEN Lab, Department of Biology, University of Florence, Sesto Fiorentino, Florence, Italy.

*Presenter: mattiamen@gmail.com

The European ant fauna is composed of approximately 630 species, a number that continues to grow each year as new species are discovered and alien species are accidentally introduced. The construction of comprehensive DNA barcoding libraries provides useful tools for detecting potential new species and introduced ones. The use of metabarcoding techniques also relies on the existence of these complete DNA libraries. Large mtDNA datasets also allow to study macroecological and macroevolutionary processes at the continental level.

We assembled the first DNA barcoding reference library based on COI sequences for European ant species, both native and alien, and we assessed their intraspecific variability. We obtained a 78.8% taxon coverage (497 species) and ~6,000 sequences (~3,800 newly sequenced and ~2,200 retrieved). We covered all 55 ant genera present in Europe, with 29 genera having all European species sequenced. We also calculated intra- and inter-specific genetic distances and generated a total of 52 genus trees, genetic and specimen maps for 480 species, and haplotype networks for 284 species. The dataset covers 37 European countries and 61 islands.

We found striking differences across groups in terms of DNA barcoding performance. We found high intraspecific genetic divergences and a large fraction of putative cryptic species. The general overlap between intra- and inter-specific genetic distances and the high level of barcode sharing can be due to a combination of biological factors (i.e., hybridisation, incomplete lineage sorting) and operational ones (i.e., poor taxonomy or identification errors). Genetic results allowed us to report new faunistic records, both at the European and country levels. Remarkable phylogeographic patterns in several species suggest the effect of glacial cycles in combination with the geographic framework in shaping the observed differentiation.

We provide a framework for the study of ants in Europe, which aims to facilitate future research, species discovery and conservation for this diverse and ecologically significant group.

Coalescent simulations as a tool to evaluate the effect of a Fishery Protection Zone on genetic diversity.

Noemi Pasini[1]*, Marta Bassitta[1], Joana F. Ferragut[1], M. Teresa Farriols[2], Natalia Petit-Marty[3], Sergio Ramírez-Amaro[1,2], Antonia Picornell[1]
[1] Genetics Area (HEGEN-UNICS Group), University of the Balearic Islands, Palma, Spain. [2] Spanish Institute of Oceanography, Balearic Oceanographic Centre, Palma, Spain. [3] Institute of Marine Research (IIM-CSIC), Vigo, Spain. *Presenter: noemi.pasini@uib.cat

The exploitation of fishery resources can drive evolutionary changes and lead to the erosion of genetic diversity, ultimately reducing a species' ability to adapt to environmental changes and human-induced pressures. For this reason, Marine Protected Areas (MPAs) have been increasingly implemented worldwide as tools to achieve both biodiversity conservation and sustainable fisheries management. Recently, the assessment of genetic diversity of Cytochrome C Oxidase subunit I (COI), a mitochondrial DNA marker, has proven to be a valuable indicator of the conservation status of both commercially exploited and vulnerable species. This study focuses on the Menorca Channel, declared a Site of Community Importance (SCI) in 2014 due to the presence of maërl and coralligenous beds, which are classified as Sensitive Habitats (SH) and Essential Fish Habitats (EFH). In 2016, in order to protect these habitats and associated marine resources, certain areas within the SCI were declared Fisheries Protection Zones (FPZs), where bottom trawling was banned.

The aim of this study was to evaluate the effect of FPZs on the restoration and conservation of fishery resources. To this end, we investigated the genetic diversity of the COI marker in four exploited species in Balearic fisheries: Mullus surmuletus, Serranus cabrilla, Scorpaena notata, and Octopus vulgaris. For each species, genetic diversity in FPZs populations was compared to that of populations from non-protected areas within the SCI and from an adjacent area outside the SCI (referred to as ADJ). Coalescent simulations were conducted to explore expected levels of genetic diversity under neutral evolutionary scenarios involving population bottlenecks and expansions, providing further insight into the effects of protection measures. Genetic diversity indices showed higher diversity levels in FPZs populations across all species, suggesting a better conservation status compared to those from non-protected areas. Unexpectedly, the lowest diversity levels in the three teleost species were observed in the SCI population. Results from coalescent simulations supported these findings, where genetic diversity values in protected populations aligned with those expected under population expansion scenarios, indicating a potential conservation benefit from the establishment of FPZs. On the other hand, observed genetic diversity values in non-protected populations, particularly for M. surmuletus and S. notata, were consistent with bottleneck scenarios, suggesting these populations may have undergone population reductions due to fishing pressure. This is supported by data from the Vessel Monitoring by satellite System (VMS), which indicates that following FPZs implementation, fishing effort in the Menorca Channel shifted towards nearby zones, with greater pressure in SCI than in ADJ, potentially contributing to population declines in those areas.

Population genetics of pygmy seahorse (Hippocampus bargibanti), from West Papua, Indonesia: insights from mitochondrial DNA analyses and RADsequencing.

Shantika Maylana Sastraprawira [1,2]*, Régis Hocde [3], Monica Arias [4], Kadarusman [5], Rizkie Satriya Utama [6], Indra Bayu Vimono [6], Charles Perrier [7], Laurent Pouyaud [2].

[1] Balearic Biodiversity Centre - University of the Balearic Islands, Palma, Spain. [2] Institute of Evolutionary Sciences of Montpellier - University of Montpellier, CNRS, EPHE, IRD, Montpellier, France. [3] Marine Biodiversity, Exploitation, and Conservation - University of Montpellier, CNRS, IFREMER, IRD, Montpellier, France. [4] Plant Health Institute of Montpellier - University of Montpellier, CIRAD, INRAE, Institute Agro, IRD, Montpellier, France. [5] Integrated Laboratory, PUJI Biodiversity, Sorong Maritime and Fisheries Polytechnic, Sorong City, Indonesia. [6] Research Center for Oceanography - National Research and Innovation Agency, Jakarta, Indonesia. [7] Biology for Population Management Centre - University of Montpellier, INRAE, CIRAD, IRD, Montpellier, France. *shantikamaylana@gmail.com

Pygmy seahorse (H. bargibanti) is a sessile marine fish, found exclusively in association with gorgonian genus Muricella spp. on which it displays similar colors as its host. However, it is yet unknown whether the variation among pygmy seahorse color morphs is due to plasticity on the gorgonian host or whether it is genetically determined and possibly corresponding to genetically divergent ecotypes or to variations at a few loci. This study used phylogenetic and genomic information of H. bargibanti to test putative genetic structure among different seahorse morphotypes and according to gorgonian-associated host specificity. Thirty-two samples were collected from Triton Bay (West Papua, Indonesia) from 4 different gorgon mitotypes and consisted of 4 distinct color morphotypes. Partial COI mitochondrial DNA gene was PCR amplified and obtained DNA sequences confirmed that all specimens belonged to the species H. bargibanti. Tajima's D test and measures of haplotype diversity revealed that all studied specimens of H. bargibanti are part of a single large and diverse population likely at equilibrium. Genomic results obtained from RADseq confirmed that H. bargibanti specimens originated from a single large population, by showing very little genetic distance between the individuals and a large effective population size. These results suggest high gene flow between individuals living in the same gorgon morphotypes, and in different gorgon morphotypes. Interestingly, there was no kinship across our samples. In addition, our genome scan did not find prominent gene associated with color morphs, further suggesting that color variation is rather plastic than genetic. Further research recommendation would be sampling and sequencing individuals from other populations, and ex-situ experiment to test the plasticity and kinetics of H. bargibanti color polymorphisms.

Genomic insights into salinity tolerance of Phillyrea angustifolia.

Silvia Manrique[1,2]*, Irene Martínez-García[2], Martina Deglialberti[2,3], Santiago Vilanova[2], Aureliano Bombarely[3], Mario X Ruiz-González[2]

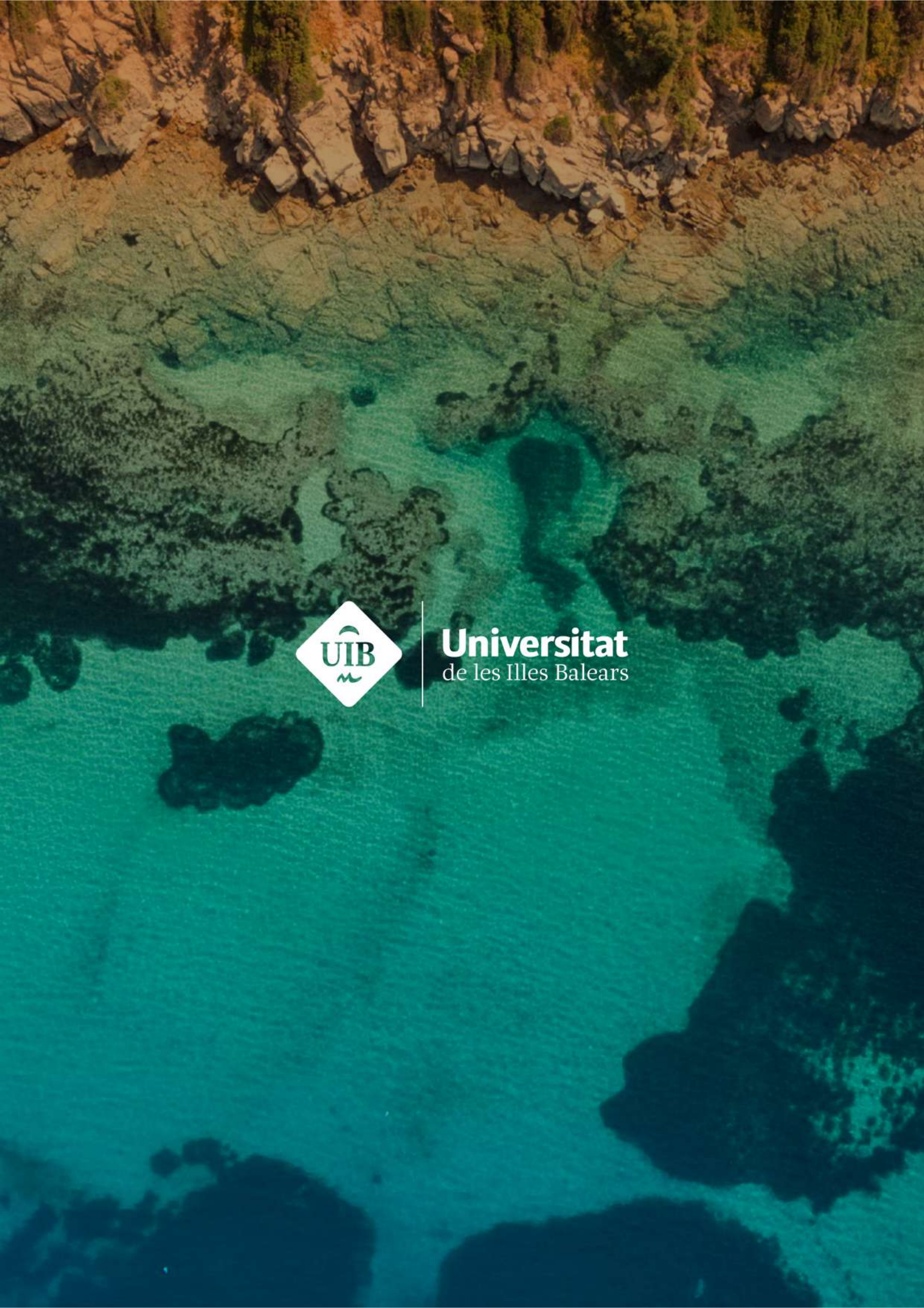
[1] Institute of Natural Resources and Agrodiversity of Salamanca (IRNASA) - Spanish National Research Council (CSIC), Salamanca, Spain. [2] University Institute for Conservation and Improvement of Valencian Agrodiversity (COMAV) - Polytechnic University of Valencia, Valencia, Spain. [3] Institute of Molecular and Cellular Biology of Plants (IBMCP-UPV) - Spanish National Research Council (CSIC), Valencia, Spain.

*Presenter: manrique.silvia@gmail.com

Phillyrea angustifolia is a species in the olive family (Oleaceae). Native to the western and central Mediterranean, it grows scattered in dense evergreen Mediterranean forests and tall shrublands. It is an androdioecious, evergreen shrub with simple, entire, leathery, dark green, opposite leaves. Flowers are small and whitish appearing at the leaf axils in spring and summer, leading to purplish-black berries in the hermaphroditic individuals.

It grows in well-preserved habitats across warm and dry areas and plays an important role in post-fire ecological dynamics. Many of the natural and semi-natural forests in which P. angustifolia grows are under decline due to climate change and centuries of intense land use, and restoration efforts are underway. In recent years, there has been a renewed interest in P. angustifolia plant production for use in general planting and restoration programs. P. angustifolia is a halotolerant species able to live in saline and non-saline environments. Its salt tolerance is based mostly in osmotic and biochemical adjustments that counteract salt-induced oxidative damage. In addition, male and hermaphroditic plants seem to display different salt-coping strategies. Male plants accumulate proline while hermaphroditic plants do not. Instead, they display a higher density of stomata.

We generated a chromosome-scale reference genome from a plant from El Saler (Valencia, Spain), encompassing around 1.5 Gb, containing 23 chromosomes and over 38K genes and a BUSCO score of 99.0% . Gene family analysis showed an enrichment in gene families related with salt tolerance when compared with other species in the Oleaceae familt, providing insights into the mechanisms sustaining salt-tolerance in this Mediterranean species.



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