NEXT GENERATION iRBiO

4t simposi

PROGRAMA

8:45 Registre i penjar pòsters

9:15 Cerimònia inaugural a càrrec de Miquel A. Arnedo

9:20 ***La revista Oryx: un pont entre ciència i societat***

9:30 Primer bloc de xerrades

Adrián Pina Hidalgo	*Phenological and spatial shifts in the migration of a pelagic seabird*
Aitor Martínez-Romero	*Identification of wasps of the family Torymidae (Hym. Chalcidoidea) emerging from the oak galls wasps of Mexico (Hym. Cynipidae)*
Ángela Palomino Gaviria	*Habitat distribution and genetic connectivity of Myliobatis aquila and Aetomylaeus bovinus in the northwestern Mediterranean: implications for conservation and management*
Inés Galán Luque	*Signs of potential loss of conserved BUSCO genes across Ctenophores*
Ashley Tejeda Meneses	*Butterflies in the city: Eco-evolutionary responses of animals to urban environments*
Maria Orriol Vernet	*Etnobotànica del Berguedà*
Ignacio Tenaguillo Arriola	*An asexual scandal! Genomic consequences of long-term asexuality in freshwater planarians*
Carlota Sánchez Campaña	*Assessing sampling efforts and completeness of aquactic Coleoptera inventories*
Caterina Marquès Gomila	*Inside a lizard's gut: Who's there and what are they doing?*
Manuel Marquerie Córdoba	*A spider on the fourth corner: Microhabitat preference and trophic guild mediate spider species sorting in a Mediterranean forest*
Guadalupe Cortés	*Temporal dynamics of weed seedbanks in organic and conventional farms: Biodiversity and management implications*

Pausa pel café + Sessió de pòsters **11:00**

Segon bloc de xerrades **12:00**

Guillermo Quevedo-Ortiz	*Flora de diatomeas de pozas desconectadas ibéricas*
Júlia Sardá Avila	*Resilience to marine heatwaves in a temperate symbiotic gorgonian*
Lucía de Uriarte López	*Molecular biodiversity of zooplankton through metabarcoding analysis and targeted population*
Mae Presas i Ferrer	*Transfer of microplastics along the coastal food webs of the southern ocean and the south western Atlantic ocean*
Claudia Amaranta Sicilia Cebrián	*The green lizards of Aiguamolls de l'Empordà: A unique Catalan population*
Biel Cassà Garcia	*The scrambled code: Unraveling massive structural rearrangements in the tunicate Oikopleura dioica*
Morena Nava	*From hidden retreats to phylogenetic trees: Resolving the evolutionary history of Iberian red devil spiders*
Nicolás Ordax Sommer	*Vultures on a schedule: Patterns in daily and seasonal foraging*
Pablo Vicent	*A comprehensive approach to integrated phenotypic evolution: Deciphering the diversification of a transcontinental lizard radiation*
Pere Amer Sureda	*Monitoratge automatitzat per comprendre i anticipar els impactes del canvi global en la funcionalitat del coral·ligen Mediterrani*
Skye Markris Brown	*Integrating acoustic telemetry and genetic connectivity for MPA management: Coastal marine predatorns in the transboundary marine protected network*

13:30 ***Stepping out of academia: failure or success?***

Entrega de premis i cloenda **13:45**

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Pòsters

Plafó		Títol
1	**Ainhoa López Rivero**	*Analyzing the impact of reference genomes on population genomics*
2	**Albert Ferré Codina**	*Avaluació dels canvis en els hàbitats al parc de la Serralada de Marina entre els anys 2010 i 2024*
3	**Alessia Cherin**	*Assessing the origin of leatherback turtles in Spanish waters through the analysis of their genome diversity*
4	**Arnau Mercadé López**	*Cartografia i cens de flora amenaçada i avaluació de l'estat de conservació dels hàbitats, dues eines fonamentals*
5	**Ashley Tejeda Meneses**	*Butterflies in the city: Eco-evolutionary responses of animals to urban environments*
6	**Biel Cassá Garcia**	*The scrambled code: Unraveling massive structural rearrangements in the tunicate Oikopleura dioica*
7	**Dídac Gómez Moreno**	*Vitibosc: Parcel·la pilot agroforestal en vinya*
8	**Fuencisla Cáceres Gala**	*Advances in ethnobotany of the Catalan linguistic area: Ongoing research and future prospects*
9	**Inés Galán Luque**	*Sings of potential loss of conserved BUSCO genes across Ctenophores*
10	**Júlia Cazorla Vila**	*El gènere Brasema (Hym. Eupelmidae) en gales de cinípids (Hym. Cynipini) en roures mexicans*
11	**Mae Presas i Ferrer**	*Transfer of microplastics along the coastal fodd webs of the southern ocean and the south western Atlantic ocean*
12	**María Morán Saiz**	*Genetic regulation of sexually dimorphic pigmentation in Cloeon dipterum*
13	**Maria Orriols Vernet**	*Anàlisi d'un receptari manuscrit de remeis a base de plantes procedents de Castellar de n'Hug (Berguedà, Catalunya)*

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Organitzadors

Aitana Merino Refoyo

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Liam Junkin Royo

Marta Olivé Muñiz

Silvia García Juan

Vadim Pisarenco

Víctor Cuesta Porta

Presentació Oral

Phenological and spatial shifts in the migration of a pelagic seabird

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Abstract. Determining migration routes and wintering areas of pelagic seabirds is essential for their conservation, especially under rapid environmental change. However, how pelagic species shift their movements and phenology remains poorly understood. Light-level geolocators (GLS) now enable tracking of seabirds throughout their full annual cycle, providing key long-term data on individual behaviour.

This study aimed to describe phenological and spatial traits of migration related to year and sex, and to assess changes in migratory timing and wintering distribution over the last decade. Our focal species, the Manx shearwater, is a long-lived pelagic seabird breeding on North Atlantic islands from May to August–September and wintering in the South Atlantic from November to February, performing a trans-equatorial migration. We tracked 39 individuals from Heimaey, Iceland using GLS devices deployed between 2006 and 2023.

Over the study period, birds reduced the duration of their northward migration from wintering grounds by an average of 11 days, which may explain the slight advance in arrival at the breeding colony. Most other phenological variables showed no clear temporal trend. Sex-related differences were evident: males spent less time in post-breeding migration and at wintering areas, departing and arriving earlier than females. Spatially, birds exhibited a gradual northward displacement of their wintering distribution, contrasting with other seabirds that often shift poleward to maintain favourable conditions.

Overall, phenological and spatial data suggest a consistent—though stronger spatial than temporal—shift over the years. Manx shearwaters may be adjusting their wintering areas and advancing migratory events in response to external pressures affecting their annual cycle. Determining whether these changes are driven by climatic or oceanographic factors is a crucial next step toward understanding how this species and seabirds more broadly respond to accelerating global change.

Keywords: Migration phenology, Migratory patterns, Shearwater, Light-level geolocation, Climate change.

Identification of wasps of the family Torymidae (Hym. Chalcidoidea) emerging from the oak galls wasps of Mexico (Hym. Cynipidae)

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Abstract. The species of the family Torymidae (Hymenoptera: Chalcidoidea) that emerge from the galls of Cynipidae (Hymenoptera) and Cecidomyiidae (Diptera) are ectoparasitoids of the last larval stage (Grissell 1997; Hanson 2006). Gall wasps (Cynipidae) are phytophagous that induce the growth of galls, abnormal structures in plant tissues, to complete their life cycle, especially in Quercus spp (Fagaceae). Torimidae and other families of the superfamily Chalcidoidea play an important role in the biological control of their populations, preventing overpopulation of oak wasps from causing damage to their host plants. The genus Torymus (Torymidae) is widely distributed, mostly in the regions of the northern hemisphere. Among the studies carried out in the Nearctic region, Grissell's review published in 1976 systematically divided the species of the genus into five groups of species by morphologically similar taxa: advenus, bedeguaris, fullawayi, tubicola and varians. The main morphological characteristics that allow distinguishing and identifying the different species groups present in the Mexican territory are presented. This study is also a first contact with an upcoming catalogue that would list all the Torymidae species that have so far been identified as Cynipini parasitoids, and those that are currently being analysed and that could also constitute new species for science, some of them being the first records of oak gall wasp parasitoids in North America.

Keywords: Chalcidoidea, Torymidae, Cynipidae, Nearctic, Parasitoids, Species Groups.

Presentació Oral

Habitat distribution and genetic connectivity of *Myliobatis aquila* and *Aetomylaeus bovinus* in the northwestern Mediterranean: Implications for conservation and management

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Abstract. This study will integrate acoustic telemetry, population genomics, and fisheries data to study the distribution, habitat use, and connectivity of the common eagle ray (Myliobatis aquila) and the duckbill eagle ray (Aetomylaeus bovinus) in the western Mediterranean. Using a multidisciplinary approach, we aim to identify critical habitats, potential migratory movements and unravel the genetic structure of regional subpopulations.

Acoustic telemetry will provide fine-scale insights into movement dynamics and residency patterns, particularly in the Gulf of Lion and along the Catalan coast, while genomic analysis using SNPs will provide detailed information on genetic diversity, gene flow, and kinship within aggregation sites. Tissue samples will be obtained during scientific surveys and through active collaboration with artisanal fishers, incorporating local ecological knowledge to strengthen conservation strategies.

The importance of this study lies in the marked decline of both species, recently categorized as “Critically Endangered” by the IUCN, and in the lack of information on their ecology in the northwestern Mediterranean. This holistic approach will contribute to understanding the ecological processes that determine the resilience of these eagle rays in a context of global change and will provide essential scientific guidance for their long-term protection.

Keywords: Myliobatiformes, distribution, connectivity, population genetics, conservation.

Presentació Oral

Butterflies in the city: Eco-evolutionary responses of animals to urban environments

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Abstract. Urbanisation is one of the major Human-Induced Rapid Environmental Changes (HIREC), creating novel conditions that species have not experienced in their evolutionary history. These changes often lead to biodiversity loss, reduced population fitness and community homogenization, mainly through habitat transformation, pollution and fragmentation. Yet, many species persist—and sometimes thrive—in such disturbed environments.

Butterflies are an excellent system for studying the mechanisms underlying adaptation to urban environments. They are well-documented, respond rapidly to environmental change and are widely recognized as indicators of biodiversity, making them ideal for identifying ecological patterns across spatial and temporal scales.

Although numerous studies have analysed how urbanisation intensity affects butterfly diversity and abundance, their findings often diverge or show no consistent trends. To improve our understanding, my research examines interspecific and intraspecific phenotypic variation in relation to morphology, thermoregulatory ability and functional ecological space along urbanisation gradients.

To do this, I combine multiple data sources, including museum specimens, citizen-science datasets from European butterfly monitoring schemes, and field measurements from populations in Barcelona. These data are analysed using models such as generalized linear mixed models (GLMM) and generalized additive models (GAM).

Although this is still work in progress, preliminary results indicate that wing size has shifted over time in response to increasing urbanisation, with species showing both increases and decreases depending on their ecological traits. Notably, species with higher mobility appear more prone to urbanisation-driven wing size changes. Additionally, while thermal buffering ability is greater in urban communities overall, this pattern does not necessarily hold at the species level.

Keywords: urbanisation, body size, thermoregulation, functional diversity.

Presentació Oral

The scrambled code: Unraveling massive structural rearrangements in the tunicate *Oikopleura dioica*

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Abstract. The planktonic tunicate Oikopleura dioica is a pivotal component of marine food webs and global carbon cycle. Beyond its ecological significance, O. dioica is a key model for Evo-Devo studies due to its compacted genome and rapid evolution. A defining feature of its genomic architecture is the presence of massive scrambling events when comparing geographically distinct populations such as Osaka, Okinawa, Barcelona, and Bergen. However, to analyze the biological impact of these rearrangements and breakpoints, a proper distinction between biological signals and technical assembly artefacts is needed.

We employed long-read genomic sequences to systematically validate massive structural variations identified by whole-genome pairwise alignments. We implemented a custom pipeline to rigorously distinguish true rearrangements from potential assembly errors by mapping raw sequencing reads back to the assembled genomes and inspecting the read depth and sequence discordance at candidate breakpoint sites.

Our investigation focused on a haplotype-resolved assembly of an individual from the Barcelona population. We reveal that massive rearrangements are not limited to comparisons between individuals; significantly, extensive structural variations, including large-scale inversions, exist between the two haplotypes of a single individual. We identified inversion breakpoints that localize within protein-coding loci. We designate these disrupted genes as "BreaKO" candidates, as their sequences span both sides of the rearrangement boundaries, resulting in the physical breakage of the coding sequences in one haplotype.

These findings imply a direct link between macrosyntenic rearrangements and gene integrity. We hypothesize that this high level of genomic scrambling serves as a reservoir for structural diversity, potentially facilitating rapid adaptation to fluctuating environments by creating novel regulatory landscapes or modifying gene dosage. While "BreaKO" events suggest a cost to this plasticity, they may also act as functional "switches", rapidly altering phenotype in response to environmental pressures without the need for slow sequence evolution.

Keywords: Oikopleura dioica, genomic scrambling, chromosomal inversion, gene disruption, adaptation.

Presentació Oral

Assessing sampling efforts and completeness of aquatic Coleoptera inventories

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Abstract. The Mediterranean Basin is considered a global biodiversity hotspot that is currently under threat. In particular, aquatic insects are exposed to multiple stressors affecting freshwater ecosystems, including drying, water pollution, and habitat fragmentation. These insects play a key role in maintaining the ecological functioning of freshwater ecosystems, highlighting the need for a deep understanding of their diversity and distribution to implement effective conservation measures. Within the Mediterranean Basin, the Iberian Peninsula harbours approximately 35% of Europe's endemic aquatic Coleoptera, but we still lack complete information on the distribution of these species. This study has two main objectives: (1) to assess the completeness of aquatic Coleoptera inventories, and (2) to identify the Species Distribution Model (SDM) that best fits the distribution of these species. We calculated the inventories' completeness at 5-minute resolution and modelled the distributions of 497 species using two SDMs (MaxEnt and Niche of Occurrence). Our preliminary results indicate that the western region of the Iberian Peninsula needs additional sampling campaigns. Model performance varied even among congeneric species; for example, the distribution Agabus biguttatus was best captured by MaxEnt, whereas Agabus brunneus was better explained by the Niche of Occurrence model. Although preliminary, these findings highlight the importance of having comprehensive and accurate information as a foundation for any effective conservation strategy.

Keywords: Coleoptera, Conservation, Biodiversity inventories, SDM.

Presentació Oral

Inside a lizard’s gut: Who’s there and what are they doing?

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Abstract. Insular populations of terrestrial vertebrates often experience resource scarcity and strong seasonal fluctuations, conditions that demand adaptations for efficient use of trophic resources and the ability to adjust to rapid changes in their availability. Gut microbes are emerging as key mediators of these processes, influencing how animals digest and metabolize food. However, how these microbes contribute to host trophic and metabolic adaptation remains poorly understood.

In this study, we investigate the functional role of the gut microbiota in local adaptation across multiple populations of the endemic Balearic lizard Podarcis lilfordi. Using shotgun metagenomic sequencing of fecal samples, we characterized the functional potential of their gut microbial communities. By annotating microbial genes and their associated metabolic pathways, we identified major microbial functions and assessed their variation across populations and seasons. Additionally, with the reconstruction of metagenome-assembled genomes (MAGs) we identified the main bacterial contributors to essential metabolic processes.

By integrating taxonomic and functional metagenomic data with lizards’ ecological information, this study aims to reveal how gut microbes shape metabolic flexibility and trophic adaptation under resource-limited conditions, providing insights into host–microbe coevolution in insular ecosystems.

Keywords: Gut microbiota, Functional metagenomics, Metagenome-assembled genomes (MAGs), Island ecology, Host–microbe interactions.

Presentació Oral

The green lizards of Aiguamolls de l'Empordà: A unique Catalan population

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Abstract. The European green lizard (Lacerta bilineata) is widely distributed across Europe, reaching the southern edge of its range in northern Spain. In the Parc Natural dels Aiguamolls de l'Empordà (PNAE), a unique and isolated population persists, remaining disconnected from the main distribution. Our project aims to characterize this population through extensive fieldwork across different areas of the PNAE. We are estimating population size, describing activity patterns, and quantifying habitat use and spatial domain. During field sampling, each captured individual is measured for morphological traits, body temperature, and photographed to obtain head-shape data using geometric morphometrics.

In parallel, we are conducting a series of laboratory experiments to examine how different phenotypic traits are integrated. These include thermal-gradient trials to generate preferred temperature curves, locomotion assays to determine maximum sprint speed, bite-force measurements as indicators of functional performance, and respirometry assays to estimate basal metabolic rate. Together, these datasets allow us to investigate correlations among thermal, morphological, behavioral, and physiological traits, ultimately revealing how trait complexes are coordinated within individuals.

Therefore, our work not only aims to improve understanding of this isolated population and provide the park with valuable data on one of its species, but also to study in detail how multiple traits are integrated at the individual level, offering insight into the functional organization of phenotypes in natural populations.

Keywords: Phenotypic integration; habitat use; activity patterns; thermal ecology; Lacerta bilineata.

Presentació Oral

Temporal dynamics of weed seedbanks in organic and conventional farms: Biodiversity and management implications

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Abstract. Long-term dynamics of weed seedbanks are critical for sustainable weed management and agroecosystem biodiversity. We evaluated 15-year changes (2008–2023) in weed seedbank richness and abundance across 12 paired organic and conventional arable fields in central Catalonia, Spain. At each site, soil samples were collected from field edges and centers, germinated in greenhouse trays under natural light for 13 months, and assessed for germinable seed density and species composition.

Organic fields consistently harbored higher observed species richness (gamma diversity): 141 species in 2008 versus 123 in conventional fields, rising to 150 by 2023 while conventional fields declined to 116. Chao1 estimators supported this trend, confirming a significant and persistent advantage for organic systems in maintaining weed diversity. In 2008, organic fields also showed greater alpha diversity (20.5 ± 2.6 species per field) and seed abundance (1125 seedlings m□^{2} ± 194 SE) than conventional fields (14.7 ± 1.8 species; 384 ± 115 seedlings m□^{2}). By 2023, seed abundance increased in both systems, yet species richness per field did not rise proportionally—particularly in conventional fields—indicating community homogenization under intensive management. A significant year × management interaction revealed a more moderate increase in seed abundance in organic systems.

In both years and across management types, field edges consistently supported higher species richness than field centers, highlighting the importance of edge habitats for weed diversity. These findings demonstrate that organic farming not only sustains but enhances weed species richness over time, whereas conventional farming leads to a decline in richness. Notably, conventional fields did not show a proportional decline in seed abundance despite reduced species numbers, indicating that conventional practices shape seedbank communities in ways that reduce diversity without necessarily suppressing overall seed density. Organic systems thereby maintain higher biodiversity while remaining effective in weed regulation.

Keywords: Farming practices, organic farming, conventional farming, biodiversity, weed seed bank.

Presentació Oral

Flora de diatomeas de pozas desconectadas ibéricas

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Abstract. Las pozas desconectadas son hábitats de transición que se forman como consecuencia de la pérdida de flujo de agua superficial en los ríos temporales. Se consideran zonas de refugio para la biodiversidad acuática durante los periodos de sequía, y pueden albergar comunidades altamente adaptadas (mediante estrategias de resistencia y resiliencia). Entre 2023 y 2024 se realizó un estudio florístico de diatomeas en pozas desconectadas de la zona mediterránea de la Península Ibérica. El análisis mediante diferentes técnicas de microscopía permitió identificar un total de 385 especies, incluyendo nuevas citas para Cataluña y el resto de la Península Ibérica. Además, muchas de ellas presentaron rasgos de adaptación probablemente ventajosos en pozas (p. ej., tamaño pequeño, carácter pionero, movilidad, etc.). Estos resultados confirman la importancia de las pozas desconectadas en los ecosistemas mediterráneos y destacan la necesidad de conservar y gestionar adecuadamente estos hábitats, a menudo olvidados por la legislación ambiental.

Keywords: Diatomeas, Flora, Península Ibérica, Pozas desconectadas, Zona Mediterránea.

Presentació Oral

An asexual scandal! Genomic consequences of long-term asexuality in freshwater planarians

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Abstract. Long-term asexuality has been considered an evolutionary dead-end, due to reduced genetic diversity and weakened purifying selection, as deleterious mutations cannot be purged through recombination, the known Muller's ratchet. As such, it is expected that asexual individuals from the same population should be clonal presenting low levels of genetic diversity. Freshwater planarians of the genus Dugesia can reproduce sexually or asexually by fission, meaning that an individual divides itself into two bodies that fully regenerate. In a recent biogeographic study of the genus, asexual populations of the Iberian-Apennines-Alps clade (conformed by D. etrusca, D. liguriensis and D. ilvana) showed an unusual phylogenetic pattern, which was associated with long-term asexuality. This hypothesis was tested through an extensive workflow, showing that this pattern was not a methodological artifact, but a genetic footprint of ancient asexuality, and these asexual populations were proposed as a new asexual scandal, being the first not presenting parthenogenetic asexuality but agametic, which implies the inheritance of somatic mutations.

To investigate this at a genomic level, we obtained chromosome-level genome assemblies for sexual representatives of D. etrusca and D. liguriensis, and SNP data was generated by mapping transcriptome reads from sexual and asexual populations to both genomes. Multidimensional scaling plots revealed higher divergence at intrapopulation level among asexuals. Interestingly, at intraindividual level, heterozygosity was higher in asexual than in sexual individuals. High heterozygosity values correspond with a high intraindividual allele divergence, which is known as the Meselson effect, a strong signal of ancient asexuality. We will also discuss potential research lines we plan to analyze to understand the genomic consequences of ancient asexuality this asexual scandal.

Keywords: Heterozygosity, Meselson effect, ancient asexuality, Dugesia.

Presentació Oral

Signs of potential loss of conserved BUSCO genes across Ctenophores

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Abstract. Ctenophores or comb jellies comprise around 200 described species and represent a key early- branching metazoan lineage whose evolutionary history remains actively debated. Clarifying their phylogenomic position is essential for understanding the origin of major animal traits such as neurons and muscles. While analyzing our newly generated dataset to address these questions, preliminary BUSCO assessments revealed an unexpectedly high proportion of genes reported as missing. The aim of this work is to determine whether these apparent absences reflect true evolutionary loss or instead result from extreme divergence that prevents their detection by conventional homology tools.

To address this, we ran BUSCO across all available datasets and generated presence-absence matrices to identify recurring patterns of gene loss. A subset of outlier assemblies showed unusually high numbers of conserved genes due to contamination and were therefore cleaned or excluded. Across the curated dataset, we identified approximately 60 BUSCO genes (~9%) that are consistently absent and conducted functional annotation to assess their associated COG categories. Preliminary results suggest that part of the missing signal reflects genuine evolutionary loss, whereas other cases may stem from incomplete assemblies or high sequence divergence. Distinguishing between these scenarios is crucial for interpreting ctenophore genome evolution and understanding how core cellular functions have been shaped in this lineage. Building on these findings, our ongoing work applies more sensitive homology detection approaches to examine functional patterns among the potentially missing genes. Ultimately, this project aims to better characterize the putatively unique genomic features of Ctenophora and assess how these may set the lineage apart from other early-diverging metazoans.

Keywords: Ctenophora, BUSCO, gene loss, genome evolution.

Presentació Oral

Resilience to marine heatwaves in a temperate symbiotic gorgonian

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Abstract. Marine heatwaves (MHWs) are increasingly impacting Mediterranean coralligenous communities, leading to mass mortality events and threatening the persistence of many habitat-forming species and their associate biodiversity. This study focuses on the temperate symbiotic gorgonian Eunicella singularis to investigate how contrasting thermal regimes, variations in nutrient and food availability and differing irradiance conditions influence its resilience to MHWs. We hypothesize that higher nutrient and/or food availability and lower irradiance conditions can help mixotrophic gorgonians to withstand thermal stress and enhance recovery mechanisms. Across different populations in the western Mediterranean basin (Catalonia, Sardinia and Sicily), we combined field observations with laboratory experiments to assess biological responses including demographic data, presence and abundance of symbiotic algae and chlorophyll content, as well as respiration and photosynthesis. Symbiont abundance and chlorophyll content were quantified and compared seasonally to examine how variation may relate to temperature, light, nutrients and local environmental conditions. We also measured respiration and photosynthesis rates during summer through individual chamber incubations and diving- PAM fluorometry. All these results, together with the demographic and reproductive data, allowed us to understand both biotic and abiotic drivers of resilience, and to assess the potential role of mixotrophy in modulating the resistance of E. singularis to MHWs, under different thermal, nutrient and food regimes. This study contributes to the understanding of the environmental and physiological mechanisms that determine coral resilience to the ongoing global change.

Keywords: Marine Ecology, Symbiosis, Corals, Global Change, Ecophysiology.

Presentació Oral

Molecular biodiversity of zooplankton through metabarcoding analysis and targeted population genomics

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Abstract. This study addresses the need for efficient and accurate methods to characterize zooplankton biodiversity in the Western Mediterranean, a system of major relevance to marine ecosystems but still insufficiently studied. The main objective is to develop and apply advanced molecular techniques to monitor the taxonomic and genetic diversity of zooplankton and to characterize benthic populations from their larval stages. To this end, two complementary approaches will be employed: (1) optimized metabarcoding using high-resolution markers such as COI, which will enable species identification and assessment of intra-species genetic variability, and (2) “Targeted Population Genomics,” an innovative methodology based on the analysis of eDNA from meroplanktonic larvae. This second technique will be applied specifically to four benthic species of ecological interest: the sea urchins Paracentrotus lividus and Arbacia lixula, and the holothurians Holothuria tubulosa and Holothuria mammata. Zooplankton samples will be collected monthlyover at least two years at two sites along the Catalan coast. We will design species-specific SNP panels, leveraging on the whole genomes already available for these four species, and through multiplex PCRs, high-throughput sequencing, and bioinformatic analyses, we aim to estimate allele frequencies and patterns of genetic differentiation between sites. The results will provide a unique dataset on intraspecific diversity for multiple species and establish baselines for long-term genetic monitoring, while also assessing the potential of meta-phylogeography as an emerging tool. This non-invasive approach represents a sustainable alternative to traditional methods and will enable the evaluation of the conservation status and the design of affordable monitoring plans for marine ecosystems.

Keywords: Zooplankton biodiversity, Metabarcoding, Environmental DNA (eDNA), Population genomics, Meta-phylogeography.

Presentació Oral

Transfer of microplastics along the coastal food webs of the southern ocean and the south western Atlantic Ocean

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Abstract. Marine fauna may ingest microplastics (MPs) directly from the environment, mistaking them for food, or indirectly through trophic transfer of contaminated prey. Although MP presence at the individual level is widely reported, their transfer along marine food webs remains poorly understood. This study aims to assess the transfer of MPs within benthic and pelagic coastal food webs in the Southern Ocean and the Southwestern Atlantic Ocean. Samples were collected from a temperate and a sub-Antarctic area in the Southwestern Atlantic, and from the Antarctic Peninsula during the austral summer of 2024–2025. These coastal food webs share a wasp-waist structure, in which the abundance of pelagic primary producers and consumers at higher trophic levels is controlled by consumers at intermediate trophic levels, enabling comparable sampling across regions. Environmental compartments (water and sediment), prey species (digestive contents of fish, squid, and krill) and predators (scats from seals and penguins) were collected in all areas. MPs were identified and categorized using light microscopy, and stable carbon and nitrogen isotope ratios were analyzed in predator scats containing MPs to assess trophic pathways. Results from Golfo San Jorge (Argentina) indicate that sediment was the most contaminated compartment (650 MPs/L), with concentrations 77 times higher than in water (8.34 MPs/L). The epibenthic detritivore Munida gregaria showed the highest MP concentration in gut contents (0.8 MPs/g), whereas the demersal carnivore Patagonotothen ramsayi exhibited the lowest burden (0.04 MPs/g). Pelagic carnivores Engraulis anchoita (0.6 MPs/g) and Loligo gahi (0.35 MPs/g) were in between. These results suggest that epibenthic detritivores are the most polluted species. Preliminary results suggest that the pelagic predators Spheniscus magellanicus and Arctocephalus australis had the highest MP concentration in scats (0.43 and 0.209 MP/g), whereas the benthic predator Otaria flavescens showed the lowest concentrations (0.099 MP/g).

Keywords: microplastics, trophic transfer, stable isotopes, marine pollution, Southwestern Atlantic Ocean, coastal food webs

Presentació Oral

A spider on the fourth corner: Microhabitat preference and trophic guild mediate spider sorting in a Mediterranean forest

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Abstract. In a time of biodiversity crisis, it is key to capture and predict its patterns to halt and prevent further decline. Nevertheless, attention should be paid not only to species richness, but to functional diversity loss as well. The composition of functional traits in a community can preserve signatures of assembly mechanisms such as species sorting. For instance, the magnitude of environmental filtering determines the variability and composition of traits in each community under a given environmental condition. Here, we aim to test whether the spider community functional diversity is driven by the heterogeneity of the habitat, and whether species with different trait compositions inhabit structurally different forests.

To understand if habitat heterogeneity drives the functional diversity of spider communities, we estimated the functional alpha-diversity of 10 forest plots in PN Sant Llorenç del Munt and calculated linear models for habitat heterogeneity, climatic and topographic distances. To explore the differences in functional composition between forests, we used an RLQ 4th corner analysis.

While habitat heterogeneity was not the main driver behind the patterns of functional diversity, the structure of the habitat was a significant predictor. The 4th corner analysis showed a positive relationship between the heterogeneity of the understory with ground-dwelling active hunters, whereas habitats characterized by bare ground and rocks were associated with vegetation-dwelling, high dispersal, and web weaving.

Both the heterogeneity of the habitat and the vegetation cover drive spider functional diversity at local spatial scales. Higher shelter and shading provided by a more complex understory benefit ground-dwelling active hunters. Moreover, a more complex tridimensional space available in habitats characterized by bare ground is positive for web weavers and good dispersers. Hence, the functional diversity of spiders varies associated with a gradient of habitat structure and heterogeneity. Efforts to preserve diversity should be focused also on preserving habitat integrity.

Keywords: Araneae, Functional diversity, Functional Traits, Community Ecology, Habitat heterogeneity.

Presentació Oral

Ethnobotany of the Berguedà district

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Abstract. Ethnobotany is the science that studies the relationship between people and plants (Harshberger, 1896). Ethnobotanists collect and preserve the traditional knowledge the elderly people have about how plants have been used through the ages with medicinal, food or other purposes. This information has generally passed orally from one generation to another without ever being written down, which makes the role of ethnobotanists clue to preserve this valuable heritage.

An ethnobotanical prospection is currently being conducted by the ethnobotanical research group of the University of Barcelona in the Berguedà district, a region in Central Catalonia, whose northern part belongs to the Catalan Pre-Pyrenees while the southern part lies in the Catalan Central Depression. This fact translates in a diverse relief of the landscape and climate conditions, which allows a wide diversity of flora to be grown in the region. When finished, this prospection will represent a noticeable contribution to the ethnobotany of the Catalan Countries.

In addition to preserve the cultural and immaterial heritage all this traditional knowledge represents, other purposes of the ethnobotanical prospection are analysing the medicinal properties people attributed to plants more deeply in order to develop new drugs or studying the viability of cultivating species that could lead us to a more sustainable food system.

Keywords: Ethnobotany, Berguedà, traditional knowledge, prospection, Catalan Countries.

Presentació Oral

From hidden retreats to phylogenetic trees: Resolving the evolutionary history of Iberian red devil spiders

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Abstract. The red devil spider genus Dysdera Latreille, 1804, is the most species-rich genus in the family Dysderidae, with 337 species, half of the currently described species. It includes ground-dwelling, nocturnal hunters with a Western Palearctic distribution, mainly limited to the circum-Mediterranean region and Macaronesian archipelagos, with at least one synanthropic species found worldwide. We present preliminary results of a multilocus phylogeny based on mitochondrial (COX1) and nuclear (18S) markers, covering 46 of the 52 Dysdera species known from the Iberian Peninsula. Additionally, we describe six new species and a species complex, broadening our understanding of the group's hidden diversity. Most specimens of the new species described were collected during extensive fieldwork following optimized protocols, highlighting the importance of standardized sampling to improve biodiversity assessments and systematic resolution. This study provides a comprehensive molecular framework for Dysdera in the Iberian Peninsula and offers insights into its evolutionary history and diversification patterns.

Keywords: Multilocus phylogeny, Dysdera, Hidden diversity, Iberian Peninsula, Standardized sampling

Presentació Oral

Vultures on a schedule: Patterns in daily and seasonal foraging

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Abstract. Vultures have long relied on patchy and unpredictable food resources like carcasses but nowadays forage in landscapes where human activity creates reliable feeding opportunities, both in time and space. I examined how Eurasian griffon vultures are attracted by these predictable food sources such as landfills or feeding stations, and how time shapes this attraction.

Using high-resolution GPS data from 51 individuals tracked for up to three years, I applied Step Selection Functions (SSFs) to assess how movement decisions depend on the distance to predictable food sources on a daily and seasonal scale. By incorporating time of day and Julian date, the models capture both daily rhythms and broad seasonal trends, offering a detailed view of how foraging behaviour shifts over time. This allowed me to explore when vultures are most likely to approach predictable food, how this behaviour changes across the annual cycle, and how consistent these patterns are across individuals.

These analyses provide a framework for understanding how a species adapted to variable food landscapes incorporates predictable, human-derived resources into its movement decisions, and offer insight into the behavioural flexibility of large avian scavengers in human-dominated environments.

Keywords: Foraging, Vultures, Resource predictability, Step Selection Functions, Movement.

Presentació Oral

A comprehensive approach to integrated phenotypic evolution: Deciphering the diversification of a transcontinental lizard radiation

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Abstract. Understanding how morphology, performance, and ecological factors interact is key to revealing the evolutionary processes shaping biodiversity. In this study, we investigate head and limb morphology, body size, and bite force in lacertid lizards, integrating geometric morphometrics, phylogenetic comparative methods, and allometric modeling. Our work is structured around three main themes: (1) the evolution of shape in relation to structural habitat, (2) patterns of body size diversification, and (3) the form–function relationship between head morphology and bite performance across biological scales. By examining these integrated phenotypes, we aim to uncover how ecological pressures and size constraints drive morphological evolution, influence functional performance, and shape diversification dynamics, providing insight into how species may respond to future environmental changes.

Key words: phenotypic evolution, phylogenetic comparative methods, functional performance, statistics.

Presentació Oral

Monitoratge automatitzat per comprendre i anticipar els impactes del canvi global en la funcionalitat del coral·ligen Mediterrani

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Abstract. El canvi global està erosionant la vida a la Terra a un ritme i escala sense precedents. La forta acceleració de la pèrdua de biodiversitat durant les dues últimes dècades, combinada amb l'augment de la dinàmica de pertorbacions i l'efecte del canvi climàtic, ha compromès la integritat dels ecosistemes, disminuint-ne la resiliència, la funcionalitat i apropant-los al col·lapse. Al mar Mediterrani, l'augment en la freqüència, intensitat i extensió de les onades de calor marines, i la seva interacció amb factors d'estrès antropogènics locals, està reorganitzant els ecosistemes marins. Un dels hàbitats mediterranis més afectats pel canvi climàtic és el coral·ligen, un ecosistema singular que alberga aproximadament un 10% de la biodiversitat d'aquest mar.

El ritme actual i el gran abast del canvi global han superat la nostra capacitat de mesurar, monitorar i predir les tendències de biodiversitat, limitant els esforços per aturar-ne la pèrdua. En concret, les metodologies actuals d'anàlisi d'imatges són manuals, basades en experts, cosa que fa que el procés sigui lent i difícil d'escalar, amb un enfocament taxonòmic que no captura adequadament les respostes funcionals dels organismes davant les pertorbacions. Basant-nos en algoritmes de deep learning generalistes, hem desenvolupat una IA per analitzar fotoquadrats de fons de coral·ligen mediterrani que ha estat entrenada amb 191 imatges i 5.213 polígons segmentats i classificats en 62 classes. Aquesta IA ens permet automatitzar la segmentació i identificació d'organismes, facilitant l'extracció d'informació funcional a gran escala i amb alta resolució temporal.

La implementació d'aquest algoritme representa un pas essencial cap a un monitoratge automatitzat, orientat a comprendre i anticipar els impactes del canvi global en la biodiversitat i la funcionalitat del coral·ligen. Aquest enfocament amplia l'abast i la resolució dels seguiments de biodiversitat, fet indispensable per avançar-nos a possibles col·lapses ecològics i millorar l'eficàcia de les estratègies de conservació.

Keywords: Coral·ligen, Canvi global, Deep learning, Pèrdua de biodiversitat, Ecologia funcional, Seguiment de biodiversitat.

Presentació Oral

Integrating acoustic telemetry and genetic connectivity for MPA management: Coastal marine predators in a transboundary marine protected network

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Abstract. Marine Protected Areas (MPAs) are a widely used conservation tool yet their effectiveness for highly mobile fish species remains uncertain. Understanding how coastal predators use and connect different habitats throughout their life cycle across protected and non-protected areas, and the genetic connectivity of their populations, is essential for informing adaptive spatial management and transboundary governance in the Mediterranean Sea.

This study integrates acoustic telemetry and population genetics to assess movement patterns and connectivity of three large marine predatory fish species: Lichia amia, Pomatomus saltatrix, and Seriola dumerili. To date, 10 L. amia and 14 P. saltatrix and 19 S. dumerili have been tagged between Gulf de Pals and Gulf de Roses in Southern Catalunya. Additionally, in the more southern Delta de Ebre, 8 L. amia, 2 P. saltatrix, and 4 S. dumerili were tagged. The reciever arrays for this study extend from the south of the Delta de Ebre, Spain to Marseille, France and include MPAs harbors, river-influenced systems, and other anthropogenized habitats, allowing evaluation of habitat use across protection levels. Concurrently, genetic samples are being collected from 3-5 sites in the Mediterranean to quantify population connectivity and assess whether individuals moving between regions originate from a shared genetic population.

By integrating individual movement with population-level genetic connectivity, this study provides a framework to inform adaptive conservation planning and governance strategies that consider the ecology of highly mobile species in a rapidly changing Mediterranean seascape.

Keywords: acoustic telemetry, marine protected areas, movement ecology, population connectivity, Mediterranean Sea.

Pòster

Analyzing the impact of reference genomes on population genomics

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Abstract. Conservation genomic studies in non-model organisms often rely on reduced representation sequencing methods, such as Genotyping-by-Sequencing (GBS), which do not require a reference genome. However, understanding the advantages and limitations of using reference genomes is essential to evaluate their impact on population genomic studies. To assess this, we analyzed published GBS data from two marine ecosystem engineers, the sea urchins Paracentrotus lividus and Arbacia lixula. We used two different approaches: a) a de novo pipeline for population structure inference, followed by mapping to the Strongylocentrotus purpuratus genome for functional annotation; and b) a reference-based pipeline using the recently published genomes for both species, including mapping, genotyping, population structure analysis, and functional characterization. Both approaches recovered consistent population structure. However, the use of species-specific reference genomes for genotyping resulted in higher population differentiation and lower inferred inbreeding coefficients. Mapping efficiency for haplotype loci, obtained through de novo strategy, was also markedly different, as fewer than 10% of loci aligned to the S. purpuratus genome, while approximately 95% of haplotype loci mapped to the respective species-specific genomes. In both approaches, haplotype loci were enriched in exonic regions, reflecting the GC content bias of the restriction enzyme used reported in previous studies. Nevertheless, functional annotation of candidate SNPs loci remained limited in both approaches due to the sparse and biased functional information available across poorly studied taxa. Our findings highlight the robustness of de novo GBS approaches for population structure inference in non-model species, while also demonstrating the added value of reference genomes for improving genomic resolution. However, they also underscore the limited functional interpretability of candidate loci in some taxa, which should be addressed in future studies.

Keywords: GBS, reference genome, de novo, population genomics, functional analysis.

Pòster

Avaluació dels canvis en els hàbitats al parc de la Serralada de Marina entre els anys 2010 i 2024

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Abstract. L'any 2010, el parc de la Serralada de Marina va ser un dels primers espais naturals de Catalunya on es va completar una cartografia dels hàbitats CORINE de detall (escala 1:10.000). L'any 2024, a fi de disposar d'informació actualitzada com a eina clau per a la gestió del parc natural, es va dur a terme l'actualització de la versió de 2010. A partir de la fotointerpretació de les ortoimatges més recents, es van revisar tots els polígons de la cartografia de 2010 i se'n van modificar els contorns o delimitar de nous en aquells casos en què s'observaven canvis de composició o estructura en els hàbitats, i es van revisitar sobre el terreny sempre que era necessari. Un cop l'actualització completada, es van sobreposar les dues cartografies, es va fer una selecció de totes les àrees en què els hàbitats no eren coincidents entre les dues versions, i se'n va identificar la causa de canvi.

En conjunt, en 14 anys un 21% de l'espai natural ha experimentat modificacions en la composició dels hàbitats. Les zones de canvi estan repartides per tot el territori, però hi ha una certa tendència a trobar-se amb més freqüència als llocs més antropitzats (zones urbanitzades, zones agrícoles...) o bé en zones que havien rebut més impactes en el passat (àrees cremades, talades...). Globalment, ha incrementat la superfície dels boscos esclerofil·les (en unes 175 ha) i aciculifolis (36 ha), i dels camps abandonats, ermots i àrees ruderals (33 ha), mentre que han perdut superfície els prats tant basòfils com acidòfils (88 ha), els matollars de ginesta (70 ha), o els conreus herbacis i llenyosos (29 ha), entre d'altres. Els principals canvis es deuen sobretot a la successió forestal (24%), l'embosquinament (16,1%), l'emmatament (10,6%) i l'abandonament agrícola (8,1%), o a la combinació de diverses causes (14,8%).

Keywords: Hàbitats CORINE, Hàbitats d'Interès Comunitari (HIC), Dinàmica de la vegetació, Ecologia del Paisatge, Parcs de la Diputació de Barcelona.

Pòster

Assessing the origin of leatherback turtles in Spanish waters through the analysis of their genome diversity

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Abstract. The leatherback turtle (Dermochelys coriacea) is the largest extant sea turtle species with populations undergoing rapid declines. Traditionally, mitochondrial DNA (mtDNA) has been used to investigate population structure and connectivity between nesting and foraging areas in marine turtles, but leatherbacks exhibit exceptionally low mtDNA variation globally, undermining reliable analysis. Advances in High-Throughput Sequencing (HTS) and the availability of a reference genome now enable genome-wide analyses using millions of markers, allowing the study of genetic diversity and population structure, as well as the assignment of individuals to their populations of origin. We first determined the genomic structure of the species across its geographical range by building a pangenome using Whole Genome Sequencing (30Gb output) on individuals taken from nesting populations in three different Regional Management Units (RMUs): Northwest Atlantic (Colombia, Dominican Republic), Southeast Atlantic (Gabon) and East Pacific (Costa Rica). We also sequenced individuals from foraging areas of Spain: Andalusia, Catalonia, Galicia, Valencian Community and Canary Islands to test the potential of genomics to assign individuals in foraging areas. We genotyped all samples by mapping their reads against a reference genome to produce a set of nuclear single-nucleotide polymorphisms (SNPs). We found a deep genetic structuring across RMUs. This genetic structuring enabled the assignment of most individuals from Spanish foraging areas to one of the RMUs. We also analysed runs of homozygosity (ROH), to assess the level of inbreeding across populations. We found that populations have different degrees of inbreeding. Our study demonstrates that whole-genome data can provide valuable insights that guide conservation strategies aimed at preserving the genetic integrity and adaptive potential of sea turtles in response to multiple pressures.

Keywords: Genomics, Sea turtles conservation, Population structure, Foraging areas.

Pòster

Cartografia i cens de flora amenaçada i avaluació de l'estat de conservació dels hàbitats, dues eines fonamentals

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Abstract. La cartografia i el cens de la flora amenaçada, així com l'avaluació i el seguiment de l'estat de conservació dels hàbitats d'un territori, constitueixen dos instruments primordials en l'àmbit de la gestió, la conservació i la restauració de la biodiversitat, a la vegada que aporten dades per a la recerca amb un doble component espacial i temporal d'elevat interès. A banda dels raonaments científics i d'aplicabilitat que justifiquen l'establiment de projectes d'estudi i seguiment de la biodiversitat, la seva implementació queda recollida a l'Estratègia del patrimoni natural i la biodiversitat de Catalunya, un document de planificació estratègica aprovat pels òrgans competents de l'administració, i també és una necessitat derivada de requeriments legals, com és el cas de la Directiva Hàbitats de la Unió Europea. Per donar compliment a aquestes demandes, s'han posat en marxa sengles programes, un per a la flora amenaçada, i l'altre per als hàbitats. En el primer cas, s'han iniciat els treballs de prospecció, cartografia i cens d'algunes espècies que formen part del Catàleg de flora amenaçada de Catalunya. Sobre els resultats obtinguts, en una segona fase s'implementaran programes de seguiment en el temps. En el cas dels hàbitats, i a través de l'establiment d'un grup de treball format per la Direcció General de Polítiques Ambientals de la Generalitat de Catalunya, el Centre de Recerca Ecològica i Aplicacions Forestals (CREAF) i el GeoVeg-IRBio de la Universitat de Barcelona, s'han establert les bases d'una metodologia estandarditzada d'avaluació i seguiment de l'estat de conservació dels hàbitats, s'ha implementat una xarxa de parcel·les estables de mostreig, i s'han engegat les tasques d'avaluació sobre el terreny. Ambdós projectes permetran l'obtenció de dades de qualitat que donaran la facultat de definir adequadament les estratègies i la presa de decisions en relació amb el patrimoni natural.

Keywords: Flora amenaçada, hàbitats, estat de conservació, seguiments de biodiversitat.

Pòster

Morphological change of butterflies in response to urbanisation

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Abstract. Urbanisation is a rapidly expanding environmental force that alters habitats and threatens biodiversity through land-use change, habitat degradation, and fragmentation. Despite these pressures, some species can persist in cities through phenotypic variation driven by plasticity or adaptive evolution. Understanding how traits shift along urbanisation gradients is therefore essential for predicting species' responses to human-modified environments.

We investigated morphological change in butterflies, focusing on how wing size varies with urbanisation. Using more than 113,000 wing size measurements from 66 butterfly species of the butterfly collection of the Natural History Museum, London, UK (1851–1971), we quantified the relationship between wing size and human population density, used as a proxy for urban intensity. Linear mixed-effects models included population density and mean annual temperature as fixed effects, and species, year, and county as random effects.

Across species, we found a significant positive association between human population density and wing size, indicating that butterflies tend to be larger in more urbanized areas. However, temperature showed no significant effect. Importantly, species differed markedly in the strength of this relationship: while some species displayed clear increases in wing size with urbanisation, others showed minimal or no response. These differences likely reflect variation in dispersal ability, life-history strategies, or selective pressures unique to urban environments. Taken together, these results suggest that urbanisation can act as a selective filter favouring larger individuals, but the extent of this effect is highly species-specific. Ultimately, this research will contribute to understanding how urban ecosystems shape the evolution and persistence of insects in a rapidly urbanising world.

Keywords: urban environment, body size, collection, insect.

Pòster

Vitibosc: Parcel·la pilot agroforestal en vinya

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Abstract. El canvi climàtic està afectant el cultiu del raïm, reduint la producció total i la qualitat organolèptica per a la producció de vi. Els sistemes agroforestals, és a dir, la introducció d'arbres i arbustos al cultiu de la vinya, s'han proposat com una solució per adaptar cultiu al canvi climàtic, i ja hi ha experiència en altres països. Els sistemes agroforestals poden millorar el microclima del cultiu, proporcionant ombra amb l'objectiu de retardar la maduració del raïm i reduir les pèrdues per evaporació de l'aigua i cremades que afecten al rendiment. Alhora també milloren la fertilitat, augmenten la biodiversitat, fixen CO2 atmosfèric i diversifiquen els beneficis amb el cultiu d'arbres fruiters o crèdits de carboni.

El projecte VITIBOSC té per objectiu establir una parcel·la ecològica agroforestal pilot en una vinya on s'avaluarà la idoneïtat de les espècies seleccionades, els costos de l'establiment, i a llarg termini, es monitoritzaran els efectes sobre la producció, biodiversitat i sòl. A més, tots els coneixements generats seran transferits al sector vitivinícola. Aquesta parcel·la pilot es va establir l'abril del 2025 a la regió vitivinícola del Penedès, a una finca de Cellers Família Torres seguint els principis de l'agricultura ecològica. El sistema agroforestal és altament divers i inclou arbres i arbustos que seran intensament podats per incorporar les restes de poda a terra, i matolls i plantes aromàtiques per augmentar la biodiversitat i fixar nitrogen.

Keywords: Agroforesteria, viticultura, agricultura ecològica, canvi climàtic.

Pòster

Advances in ethnobotany of the Catalan linguistic area: Ongoing research and future prospects

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Abstract. Traditional knowledge in rural areas of industrialized societies is rapidly declining, making ethnobotanical research urgent and essential for documenting and preserving this valuable heritage. Additionally, returning this knowledge to local communities is both an ethical duty and a key strategy for its conservation. The Catalan linguistic area stands as one of the most extensively studied European regions in ethnobotany, and there is still ongoing and foreseen research. The 'Ethnobotany of the Catalan Countries' website (https://etnobotanica.iec.cat) serves as a platform to explore traditional plant knowledge gathered since 1990. This poster presents an updated overview of the territories studied and those currently under research, while also identifying gaps in ethnofloristic studies. Currently, the open-access database hosts nearly 80,000 plant name entries, 55,000 medicinal use records, and around 30,000 food-related entries (apart from a separate dataset on plant-based beverages), with an additional 30,000 records on other plant uses, harmful or toxic effects and other information is set for inclusion within the next two years. This extensive dataset not only conserves cultural and botanical heritage, but also provides an accessible resource for future generations. Moreover, recent efforts have focused on meta-analytical studies comparing regional plant uses and examining broader ethnobotanical trends. A novel phylogenetic approach has also been introduced, aiming to identify key evolutionary nodes where traditional plant knowledge is concentrated. By integrating these perspectives, among others, we seek to deepen our understanding of plant use patterns and their implications for human well-being.

Keywords: Biocultural diversity, Catalan linguistic area, Database, Ethnobotany, Plant uses, Traditional knowledge.

Pòster

Signs of potential loss of conserved BUSCO genes across Ctenophores

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Abstract. Ctenophores or comb jellies comprise around 200 described species and represent a key early- branching metazoan lineage whose evolutionary history remains actively debated. Clarifying their phylogenomic position is essential for understanding the origin of major animal traits such as neurons and muscles. While analyzing our newly generated dataset to address these questions, preliminary BUSCO assessments revealed an unexpectedly high proportion of genes reported as missing. The aim of this work is to determine whether these apparent absences reflect true evolutionary loss or instead result from extreme divergence that prevents their detection by conventional homology tools.

To address this, we ran BUSCO across all available datasets and generated presence-absence matrices to identify recurring patterns of gene loss. A subset of outlier assemblies showed unusually high numbers of conserved genes due to contamination and were therefore cleaned or excluded. Across the curated dataset, we identified approximately 60 BUSCO genes (~9%) that are consistently absent and conducted functional annotation to assess their associated COG categories. Preliminary results suggest that part of the missing signal reflects genuine evolutionary loss, whereas other cases may stem from incomplete assemblies or high sequence divergence. Distinguishing between these scenarios is crucial for interpreting ctenophore genome evolution and understanding how core cellular functions have been shaped in this lineage. Building on these findings, our ongoing work applies more sensitive homology detection approaches to examine functional patterns among the potentially missing genes. Ultimately, this project aims to better characterize the putatively unique genomic features of Ctenophora and assess how these may set the lineage apart from other early-diverging metazoans.

Keywords: Ctenophora, BUSCO, gene loss, genome evolution.

Pòster

El gènere Brasema (Hym., Eupelmidae) en gales de cinípids (Hym., Cynipini) en roures mexicans

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Abstract. Les gales són unes deformacions vegetals formades per l'activitat d'un organisme inductor, com poden ser les picades alimentaries o la posta dels ous dins dels teixits vegetals. En l'últim cas, les gales protegeixen i alimenten a l'inductor. Les gales més complexes són les formades per cinípids (Hym., Cynipini) en roures. Aquests cinípids solen ser atacats per parasitoides de la superfamília Chalcidoidea, que s'alimenten de larves de forma ecto- o endoparasitoide.

Dins d'aquesta superfamília es troba la família Eupelmidae, ectoparasitoides de larves o prepupes d'insectes, generalment en plantes o capolls, o endoparàsits d'altres insectes o ous d'aranyes. Actualment, inclou 3 subfamílies, 39 gèneres i unes 900 espècies. Els gèneres més comuns a Amèrica són Eupelmus Dalman, 1820 y Brasema Cameron, 1884 i constitueixen la major part de diversitat d'eupèlmids en gales de cinípids

L'objectiu principal d'aquest estudi és conèixer les espècies d'eupèlmids emergents de gales de cinípids en roures mexicans.

Es procedeix a estudiar 97 mostres de gales recollides en 16 estats mexicans diferents des de l'any 2015.Per a la identificació d'espècies s'han preparat 194 mostres entomològiques d'eupèlmids emergits de les gales mostrejades i s'han il·lustrat els representants dels diferents morfotipus a través de macrofotografia i microscòpia electrònica (SEM).

En relació amb el gènere Brasema s'han reportat cinc espècies emergents de gales de cinípids en roures mexicans; tres espècies ja descrites: B. dryophantae (Ashmead, 1886), B. macrocarpae (Ashmead, 1888), B. speciosum (Girault, 1916) i dues noves espècies: **B. mexicanum** Cazorla-Vila & Pujade-Villar 2025 i **B. obscurum** Cazorla-Vila & Pujade-Villar, 2025. Les noves espècies estan suportades per evidències morfològiques i moleculars. Ha estat redactada la primera clau d'identificació d'espècies de Brasema emergents de gales de cinípids i també una primera aproximació a la filogènia d'aquest gènere. Per altra banda, del gènere Eupelmus, es reporten dues espècies: E. cynipidis Ashmead, 1882 i E. pulchriceps (Cameron, 1904).

Keywords. Hymenoptera, Eupelmidae, taxonomia, morfologia, filogènia.

Pòster

Assessing the trophic transfer of microplastics in marine mammals

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Abstract. Marine mammals may ingest microplastics (MPs) directly from the environment or indirectly through trophic transfer of contaminated prey. While the occurrence of these pollutants at the individual level has been extensively reported, there are few studies addressing the trophic transfer of MPs along marine food webs including marine mammals. Here, we conducted a systematic literature review on this topic, following the PRISMA procedure. Out of 2755 screened studies, only 8 met the established selection criteria. A total of nine marine mammal species, including mysticetes, odontocetes, polar bears and pinnipeds, were included. Modeling and meta-analysis studies represent 62.5% of the reviewed research, while field studies cover the remaining 37.5%. In field studies, KOH was used to digest organic matter in two out of three cases, and Fourier-Transform infrared (FTIR) spectroscopy was used in all of them to polymer identification. Trophic transfer of MPs to marine mammal was rejected in three of the studied food webs and confirmed in five studies. Only one out of the five studies used the Trophic Magnification Factor (TMF) to quantify the trophic transfer of MPs. This model-based study obtained a TMF value of 6.17 for the first run of the model. We attempted to quantify trophic transfer in the remaining studies but due to the absence of standardized data, we could only calculate the Biomagnification Factor in one field study, obtaining a value of 1.5, suggesting biomagnification of MPs. The complexity of analyzing food webs, the challenges of working with marine mammals in a non-invasive way and the lack of standardized data are some of the shortcomings in this area of research. Addressing these issues through further studies is essential to better understand the trophic transfer of MPs to marine mammals.

Keywords: microplastic, trophic transfer, marine mammal, PRISMA

Genetic regulation of sexually dimorphic pigmentation in *Cloeon dipterum*

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Abstract. Sexual dimorphism can be displayed in many forms, such as distinct organs or body pigmentation. Although this is a wide-spread characteristic in animal species, little is known about the genes regulating sex determination and sexual dimorphism in key groups of insects, such paleopterans (Ephemeroptera and Odonata). The emergent evo-devo model Cloeon dipterum is an Ephemeroptera species, whose adults exhibit sexual differences in body pigmentation. Therefore, we aim at understanding the genetic control of sex determination in this species and how the sex determination cascade defines sexual dimorphic body colouration. First, we described a transcription factor involved in arthropod sexual differentiation: Doublesex (Dsx). For this, we built a phylogenetic tree using orthologs from other insect species, and we identified three paralogs of Dsx: Dsx, Dsx-like and a novel gene that we named as Dsx-y. Second, Raman spectroscopy allowed us to identify pigments in both sexes: melanin in the thorax and an unknown pigment in the pattern of the abdomen. Finally, we examined the transcriptomes of male and female epidermis and found differential expression in melanin-associated genes. Different paralogs of yellow gene were upregulated in both sexes, and ebony showed a female-biased expression. In addition, we found other pigmentation-related genes that were differentially expressed, such as vermilion, which suggests that the unknown pigment in the abdomen of both sexes may be an ommochrome. These results provide new insights into the regulation of pigmentation downstream of the sex determination cascade in *C. dipterum*.

Keywords: pigmentation, doublesex, sex determination cascade, mayfly, sex dimorphism.

Pòster

Analysis of a handwritten manuscript of plant-based remedies from Castellar de n'Hug (Berguedà, Catalonia)

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Abstract. An ethnobotanical prospection is currently being conducted in the Berguedà district, an area in Central Catalonia whose northern part belongs to the Catalan Pre-Pyrenees. In addition to applying the standard ethnobotanical method—interviewing native inhabitants or long-term residents—we are also examining documents of ethnobotanical interest. One such document is a handwritten recipe book that contains information about plants used in remedies for treating various ailments. This manuscript dates from the 1930s and was provided by a resident of La Pobla de Lillet, a municipality adjacent to the village from which the manuscript originates: Castellar de n'Hug. The document was written by the son of the woman who possessed all the knowledge it contains. Although she was born in Cadaqués, a coastal town, she lived for many years in Castellar de n'Hug, where she died in 1960.

This manuscript has provided highly valuable information for the ethnobotany of Berguedà. By comparing the data collected in ethnobotanical interviews conducted so far with the information extracted from the manuscript, we find that popular plant names often coincide, confirming that these species have long been used for medicinal purposes. Nonetheless, the manuscript also includes plant names that had not been recorded in the interviews and that, in some cases, have led to the identification of new taxa within the region's ethnobotanical corpus. One example is Ranunculus parnassifolius L., known locally as "herba del mal gra".

Keywords: Ethnobotany, Berguedà, manuscript, medicinal plants, popular plant names.