



Programme flow 2026

Day 1, Thursday, October 1st:

9.00h – 09.15h: Registration

9.15h – 09.30h: Reception and welcome

930h–955h	Eirini Trypidaki CREAF (UAB)	Advancing High-Resolution Drought Monitoring: Evaluating Remote Sensing Soil Moisture Products
955h–1020h	Júlia Froxán-Grabalosa CEAB (CSIC)	West Nile Virus Disease Ecology in Avian Hosts
1020h–1045h	Adrià Casacuberta Dept. Biologia Evolutiva, Ecologia i Ciències Ambientals (UB)	Using Treated Urban Wastewater for Riparian Restoration: Plant Performance, Diversity, and Ecosystem Services
1055h–1110h	Ashley Tejeda IRBio (UB)	Morphological responses of butterflies to long-term urbanisation
1110h–1135h		Coffee break
1135h–1200h	Caterina Marquès Dept. Biologia Evolutiva, Ecologia i Ciències Ambientals (UB)	Gut microbiomes and ecological adaptation in an insular lizard
1200h–1225h	Gerard Mas CEAB (CSIC)	Demography, population dynamics and thermotolerance of the two dominant species of gorgonians in the Canary Islands, Subtropical Eastern Atlantic Ocean
1225h–1250h	Agustín Carabajo CEAB (CSIC)	Wild dynamics, wild future: Dynamics of the Iberian Lynx Gut in captive breeding, insights in conservation
1250h–1315h	Gema Cambero IRTA	Landscape and field management drivers of biodiversity and ecosystem services in rice agroecosystems

	1315h–1445h	Lunch served at CEAB
1445h–1510h	Krati Sharma CEAB (CSIC)	Unravelling the role of salinity and sediment moisture on greenhouse gases emissions in shallow saline lakes
1510h–1535h	Joana Krause-Massaguer IBE (CSIC)	Isolation, Culturing and Characterization of Protist Symbionts from Mediterranean Corals
1535h–1600h	Enric Gomis CEAB (CSIC)	Natural seagrass recovery enhances biomass and soil carbon sequestration and avoids erosion-driven CO ₂ emissions
1600h–1625h	Maria Estarellas IBE (CSIC)	Disarming the venom arsenal of <i>Atractaspis andersonii</i> through a multi-omics approach

The PhD Odyssey. Open discussion of challenges and opportunities
(Snacks and cheap drinks will be available!)

1625h–2000h	During this final part of the day, we will dedicate time to having an open and friendly discussion about the challenges and opportunities of pursuing a PhD. We will have a round table discussion about anything that may be on your mind, with the chance to start conversations and get feedback from the senior scientists and your fellow PhD students.	
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Day 2, October 2nd.

09.30h–10.30h	Volker Grimm, Helmholtz Centre for Environmental Research – UFZ, Leipzig (Germany)	The integrative honey bee colony model BEEHAVE: lessons learned and to be learned
	10.30h – 11.00h	Coffee break
11.00h–12.00h	Marta Coll, Institut de Ciències del Mar (ICM-CSIC)	Who Eats Whom—and Why It Matters: Food-Web Models for Understanding Marine Ecosystem Dynamics
12.00h–13.00h	Graciela Gil-Romera, Instituto Pirenaico de Ecología (IPE-CSIC)	Time Continuum: unifying palaeo and neoecology
Closure		

List of Abstracts

PLENARY TALKS

Volker Grimm

Helmholtz Centre for Environmental Research – UFZ, Leipzig (Germany)

The integrative honey bee colony model BEEHAVE: lessons learned and to be learned

The mortality rate of honeybee colonies has increased over the last two decades due to the cumulative impact of various stressors, including diseases, pesticides, changes in land use, and beekeeping practices. It is virtually impossible to empirically explore the relative importance of these stressors, as honeybee colonies exhibit trait variation that is orders of magnitude higher than that of most other animal species. Hence, the BEEHAVE model was developed. It represents a single colony and includes a detailed depiction of foraging in agricultural landscapes. Since its release in 2014, BEEHAVE has been used in over 30 studies. In this presentation, I will explain the rationale behind the model, demonstrate how it is used, and summarise what we have learnt from it so far, including its limitations and future developments. Overall, this is an example of ecological modelling for decision support, not via predictions, which are impossible, but via a better understanding of the underlying mechanisms.

Marta Coll

Institut de Ciències del Mar (ICM-CSIC)

Who Eats Whom—and Why It Matters: Food-Web Models for Understanding Marine Ecosystem Dynamics

Ecosystems are connected by feeding interactions that move energy and matter among species, habitats and regions. These trophic connections influence how ecological communities function and respond to pressures such as fishing, climate change, species invasions and other disturbances. They also underpin ecosystem services and nature's contributions to people, including food provision, climate regulation, nutrient cycling and cultural benefits. Yet ecosystems are often studied one species, one habitat or one pressure at a time, potentially overlooking indirect effects, feedbacks and ecological surprises.

In this lecture, I will explore how food-web models help us move from observations of individual trophic links to an integrated and dynamic understanding of marine ecosystems. I will introduce complementary approaches for characterizing food webs, from empirical trophic data and qualitative ecological networks to quantitative and spatially explicit marine ecosystem models. I will then show how combining food-web dynamics with species distributions, environmental conditions and human pressures allows us to investigate how change propagates across species, habitats and trophic levels—and how these ecological changes may affect the benefits that people derive from marine ecosystems.

Using scenarios that combine fishing and climate-change pressures with alternative spatial-management options, I will illustrate how these models can reveal ecological interdependencies and trade-offs that remain hidden when species are considered in isolation. They can also support more realistic projections, since trophic interactions may amplify, redistribute or buffer the effects of global change. By linking changes in food-web structure and functioning to

ecosystem services and nature's contributions to people, these approaches can help evaluate the wider ecological and societal consequences of management decisions.

Rather than viewing food webs as static diagrams of “who eats whom,” I will argue that they should be understood as dynamic maps of ecological dependence. I will conclude by discussing what food-web models can and cannot tell us, the importance of data and uncertainty, and the interdisciplinary collaborations needed to better understand, anticipate and manage future marine ecosystems.

Graciela Gil-Romera

Instituto Pirenaico de Ecología (IPE-CSIC)

Time Continuum: unifying palaeo and neoecology

Global Change is arguably the most transformative process shaping our planet — driven by a single species and potentially irreversible. Estimating its true extent and working towards mitigation demands a broad spatio-temporal perspective, one that only long-term ecological records can provide. My research sits at this intersection: understanding how ecosystems have responded to environmental change over the Quaternary allows us to define baseline conditions and thresholds of resilience against which present and future disturbance can be measured. This is inherently interdisciplinary work, bridging palaeoecology, evolutionary biology, biodiversity science, and modern quantitative ecology.

In this talk, I argue that fully realising this potential requires actively integrating palaeoecological and neoecological approaches, rather than treating them as separate traditions. I illustrate this with our recent work reconstructing 14,000 years of plant community assembly in the Pyrenees and the Bale Mountains (Ethiopia), where we apply Granger causality — a method rooted in modern time-series ecology — to fossil pollen and charcoal records, revealing how fire reorganises predictive relationships among taxa across millennia.

This integrative approach also reflects my commitment to open, collaborative science, embodied in my roles within the European Pollen Database and Neotoma, and in building baselines that can genuinely inform conservation and forecasting in a rapidly changing world.

PhD students

List of oral proposals

(Sorted out by *alphabetic order*, name of the candidate in yellow)

(Those accepted for presentation are framed in orange)

Title: A nature-based solution to mitigate the impact of reclaimed water discharge into a river under water scarcity conditions

Ana Karen Agustin Navarro - Universitat de Girona / Environmental Chemistry and Physics departments

📄 Resum (màxim 300 paraules)

Water scarcity in the Mediterranean is an escalating concern. In Eastern Spain, projections indicate a rise in heatwaves and prolonged droughts. These conditions exacerbate the impact of anthropogenic residues on aquatic ecosystems (Sepp et al. 2025). A primary source is reclaimed water from Wastewater Treatment Plants (WWTPs). Although aquatic ecosystems possess natural attenuation capacities, these mechanisms are compromised when flow dilution is reduced by drought (Abily et al. 2021). The BIODAPH NbS tertiary treatment reduces particulate pollutant loads, improving the water quality of the Onyar River and acting as a buffer for the aquatic ecosystem against the risks associated with low-flow conditions and water scarcity. My research analyzes particle transport and sedimentation patterns upstream and downstream of WWTP discharge to establish a model forecasting the impact of the BIODAPH Nature-based Solution (NbS). Additionally, an efficiency assessment of the technology is performed to track the enhancing potential of *Daphnia* filtration of particle-like pollutants of emerging concern, such as microplastics, and those associated with particle adsorption, such as PFAS. The BIODAPH system is an efficient nature-based solution for improving the quality of reclaimed water. Its implementation may successfully mitigate the impact of WWTP discharges on Mediterranean rivers, especially during periods of water scarcity where dilution capacity is low. This technology supports the maintenance of ecological flows and helps meet sustainable water management goals by restoring degraded aquatic habitats.

📄 Any en què es troba el Doctorat: Primer any

Flow reduction amplifies sediment-driven impacts on stream biofilms

Neus Besoli-Mestres^{1,2}, Paula Esparraguera¹, Anna Freixa¹ & Sergi Sabater^{1,2}.

¹Catalan Institute for Water Research (ICRA), Carrer Emili Grahit, 101, Parc Científic I Tecnològic de la Universitat de Girona, 17003, Girona, Spain

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2nd year of PhD

Mediterranean rivers are naturally adapted to water flow intermittency. However, water diversion or damming alter these natural hydrological and sediment dynamics and may push these systems beyond their natural operating range, with undefined short- and long-term consequences.

We here performed a 14-days laboratory experiment using artificial channels, in which we assessed the combined effects of fine sediment deposition and water flow reduction on stream biofilm's structure and functioning. By performing a sequential experimental design, we identified a water flow threshold at which sediment mobilization and deposition shifted. The progressive reduction in water flow (from 360 L h⁻¹ to 108 L h⁻¹) modified the hydraulic conditions at the streambed and promoted varying levels of fine sediment deposition. Low-flow conditions, associated with sediment deposition, affected microbial structure and functioning due to sediment clogging and reduction of light availability. Biofilms decreased their basal fluorescence, primary production efficiency related to chl-a content, organic matter capacity degradation, and P-uptake. This experiment illustrates the implications of strong hydrosedimentary pressures on the structure and functioning of biofilm communities, with potential effects for other biological components in river ecosystems.

Títol: Salinity constrains methane while in-stream processes regulate CO₂ dynamics in a tropical estuary

Nom: Elsa Bisbal Regidor

Afiliació: Department of Evolutionary Biology, Ecology and Environmental Sciences, Universitat de Barcelona.

Any de doctorat: 1st

Abstract:

Salinization is an increasing pressure on inland waters worldwide, driven by sea-level rise, climate change, and human activities. While this process threatens freshwater ecosystems, tidal rivers and estuaries naturally experience salinity gradients that can provide insight into how salinization alters biogeochemical functioning. However, how these gradients translate into changes in carbon cycling and greenhouse gas dynamics remains poorly constrained, particularly in tropical systems. The Gambia River in West Africa offers a natural setting to examine these processes along a relatively undisturbed river–estuary continuum. Despite its regional importance, its role in carbon cycling remains largely uncharacterized. At the same time, the system may be threatened by salinization, given a planned upstream dam and increasing water abstraction. Here, we quantify the concentrations, isotopic composition ($\delta^{13}\text{C}$), and atmospheric fluxes of CO₂ and CH₄ across 3 hydrological conditions and along a 400 km freshwater to ocean gradient. We show that CO₂ and CH₄ respond differently along the river continuum. CO₂ concentrations exhibit a maximum at ~200 km from the river mouth that is consistent across seasons, indicating enhanced carbon processing within the estuarine mixing zone that is not explained by the increasing salinity alone. In contrast, CH₄ concentrations decline with increasing salinity and display strong spatial variability, consistent with salinity-driven shifts in redox conditions that suppress methanogenesis. These results demonstrate that salinity does not act as a universal control on greenhouse gas dynamics in this system. Instead, spatial structure along the river–estuary continuum governs CO₂ dynamics, while CH₄ is primarily regulated by local biogeochemical conditions. The decoupling between CO₂ and CH₄ indicates that the influence of salinity on GHG dynamics is gas-specific, and suggests that tropical tidal rivers such as the Gambia, characterized by low freshwater input and strong marine intrusion in semi-arid settings, may deviate from existing conceptual models.

ΣPhD Ecological Symposium (4th edition)

Estel Blanch Ojea, Second year of PhD

1. Ecological and Forestry Applications Research Centre (CREAF), C Building, Faculty of Biosciences, Cerdanyola del Vallès, 08193, Spain
2. Departament of Animal Biology, Plant Biology and Ecology, Autonomous University of Barcelona (UAB), C Building, Faculty of Biosciences, Cerdanyola del Vallès, 08193, Spain
3. BiBio Research Group, Natural Sciences Museum of Granollers, Av/Francesc Macià 51, 08402, Granollers, Spain
4. BETA Technological Centre, Ctra de Roda 70, 08500 Vic, Spain

Abstract

Beneath the Earth's surface: long-term temperature monitoring network in underground roosts.

Climate change is now on everyone's agenda because of the multiple severe effects we are already facing as a society. Rapid temperature changes have terrible consequences for troglodyte fauna. Yet, very few studies have monitored this Climate Change driver beneath the Earth's surface, mostly due to the inaccessibility and remoteness of these habitats.

Some bat species strongly depend on underground cavities during their life cycle, and many of them are heavily threatened. The Bat Monitoring Program (www.batmonitoring.org), established in the northeastern Iberian Peninsula, includes long-term annual standardised cave-dwelling bat populations' monitoring through citizen science. Within this framework, in this project, we initiated systematic temperature monitoring in the most valuable and threatened underground roosts.

Since 2024, we have established a network of 100 recently developed long-term temperature dataloggers (T7.3 EnvLogger, Electricblue), being the first network of its kind globally. These pioneering, miniaturised, and user-friendly dataloggers will record temperature conditions over a 15-year period, every 60 minutes.

Due to the data provided by this network, we have characterised the roost temperatures used by cave-dwelling bats during different seasons. Preliminary results show clear differences in roost temperature among different bat species across their annual periods: hibernation, migration, breeding and mating. The barbastelle bat used the coldest roosts, hibernating at around 2.5 °C, while other species were recorded in warmer hibernation roosts, at around 11°C. In contrast, during migration and mating, the roost temperatures were more similar between species. We have also analysed the annual temperature variation in the different caves, which showed a relatively constant dynamic, as the average temperature change along the whole year is 4 °C.

Temperature is a key driver in bat roosts under the umbrella of Climate Change. Therefore, this long-term monitoring scheme will provide crucial data to study the effects of climate change in underground habitats over time.

Movescapes of Mediterranean Coastal Predators: Movement Ecology and Habitat Connectivity Across the Catalan and French Coast

Skye Brown¹, Eneko Aspillaga², Bernat Hereu¹

¹ Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Barcelona, Spain.

1st Year PhD Candidate: University of Barcelona

Movement of mobile marine species is fundamental to ecological connectivity across coastal seascapes, linking habitats, supporting trophic dynamics, and sustaining ecosystem resilience. However, understanding how species move through increasingly anthropogenized coastal environments remains a major challenge for conservation and spatial management, particularly in the Mediterranean Sea, where coastal habitats are highly fragmented and heavily exploited.

This study uses acoustic telemetry to investigate movement patterns and habitat use of several ecologically and socioeconomically important mobile coastal teleosts (*Seriola dumerili*, *Pomatomus saltatrix*, and *Lichia amia*) across the Catalan coast and adjacent transboundary waters, assessing how these species utilize diverse coastal habitats, including Marine Protected Areas (MPAs), harbours, and coastal corridors.

Preliminary findings reveal species-specific movement strategies and varying degrees of site fidelity, seasonal displacement, and habitat coupling, highlighting the importance of dynamic coastal mosaics in supporting mobile predators and fisheries-associated species. Many of the key habitats and movement corridors identified extend beyond static MPA boundaries, underscoring the need for adaptive, connectivity-based conservation approaches that integrate habitat mosaics, fisheries regulation, and transboundary management.

Beyond these initial results, this work lays a movement ecology foundation for addressing further questions, such as how migration patterns and life-history traits shape population connectivity, ultimately contributing to a growing understanding of Mediterranean coastal movescapes and how movement ecology can inform adaptive spatial management and conservation planning.

Title: The Effect of Water Stress on the Dielectric Properties of Plants.

Name: Marc Busuldu Tris.

Affiliation: Centre de Recerca Ecològica i Aplicacions Forestals (CREAF).

Year of the PhD: 2nd.

Abstract

Increasing atmospheric demand and the rising frequency of severe droughts are intensifying water stress in forest ecosystems, with major implications for plant survival, ecosystem functioning, and climate feedbacks. Accurate monitoring of vegetation water status is therefore essential for understanding drought impacts across scales. Microwave remote sensing offers unique sensitivity to vegetation water content through the dielectric properties of plant tissues; however, the dielectric mixing models used to interpret remote sensing signals are based on assumptions that remain insufficiently validated at the tissue level.

This research investigates the relationship between leaf water status and dielectric permittivity during dehydration. Microwave measurements of leaf dielectric properties are combined with pressure–volume analysis to characterize changes in tissue water compartments across a wide range of water potential states. By linking dielectric responses to physiologically meaningful variables such as water potential, turgor loss, and tissue water content, the study aims to evaluate and improve the permittivity models commonly used in vegetation remote sensing.

The results will contribute to a more physically grounded interpretation of microwave observations of vegetation, improving the retrieval of plant water status from remote sensing data and enhancing ecosystem monitoring under increasing drought stress.

Beyond the traditional blue carbon approach: Unveiling coastal carbon pathways in Mediterranean seagrass meadows using benthic chamber incubations

Sinéad Cahill

Institut de Ciències del Mar (ICM-CSIC), Barcelona, Spain

2nd year PhD candidate

Seagrass meadows are key blue-carbon ecosystems, yet their net role in coastal carbon budgets remains uncertain. While these ecosystems can store large amounts of particulate organic carbon in sediments, other carbon sequestration pathways such as dissolved carbon export and total alkalinity (TA) outwelling remain poorly constrained. Moreover, the strong biogeochemical heterogeneity that characterizes coastal seascapes adds uncertainty to these carbon pathways. Here, we used in situ benthic chamber incubations to assess how seawater biogeochemical heterogeneity modulates short-term carbon fluxes in Mediterranean seagrass meadows across species (*Posidonia oceanica*; *Cymodocea nodosa*), locations (based on depth and anthropogenic influence) and seasons (spring, fall). We quantified changes in seawater pH, TA, dissolved inorganic carbon (DIC), greenhouse gas (GHG) fluxes and characterized sediment organic and inorganic carbon content, grain size and total living biomass. Preliminary results reveal pronounced spatial and diel variability in carbonate chemistry and GHG fluxes. pH exhibited strong diel cycles in both species, with larger daytime increases and stronger nighttime decreases in *C. nodosa*, while *P. oceanica* showed marked depth and seasonal contrasts: surface meadows displayed stronger spring pH increases and deep meadows stronger fall decreases. TA and DIC fluxes also differed between species, with higher export in *C. nodosa*, particularly in the fall, and seasonally contrasting dynamics in *P. oceanica*, ranging from uptake in spring to neutral or export or conditions in fall. CH₄ increased in all incubations, with higher fluxes in seagrass compared to adjacent sand, and clear regional and seasonal patterns. CO₂ exhibited strong diel oscillations, with net balances ranging from neutral or slightly positive in the *C. nodosa* to net uptake in *P. oceanica* surface meadows in fall. N₂O changes were small but structured across species and seasons. Together, these results demonstrate that spatial, seasonal and habitat heterogeneity strongly modulate short-term carbon and GHG dynamics in seagrass ecosystems, and that neglecting this variability may bias blue-carbon budgets and mitigation strategies.

Landscape and field management drivers of biodiversity and ecosystem services in rice agroecosystems

Gema Cambero-Conejero (third-year PhD candidate)

IRTA, Marine and Continental Waters, Carretera Poble Nou Km 5.5, 43540 La Ràpita, Catalonia, Spain.

Agricultural intensification is a major driver of landscape simplification and biodiversity loss. To investigate how landscape context influences biodiversity in rice agroecosystems, we conducted a meta-analysis based on 456 effect sizes from 18 papers across 9 countries. Overall, landscape complexity had a positive effect on rice-associated biodiversity, although responses varied among taxonomic orders.

However, under intensive agricultural conditions, it remains unclear whether landscape complexity or field management is the primary driver of biodiversity. To address this question at a regional scale, we surveyed seven taxonomic groups (waterbirds, amphibians, adult odonates, spiders, aquatic insects, fish and crayfish) across 24 rice fields in the Ebro Delta, representing a gradient of landscape complexity. We characterized field-scale management practices and quantified landscape metrics at multiple spatial scales to assess their influence on abundance and diversity.

Waterbird diversity declined with pesticide use, dry seeding, and increasing distance to lagoons, while abundance decreased with larger field size. In contrast, amphibian abundance increased with field size. Aquatic insect and crayfish abundance were positively associated with the rice area within a 200-m buffer, whereas crayfish abundance and odonate diversity increased with channel area within a 1000-m buffer. Spider and dragonfly abundance benefited from field margin vegetation, the sole field management predictor showing consistent positive effects across taxa. Fish communities showed no association with any landscape or local predictor.

We also evaluated three different ecosystem services in the aquatic-terrestrial interface of rice fields: pest predation, weed seed predation and organic matter decomposition. Preliminary results indicate that aquatic insect and crayfish abundances enhanced ecosystem services in the water layer, whereas odonate abundance and field management were important drivers in the terrestrial component.

These findings support the design of agri-environment schemes that integrate landscape and field-level management to enhance biodiversity, ecosystem service provision, and agroecosystem sustainability.

Wild dynamics, wild future: Dynamics of the Iberian Lynx Gut in captive breeding, insights in conservation.

Agustín Carbajo Usano, Centre d'Estudis Avançats de Blanes CEAB. At 3rd year of phd.

The gut microbiome of wild mammals is a dynamic ecosystem that influences host health and conservation outcomes. For the critically endangered Iberian lynx (*Lynx pardinus*), little is known about how ecological and management factors shape microbial community trajectories. We collected 16S rRNA amplicon data from fecal samples across two breeding stations. A dynamical-systems approach yielded individual-specific parameters (e.g., turnover rates, stability indices). Principal component analysis and hierarchical clustering identified distinct microbiome-dynamic profiles. Redundancy analysis (RDA) tested the influence of environmental variables (station, medical treatments). Functional potential was inferred with PICRUSt to generate enzyme commission (EC) profiles, and pathway-level selection was assessed via non-neutrality metrics. Two robust microbiome-dynamic clusters emerged, differing in turnover and stability. RDA revealed that breeding station and medical interventions significantly explained the variance in community dynamics. Taxonomic shifts did not translate into large functional changes, indicating functional redundancy; however, specific metabolic pathways, displayed non-neutral signatures.

Our integrative dynamical–functional framework demonstrates that environmental management and medical treatment are key drivers of gut microbiome dynamics in the Iberian lynx. These findings underscore the necessity of incorporating microbiome monitoring into conservation strategies and highlight the potential for targeted interventions to maintain microbial resilience in endangered species.

Using Treated Urban Wastewater for Riparian Restoration: Plant Performance, Diversity, and Ecosystem Services

Adrià Casacuberta Vilaró (Third-year PhD student)

Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona

Wastewater discharges in Mediterranean streams stress riparian vegetation and worsen regional water quality. Within a One Health framework, this thesis aims to inform restoration strategies that simultaneously improve water quality and vegetation water availability. Specifically, we evaluated the effects of treated urban wastewater on the growth and physiological condition of Mediterranean riparian plant species representing different life forms and assessed the role of plant diversity in carbon sequestration and nutrient retention.

Two mesocosm experiments were conducted at the Urbar River Lab outdoor facility located at the Montornès del Vallès Wastewater Treatment Plant (WWTP), near Barcelona, Spain. Native herbaceous and woody species commonly used in fluvial restoration were planted in 12 m-long experimental flumes irrigated with WWTP effluent. Growth and functional performance indicators – including stem diameter, biomass production and allocation, and leaf chlorophyll content – were monitored throughout the experiments.

In the first experiment, which lasted eight months, we assessed the tolerance of *Iris pseudacorus*, *Cornus sanguinea*, and *Alnus glutinosa* to treated wastewater and their phytodepuration potential. Based on the chemical composition of the WWTP effluent, we hypothesised that species tolerant to root anoxia would show superior performance. The results revealed contrasting, species-specific responses. Accumulation of metals (Cu, Ni, Cd, and Fe) was observed in all species, primarily in root tissues, suggesting limited translocation to aboveground biomass.

In a second, 13-month experiment, we expanded the approach to evaluate the effects of plant biodiversity. Species mixtures of three, six, and nine species were established, selected to maximise functional trait complementarity (*I. pseudacorus*, *C. sanguinea*, *A. glutinosa*, *Schoenoplectus lacustris*, *Salix atrocinerea*, *Fraxinus angustifolia*, *Carex pendula*, *Crataegus monogyna*, and *Populus nigra*). Growth responses to increasing mixture complexity were species-specific. While total biomass accumulation depended strongly on species composition, nutrient retention increased in more diverse plantations.

Overall, these results suggest that treated urban wastewater can sustain riparian plant development under suitable conditions. However, careful selection of species with appropriate functional traits is essential to ensure the long-term success of wastewater-irrigated plantations and riparian restoration initiatives.

This work was supported by the Riparian EcoRest project (PID2022-1413300B-I00), funded by MICIU/AEI/10.13039/501100011033 and by the 'European Union' / 'ERDF A way of making Europe'. Adrià Casacuberta Vilaró acknowledges the FPI predoctoral fellowship [PREP2022-000541] funded by the MICIU/AEI/10.13039/501100011033 and by the ESF+.

What grazing leaves behind: plant and butterfly responses to management in subalpine grasslands

2nd year PhD Student

Cristina de Gracia i Marin

CEAB – CSIC

Natural Science Museum of Granollers

Abstract

Grazing influences the spatial and temporal dynamics of vegetation heterogeneity and structure. Whether due to intensification or abandonment, changes in grazing dynamics may cause a variety of habitat responses at different spatio-temporal scales that significantly influence ecological communities. Despite extensive knowledge on the effects of grazing on mountain ecosystems, there is still a limited understanding of how different grazing histories and their legacy (i.e. past long-term effects) interact to shape biodiversity across broad spatial gradients. We aimed to identify the optimal stage of vegetation conditions resulting from particular grazing dynamics and their legacy effects that would maximise butterfly and plant biodiversity across a large geographical range in the Pyrenees. We sought to assess how grazing (either through legacies or immediate effects) influences the richness, abundance, community composition and functional group structure of both plant and butterfly species. We conducted butterfly and plant surveys in 60-x-60m plots in 12 valleys in the Catalan Pyrenees (western Mediterranean) under four different grazing legacy regimes representing different vegetation conditions, ranging from heavily grazed grasslands to densely scrub-encroached areas. We also conducted participatory mapping with local cattle-herders to gain insights into the spatial-temporal dynamics of the grazing legacy regimes. Intermediate grazing stages exhibited significantly higher plant and butterfly richness and abundance, and also harboured, species of greater conservation concern. Grazing legacy was the main driver for butterfly and plant diversity, community composition and functionality. Maintaining low to medium grazing intensity is essential for preserving vegetation heterogeneity and enhancing both butterfly and plant richness and abundance.

Comparative assessment of DNA metabarcoding and morphological identification for the detection of meroplanktonic larvae in Mediterranean zooplankton communities

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Marine zooplankton communities play a fundamental role in pelagic food webs, biogeochemical cycles, and the dispersal of benthic marine organisms through their meroplanktonic larval stages. However, the characterization of these communities and the assessment of population connectivity remain challenging due to the high taxonomic diversity and morphological similarity of many larval forms. Recent advances in environmental DNA (eDNA) metabarcoding and high-throughput sequencing provide new opportunities to overcome these limitations, enabling both biodiversity assessment and population-level analyses from environmental samples. This study aims to characterize the taxonomic diversity, seasonal dynamics, and connectivity patterns of zooplankton and meroplankton communities along the Catalan coast using eDNA-based approaches. Monthly zooplankton samples were collected in Barcelona and Blanes and processed through DNA extraction, mitochondrial COI metabarcoding, and high-throughput sequencing. Bioinformatic analyses were conducted using the MJOLNIR pipeline, focusing on the detection of larvae from four benthic echinoderm species of ecological importance in the western Mediterranean: *Paracentrotus lividus*, *Arbacia lixula*, *Holothuria tubulosa*, and *H. mammata*. Molecular identifications were compared with traditional morphological observations to evaluate the complementarity and taxonomic resolution of both approaches.

To further investigate connectivity, species-specific population genomic tools are being developed through the identification of informative nuclear SNP markers from available genomic resources. Multiplex PCR panels targeting approximately 96 loci per species will be validated using adult specimens before being applied to environmental plankton samples. Sequencing data will then be used to estimate allele frequencies and assess spatial and temporal patterns of genetic differentiation among populations. Preliminary results demonstrate the successful detection of all four target species using both morphological and metabarcoding approaches. The integration of metabarcoding and population genomics from environmental samples represents a promising non-invasive framework for monitoring marine biodiversity, larval dispersal, and population connectivity, providing valuable tools for conservation and long-term ecosystem management in the Mediterranean Sea.

(First year of PhD).

Disarming the venom arsenal of *Atractaspis andersonii* through a multi-omics approach

Maria Estarellas¹, Sergi Tulloch¹, Juan D. Bayona-Serrano², Bernat Burriel-Carranza^{1,3}, Laura Blascón⁴, Gabriel Mochales-Riaño¹, Adrián Talavera¹, Ahmed Al Busaidi⁵, Sulaiman Al Hashmi⁵, Inácio de Loiola Meirelles Junqueira-de-Azevedo², Salvador Carranza¹

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Burrowing asps (*Atractaspis* spp.) are a distinctive group of fossorial snakes distributed across Africa and parts of the Middle East and Arabia. Adapted to a subterranean lifestyle, these nocturnal predators primarily feed on lizards, small snakes, small mammals and frogs which they subdue using their highly specialized venom. Their fangs are particularly extraordinary: long, hollow, and highly mobile, these fangs can rotate laterally, enabling venom delivery without fully opening their mouths. This adaptation allows them to strike effectively in tight spaces, such as burrows or crevices. Despite their medical importance and unique venom properties, there is currently no antivenom available for *Atractaspis* envenomations worldwide. In this study we assembled a chromosome-level reference genome for *Atractaspis andersonii*, annotated it using RNA sequencing data from 12 different tissues and analyzed the venom-gland transcriptome, identifying all the venom-coding transcripts. The most expressed toxin loci were then manually annotated in the genome.

The genome of *A. andersonii* consisted of 22 putative chromosomes (10 macro and 10 micro chromosomes) + Z and W. We were able to annotate the locus of the Sarafotoxin, the most abundantly expressed toxin in the venom gland transcriptome (36%), and a toxin that is unique to the *Atractaspis* genus. Other highly expressed toxins were Cystatins (22%) and Phospholipases A2 (19%). Phospholipases A2 type E have expanded in *Atractaspis andersonii*. Another interesting finding was the detection of the three types of Snake Venom Matrix Metalloproteases (svMMP), which were previously only found in members of Colubroidea. Overall, these findings highlight the importance of having chromosome-level reference genomes as they allow the annotation of complete toxin loci, facilitating the identification of novel gene duplications and contractions.

West Nile Virus Disease Ecology in Avian Hosts

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Abstract

Introduction. West Nile virus (WNV) is a multi-host vector-borne pathogen maintained in an enzootic cycle between *Culex* mosquitoes and wild birds. Transmission depends on avian communities whose species differ strikingly in host competence—their ability to sustain and transmit infection. Despite its epidemiological importance, host competence has been characterised largely in isolation, one species at a time, while the ecological and evolutionary determinants of these differences remain unknown.

Materials and methods. We synthesized WNV experimental infection data and extracted four complementary dimensions of WNV host response: viral load, kinetics, tolerance, and survival. Using phylogenetic comparative methods, we tested whether competence variation reflects life-history-mediated constraints on immune investment, where size and reproductive effort trade off against survival, or whether greater exposure to parasite diversity, through geography and ecology, selects for stronger host responses.

Results. Viral load and survival appear inversely related, revealing deep constraints on avian immunity shaped by life-history trade-offs and long-term parasite exposure. Smaller but long-lived species develop higher viral load and suffer greater mortality. Additionally, species with minimal parasite exposure (residents, high-latitude breeders, restricted ranges) show substantially higher viral load and mortality, yet this gradient is reversed in long-distance migrants. In contrast, infection kinetics responds to distinct pressures: higher metabolic rates accelerate viral clearance, while greater pathogen exposure (through wetland habitats, animal-based diets, and social aggregation) selects for faster immune responses.

Discussion and conclusions. Our results suggest that WNV host competence is not a single biological axis, but a multidimensional phenotype whose components are partially decoupled. Linking these dimensions to ecological, life-history, and phylogenetic predictors can help extend inference beyond experimentally tested species, providing a framework to predict host responses and identify likely amplifying hosts across avian communities.

Hidden Carbon Sinks: Rewetting events drive unexpected CO₂ fixation in Saline Endorheic Lagoons

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Saline endorheic aquatic systems (SEAS) represent a substantial fraction of global inland waters, accounting for ~40% of total lake volume and ~20% of surface area worldwide, especially in arid regions. Growing evidence suggests that lakes can act as significant carbon sinks through the burial of organic carbon in sediments; however, their overall role in the carbon cycle is complex, as many lakes simultaneously emit CO₂ and may function as net carbon sources depending on environmental conditions.

In this context, the interaction between hydrological fluctuations (including drying events) and salinity may play a substantial role in regulating carbon fluxes in these systems. Under the global climate crisis, with increasing aridity and salinization of inland waters, it is critical to understand how these stressors influence CO₂ emissions.

Here, we investigated the implications of salinity in the response of CO₂ fluxes to rewetting using lab incubations of benthic sediments after a drying period. To this end, we investigated 12 endorheic shallow lagoons across the Iberian Peninsula, encompassing a natural salinity gradient. Paired incubations of rewetted sediment under light and dark conditions were conducted, and rates of CO₂ emission and or fixation were measured. Preliminary results revealed that freshwater and hyposaline lagoons showed net CO₂ release after rewetting, whereas mesosaline and hypersaline systems exhibited similar net CO₂ uptake under both light and dark conditions.

A further experiment with sterilized sediments confirmed that biologically mediated processes largely explain the observed CO₂ fixation, although a minor abiotic contribution was also detected. Ongoing experiments using ¹³C-CO₂ isotopic tracers and gene expression analyses of key C cycling genes aim to track C incorporation into microbial biomass and identify the metabolic pathways driving these processes.

Overall, the contrasting responses of freshwater and saline lagoons to post-drought rewetting underscore the need to revise current carbon balance models for inland waters.

Natural seagrass recovery enhances biomass and soil carbon sequestration and avoids erosion-driven CO₂ emissions

Enric Gomis^{1,2,3} (3rd year PhD candidate)

Supervisor: Oscar Serrano

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Abstract

Extreme climatic events can trigger the collapse of seagrass ecosystems and the loss of the ecosystem services they provide. However, the return of ecosystem services with the recovery of seagrasses, including blue carbon, remains largely unknown. Here, we retrospectively studied CO₂ emissions resulting from seagrass loss during the 2010/2011 marine heatwave in Shark Bay (Western Australia) and estimated soil enhanced carbon sequestration and avoided emissions linked to seagrass recovery. The study of carbon dynamics across resilient, lost, and naturally recovered meadows dominated by *Posidonia australis* and *Amphibolis antarctica* showed that 13.3 ± 1.9 Mg CO_{2-eq} ha⁻¹ yr⁻¹ have been emitted over 12 years due to erosion-driven depletion of soil organic carbon. Naturally recovered *P. australis* meadows accumulated soil and biomass carbon at rates of approximately 15.6 ± 1.8 Mg CO_{2-eq} yr⁻¹ and avoided 8.1 ± 2.4 Mg CO_{2-eq} yr⁻¹ of emissions, within seven years of canopy re-establishment. Recovery trajectories were species-specific, with *A. antarctica* meadows exhibiting ~37% lower carbon gains than *P. australis*. We demonstrate that seagrass recovery can reinstate soil carbon stabilization and accumulation, generating measurable carbon additionality through both enhanced sequestration and avoided emissions from soil erosion. This study provides conversion factors for carbon additionality assessments in seagrass meadows, supporting abatement policy settings for active or passive seagrass restoration actions linked to carbon credits.

TÍTOL:

Environmental DNA uncovers hidden parasite biodiversity in high mountain lakes

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Afiliació: CEAB-CSIC - Integrative Freshwater Ecology Group (IFE)

Any de doctorat: 2nd

Resum:

Parasites play a key role in ecosystem balance by affecting and regulating host populations; however, they are among the most overlooked groups in aquatic ecology. In addition, classical methods based on host examination or microscopy leave considerable gaps in our knowledge of these communities, as they face several constraints in detecting cryptic taxa and complex life cycles. The diversity of remote oligotrophic freshwater environments is even less well understood. To address these limitations, we applied environmental DNA (eDNA) metabarcoding targeting the 18S rRNA gene in 26 high mountain lakes in the Pyrenees. A total of 52 samples were analysed using a paired sampling design consisting of littoral material and surface sediment, testing a double habitat approach. The results revealed a high and previously unknown diversity of parasite OTUs comprising multiple phyla. Assemblage structures differed clearly between littoral and sediment samples, with multivariate analyses showing significant separation between the two habitats. Surface sediments acted as important reservoirs of parasite DNA, which were complementary to those detected in the littoral zone and were not merely duplicates of the same signal. Additionally, parasite signals varied among samples according to the dominant host group, indicating a marked influence of each lake's host composition on parasite assemblages. A small number of OTUs constituted the majority of the total reads, revealing a clear dominance of DNA signal patterns. This study highlights the hidden diversity of parasites in high mountain lakes and demonstrates the value of incorporating eDNA and multiple habitat sampling in aquatic parasitology studies. These findings reinforce the potential of metabarcoding as a tool to advance parasite ecology and freshwater biodiversity monitoring and open the door for future research.

Title: Wetlands of the Past; Reconstructing Changes in Aquatic Systems of the Ebro Delta Over Decadal, Centennial and Millennial Scales.

Authors: Anastasia Ivanova¹, Santi Riera², Teresa Buchaca³, Marc Ventura³, Miquel Vilà⁴, Isabel Cacho⁵, Xavier Benito¹

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Abstract:

Mediterranean deltas are transitional aquatic ecosystems shaped by highly fluctuating environmental regimes that change at different spatial (basin and deltaic plain) and temporal (from decadal to centennial and millennial) scales. The ecological rules linking processes at such varied spatiotemporal scales in deltaic systems are vastly unknown, because, among others, relationships between communities and environmental conditions are often multivariate and weak. Under situations where human activities have altered the ecology of deltas, long-term reconstructions could provide insights into analog situations of global change impacts such as sea-level rise and hydrological perturbations. We are using a plethora of palaeoecological datasets including aquatic benthic assemblages (diatoms and foraminifera), sediment geochemistry (X-Ray fluorescence, isotopic and carbon analyses), and sedimentary DNA, to understand past ecosystem change and its potential drivers in the Ebro Delta.

The study is part of an ongoing PhD thesis year 1 from which two contrasting coastal wetlands have been already cored: Ullals of Baltassar (peat-forming freshwater marsh) and the recently restored Violi wetland. In this presentation I will show preliminary results in the Ullals area where three main sedimentary regimes were developed during the last *ca* 5000 years under different riverine and marine forces. Similarly, the more recent Violi record will provide insights into pre-anthropogenic ecological changes for the last *ca* 300 years provided by distinct responses of benthic foraminifera communities. In the presentation I will also discuss the value of long-term ecological datasets to gain insight into ecosystem dynamics over time for applied research in Mediterranean deltas.

Current PhD Year: First Year (Started in March 2026)

Isolation, Culturing and Characterization of Protist Symbionts from Mediterranean Corals

Joana Krause-Massaguer¹, Javier del Campo¹

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Corals live in association with a wide and diverse microbial community that influences the host's physiology, evolution, and ecological function. Together, the coral host and its associated microbial community form the coral holobiont. Some of the members of the holobiont, the Symbiodiniaceae dinoflagellates and the bacterial community, have been studied extensively. However, other components, including viruses, archaea, fungi, endolithic algae, and protists, remain largely overlooked. In this study, we isolated and characterized several protist symbionts from multiple Mediterranean coral species across different families. Small fragments of coral tissue were homogenized and incubated in filtered and autoclaved seawater and/or in f/2 medium, resulting in mixed cultures containing coral cells and various associated microorganisms. Protist strains were subsequently isolated using dilution-to-extinction, size-fractionation filtration, or fluorescence-activated cell sorting (FACS), enabling the establishment of independent cultures. Genomic DNA was extracted from the established cultures, and the 18S rRNA gene was amplified by polymerase chain reaction (PCR) and sequenced using Sanger sequencing for phylogenetic identification. The isolated protists were additionally characterized morphologically using light microscopy and Ultrastructure Expansion Microscopy. Our findings expand current knowledge of coral-associated protist diversity in the Mediterranean Sea and provide cultured representatives that establish a foundation for future phylogenetic, ecological, and genomic studies.

Joana Krause-Massaguer is a third year PhD student.

Organ-specific variations in the hormonal profile of *Posidonia oceanica* during flowering

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Posidonia oceanica is a marine angiosperm endemic of the Mediterranean sea that forms seagrass meadows with an enormous ecological value. Although it primarily propagates vegetatively, it also produces flowers and fruits. However, we know very little about the hormonal variations in the rhizomes and leaves and their possible functions in the regulation of flowering. Here, we aimed at studying organ-specific variations in hormones during flowering to infer whether the rhizome and/or leaves may contribute to the regulation of flowering in this plant species. Samplings were conducted at two sites along the Costa Brava with contrasting environmental features (a Marine Reserve in the Medes Islands, and an unprotected area in Palamós, both located in NE Spain). Aside from visual differences in terms of density between both sites, the hormonal profile of rhizomes—distinguishing between plagiotropic and orthotropic rhizomes—, leaves and inflorescences largely varied both depending on the site as well as during the different stages of the reproductive cycle. The hormonal profile of rhizomes and leaves strongly differed between the pre-flowering and flowering periods, with large differences as well between reproductive and non-reproductive individuals. Overall, we found a prominent role in the variations of cytokinins during flowering, suggesting a major involvement for this group of phytohormones in the regulation of sexual reproduction. This will undoubtedly help us to better understand the physiological basis of flowering in these meadows thus ultimately contributing to develop appropriate management strategies for the conservation of *Posidonia oceanica*, a key species for Mediterranean marine biodiversity.

Gut microbiomes and ecological adaptation in an insular lizard

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Insular vertebrates often experience resource scarcity and strong seasonal fluctuations, conditions that require an efficient use of trophic resources and the ability to adjust to rapid changes in their availability. Increasing evidence suggests that gut microbial communities play a key role in these processes by influencing how animals digest and metabolize food. Yet how these microbes contribute to host ecological adaptation in natural populations remains poorly understood.

In this talk, I will explore the relationship between gut microbiomes and trophic adaptation in populations of the endemic Balearic lizard (*Podarcis lilfordi*), a species inhabiting small Mediterranean islets. Using shotgun metagenomic sequencing of more than 200 fresh fecal samples collected from multiple populations over three years and across two seasons, we characterized the taxonomic and functional composition of their gut microbial communities and evaluated how these vary across ecological and host intrinsic variables. As these lizards are primarily omnivorous but consume substantial amounts of plant material, we tested the hypothesis that gut microbes facilitate lizard herbivory by investigating microbial pathways involved in the processing of plant-derived fibers.

We observed a remarkably conserved microbial taxonomic and functional profile across populations, despite thousands of years of geographic isolation. This pattern suggests the existence of a core microbial assemblage associated with essential metabolic functions in lizards, largely independent of major geographical, ecological and host-specific variables. At finer scales, however, we detected a more plastic component that varied across populations and seasons, potentially reflecting adaptation to local ecological conditions and fluctuations in resource availability.

By integrating microbiome data with long-term ecological information, this work provides new insights into how host–microbe interactions contribute to metabolic flexibility and trophic adaptation in insular vertebrate populations.

Demography, population dynamics and thermotolerance of the two dominant species of gorgonians in the Canary Islands, Subtropical Eastern Atlantic Ocean.

Gerard Mas^{1,2}

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Abstract

The current global warming scenario threatens biodiversity and has raised increasing concern about the persistence and functioning of ecosystems. Although the importance of biodiversity, significant knowledge gaps remain for many species worldwide, particularly key species that play essential roles in maintaining ecosystem processes. In this context, habitat-forming organisms such as gorgonians are crucial, as they enhance biodiversity through their three-dimensional structures, which modify hydrodynamic conditions and support diverse associated communities. In the Canary Islands (subtropical eastern Atlantic Ocean), the two dominant gorgonian species, *Leptogorgia ruberrima* and *Leptogorgia viminalis*, remain poorly studied, despite the fact that this region is experiencing the fastest warming among the four eastern boundary current systems. These species inhabit depths ranging from approximately 10 to 150 m and can form sparse but extensive forests below 25 m depth. Here, we address gaps in the knowledge of their demography, population dynamics, and resistance to heat stress. Both species exhibit a stable population size structure dominated by intermediate-sized colonies, with a low representation of small colonies. Notably, *L. ruberrima* shows slow growth rates (around 1 cm yr⁻¹), whereas *L. viminalis* grows faster (approximately ~5 cm yr⁻¹), likely attributed to morphological differences. High mortality rates observed in small colonies contrast with the low mortality and good condition of larger, adult colonies, which sustain an overall healthy population status. Moreover, the absence of a significant increase in mortality during and after the warmest heatwave recorded in the region (summer 2023), together with *ex situ* thermotolerance experiments showing a gradual biomass decrease prior to the onset of partial mortality rather than acute mortality, suggests that temperatures at or above the natural thermal maxima (~25 °C) do not yet compromise their persistence. Nevertheless, slow growth, high juvenile mortality, and episodic recruitment indicate potential vulnerability in terms of population renewal and resilience to future disturbances.

I'm currently in the third year of my PhD.

Nom: Berta Mateos Vivar

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Any Doctorat: 3r

Metabarcoding primer evaluation for environmental DNA monitoring of freshwater biodiversity

Freshwater ecosystems have suffered the strongest global biodiversity declines. Covering just 2.3% of land, they hold 9.5% of described animal species, including one-third of vertebrates. Their protection requires robust monitoring tools. Traditional biomonitoring approaches rely on capture-based methods and morphotaxonomic identification, which are time-consuming, invasive and dependent on taxonomic expertise. Next-generation sequencing has enabled a more holistic view of biodiversity through environmental DNA (eDNA) metabarcoding. This non-invasive, taxonomically inclusive approach that detects organisms regardless of size, life stage or mobility. However, the application of eDNA for monitoring freshwater ecosystems remains a novel field and still faces several challenges. Between them, PCR primers chosen to amplify target genes is maybe one of the main method validation steps, while metabarcoding performance analysis depends on the primer election.

To address this challenge, we thoroughly assessed nine metabarcoding primers targeting metazoans, vertebrates and plants. We used eDNA from 52 littoral and surface-sediment samples from Pyrenean lakes to evaluate primer specificity, taxonomic coverage, off-target amplification, and taxonomic resolution.

Our results reveal strong primer-specific differences in detection profiles, with substantial variability in the proportion of non-target sequences, the number of OTUs recovered, and the depth of taxonomic assignment. Off-target amplification varied widely across markers, metazoan primers differed between low values in 16S based primers (3-17%), to much higher proportions in the COI primers (46-93%). OTU richness also differed markedly among primers and biological groups: metazoan markers ranged from 391 to 1,118 OTUs, vertebrate primers from 59 to 162 OTUs, and plant primers from 372 to 576 OTUs. Differences between littoral and surface-sediment samples were also evident; with higher richness in the littoral. These patterns highlight substantial variability in detection capacity, taxonomic resolution and ecological representativeness across markers and sample types. By identifying markers that optimally balance these properties, our results provide a solid methodological basis for selecting the most effective primers for freshwater biomonitoring.

Community composition and functional diversity across brown macroalgal forests.

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Year of PhD: 2nd

Abstract: In coastal marine environments, large brown seaweeds create complex habitats (i.e., macroalgal forests). Depending on the region, they are dominated by different structural species associated to a specific understorey community of smaller algae, which occur as a consequence of the canopy structure. Although all macroalgal forests support a wide array of ecosystem functions and services, the relationship between the different species associations and the particular functions remains poorly understood. Here, we studied four macroalgal forests, each dominated by a different structural species: *Laminaria hyperborea* (N Scotland), *Laminaria ochroleuca* (SW England), *Saccorhiza polyschides* (N Portugal) and *Laminaria rodriguezii* (E Spain). We compared their macroalgal communities using traditional taxonomic-based biodiversity indices and species composition, and further quantified their functional diversity using species-specific traits. Preliminary results show that taxonomic biodiversity indices and trait-based functional diversity exhibit different patterns, and that species composition and functional diversity relatively vary among forests. These results suggest that the replacement of these forests, driven by direct human impacts and climate-driven shifts in the structural species, may lead to changes in ecosystem functioning with significant implications for the conservation and management of these habitats.

Waterbird contribution to rice water weevil pest control and rice production in the Ebro Delta

Alejandro Muñoz-Escribano (2nd year PhD)

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Vertebrates play a key role in agroecosystems through top-down interactions (direct or indirect impacts of higher trophic level organisms on lower ones). These interactions preserve biodiversity and ecosystem's structure and functions at the same time as provide valuable ecosystem services for humans, e.g. pest control. Rice fields present distinctive characteristics compared to other crops as they are typically cultivated in flooded conditions, which causes the vertebrate community to be mainly composed by waterbirds.

The rice water weevil (*Lissorhoptrus oryzophilus*, Kuschel) is an invasive pest species that has been recently introduced in the Ebro Delta. It is unknown whether local predators can feed on this pest but considering the need to reduce the use of agrochemicals, it is crucial to study and promote their capacity as biological pest controllers.

In this study we conducted a predator exclusion experiment preventing waterbirds from entering experimental plots located in five rice fields in the Ebro Delta. We compared *Lissorhoptrus* pest abundance, leaf and root damage, and rice yield between exclusion and control plots. The results showed a tendency for reduced pest abundance and leaf damage in the presence of bird predators, but no difference in root damage. Rice yield was also higher in non-exclusion plots.

We conclude that biological control of the *Lissorhoptrus* pest by waterbirds is possible but limited, mostly occurring in the early stage of the crop growth. Other local field factors may modulate this top-down interaction. Nevertheless, waterbird populations can promote rice yields (via pest control and/or other mechanisms). These findings will help develop measures supporting both waterbird conservation and rice production simultaneously.

Habitat complexity does not affect fish escape behavior in response to underwater human presence

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Habitat complexity can play an important role in predator-prey behavioral interactions by modulating perceived risk. For instance, a more complex habitat can provide greater availability of safe shelters, thereby reducing the magnitude of escape responses. Antipredator behavior can also be shaped by human activity, with animals maintaining greater distance from risky humans (e.g., hunters, fishers) than non-risky ones (e.g., hikers, snorkelers). Understanding how habitat complexity affects antipredator response to humans is therefore crucial for determining whether it modulates the perceived risk in human-wildlife interactions and whether this effect varies across activities that represent different levels of risk. Here, we investigated how flight initiation distance (i.e., the distance at which a predator can approach a prey before it flees) and post-flight behavior (i.e., the type of response after the prey flees) in white seabream (*Diplodus sargus*) varied across different habitat complexity levels when a risky spearfisher or a non-risky snorkeler approached fish. Our results indicated that habitat complexity did not modulate antipredator responses differently according to the level of risk associated with each human activity. Overall, flight initiation distance and post-flight behavior did not differ significantly across complexity levels, while fish fled earlier and more rapidly when approached by spearfishers than by snorkelers. These findings advance our understanding of human-wildlife interactions, suggesting that the behavioral disturbance produced by underwater activities depends strictly on the risk associated with the activity itself, and is not reduced by the complexity of the habitat where the interaction occurs.

Current year of PhD: 2nd year

Unravelling the role of salinity and sediment moisture on greenhouse gases emissions in shallow saline lakes

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Abstract: Globally, saline lakes are shrinking due to climate change and extreme water consumption by human activities, potentially leading to the release of buried organic matter from the sediments to the atmosphere as greenhouse gases (GHGs). However, chronically desiccating saline lakes are scarcely studied and thus, are their emissions, creating a blind spot in global biogeochemical cycles. To address this gap, we investigated the GHGs emissions from Gallocanta and seven additional saline lakes in the Monegros Desert (Aragón, Spain): Salobral, Salineta, Playa, Pito, Muerte, Camarón, and Chiprana, spanning a broad salinity gradient. The GHGs fluxes (FCO₂, FCH₄, and FN₂O) were measured across three hydrological zones within each lake i.e., inundated, exposed - wet, and exposed - dry zones.

Overall saline lakes exhibited high electrical conductivity (proxy of salinity, $23.6 \pm 20.1 \text{ mS cm}^{-1}$), whereas, sediment moisture increase from exposed - dry ($0.30 \pm 0.08 \text{ g g}^{-1} \text{ wW}$) to exposed - wet ($0.37 \pm 0.09 \text{ g g}^{-1} \text{ wW}$), and inundated zones ($0.49 \pm 0.11 \text{ g g}^{-1} \text{ wW}$). Across all sites, substantial FCO₂ ($4.9 \pm 14.2 \mu\text{mol m}^{-2} \text{ s}^{-1}$) and FN₂O ($0.78 \pm 2.7 \text{ nmol m}^{-2} \text{ s}^{-1}$) were observed, while FCH₄ remained low ($0.002 \pm 0.004 \mu\text{mol m}^{-2} \text{ s}^{-1}$). Sediment moisture exerted contrasting controls on GHG fluxes. FCO₂ were consistently higher in exposed - dry ($10 \pm 20.4 \mu\text{mol m}^{-2} \text{ s}^{-1}$) compared to exposed - wet zones ($1.58 \pm 3.92 \mu\text{mol m}^{-2} \text{ s}^{-1}$), highlighting the importance of desiccated sediment in enhancing CO₂ emissions. In contrast, FCH₄ increased with sediment moisture, reflecting the development of anaerobic conditions favorable for methanogenesis. Salinity showed strong correlations with both FCO₂ and FCH₄, further modulating emission dynamics.

Overall, our findings indicate that the desiccation of saline lakes may enhance FCO₂ and FN₂O, while FCH₄ remains relatively low but detectable, underscoring the need to incorporate chronically desiccating saline lakes into global carbon and nitrogen cycle assessments.

Keywords: Saline Lake, Greenhouse gas emissions, Sediment moisture, Salinity, Gallocanta, Monegros

Oral presentation

Title: Seawater intrusion affects river contributions to people in The Gambia

Ana Elena Solórzano Ruiz

IDAEA-CSIC

Universitat de Barcelona

Abstract:

Freshwater ecosystems are undergoing profound transformations under climate and human pressures. In the River Gambia, climate variability and the construction of an upstream dam are altering salinity dynamics and impacting the contributions communities derive from the river. Based on the IPBES framework on Nature's Contributions to People (NCP), we conducted 90 semi-structured interviews in nine communities distributed along a salinity gradient. River-dependent actors, such as fishers, rice farmers, fishmongers, and community representatives, identified both positive and negative contributions associated with the river. Food and feed emerged as the most prominent positive contributions, highlighting the importance of fishing and rice cultivation for livelihoods. Supporting identities and freshwater regulation were also widely recognized contributions, underscoring the river's non-material importance and its regulatory aspects. At the same time, respondents reported significant negative contributions. Food security was simultaneously described as increasingly precarious, reflecting declining rice productivity and changing fish availability. Physical and psychological stress associated with environmental uncertainty was frequently mentioned, along with concerns about deteriorating freshwater quality. Taken together, these findings show that positive and negative contributions increasingly coexist within the same categories, as the river processes that sustain livelihoods also become impacts for the people. This coexistence highlights how salinization is reshaping livelihoods along the river and underscores the need to integrate local perspectives into freshwater governance to support adaptation under interacting climatic and anthropogenic pressures. These findings reveal how salinization is reshaping the ways people experience and benefit from the river. While key contributions such as food provision, freshwater regulation, and cultural identities remain central to local well-being, their capacity to support livelihoods is increasingly threatened by interacting climatic and anthropogenic pressures. This highlights the need to integrate local perspectives into freshwater governance and adaptation planning.

Morphological responses of butterflies to long-term urbanisation

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Urbanisation is a major driver of rapid environmental change that can alter phenotypic traits across animal populations. Here, we investigate whether long-term urbanisation has influenced butterfly wing size and whether responses are modulated by species mobility.

We analysed over 113,000 specimens from 56 butterfly species collected across the United Kingdom between 1901 and 1971, using digitised records and morphological measurements from the Natural History Museum (London). Wing size, a reliable proxy for body size in Lepidoptera, was modelled against human population density as a proxy for urbanisation, derived from historical census data interpolated annually via generalised additive models across 65 counties.

A global mixed-effects model revealed a positive association between urbanisation and wing size, and a negative effect of temperature, consistent with expectations for ectotherms. Species-level models confirmed that responses varied considerably across taxa, with some species increasing and others decreasing in wing size along the urbanisation gradient. To understand what drives this variation, we explored the role of species mobility and found that low-mobility species tend to show stronger positive responses to urbanisation than their more mobile counterparts, suggesting that dispersal ability modulates the degree to which species are exposed to - or respond to - local urban conditions.

Together, these findings show that urbanisation shapes butterfly morphology in a species-specific manner, and that dispersal ability is a key trait associated with the magnitude of this response. Our results highlight the value of natural history collections for detecting long-term phenotypic change driven by urbanisation.

Specialized plant metabolites play a central role in responses to abiotic and biotic environments. However, their extreme diversity limits functionally informative integration into ecological processes, which remains a significant challenge in functional ecology. Recent work has proposed summarizing metabolomes using chemical properties as metabolomic traits, yet their global patterns, ecological relevance, and evolutionary constraints have not been explored.

Here, we aim (1) evaluating the metabolomic trait concept across a global dataset of vascular plants; (2) assessing the biogeographical distribution of metabolomic traits in relation to macroenvironmental gradients; (3) quantifying their phylogenetic signal and disentangle the relative roles of phylogenetic versus niche conservatism; and (4) examining coordination between metabolomic and key classical plant functional traits.

We compiled metabolomic traits for more than 9,300 plant species and identified six chemical properties that effectively summarize variation in three specialized metabolite pathways (alkaloids, terpenoids, and phenolics). These metabolomic traits showed weak biogeographical patterns across major environmental gradients, suggesting that large-scale edaphoclimatic factors are not primary drivers of species-level metabolomic differentiation. Instead, metabolomic variation appears strongly structured by phylogeny, indicating substantial evolutionary conservatism across species.

We detected significant but generally weak correlations between metabolomic and functional traits. These relationships were largely phylogenetically structured, suggesting shared evolutionary constraints linking chemical composition and plant functional strategies.

Overall, our results support the use of metabolomic traits as a meaningful extension of the plant functional trait framework. However, their ecological signal appears to operate more strongly through evolutionary history than through contemporary edaphoclimatic filtering. This may indicate that filtering operates at finer scales, or that key drivers of specialized metabolome, including biotic interactions, such as competition and herbivory, remain insufficiently captured at large scales. Integrating metabolomic traits into experimental stress studies and community ecology frameworks may help elucidate the role of specialized metabolites in plant function and species coexistence.

Title: Advancing High-Resolution Drought Monitoring: Evaluating Remote Sensing Soil Moisture Products

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Current year of PhD: 3rd year PhD

Abstract

Drought is a natural hazard caused by a precipitation deficit and consequent hydrological imbalance (Pachauri et al., 2014; Trenberth et al., 2014), with significant economic and environmental impacts, particularly in agriculture and forest. Although, ground-based observations provide high accuracy for drought-related parameters such as precipitation, temperature, and soil moisture, they lack in coverage and cost, making them unsuitable for large-scale, high-resolution assessments. In contrast, remote sensing technologies offer a cost-effective alternative, providing continuous spatial information over large regions.

This study is conducted as part of the Open Earth Monitor (OEMC) project, which aims to develop a global, high-resolution system for drought monitoring. Our research focuses on identifying and improving existing approaches to create high-resolution monthly drought maps by exploiting drought indicators from ground station meteorological data and remotely sensed soil moisture. Soil moisture plays a key role in drought monitoring and prediction, especially in water-limited ecosystems (D'Odorico et al., 2007; Moran et al., 2004; Peters-Lidard et al., 2008), such as the Ebro Basin at northeast of Spain, the study area.

In terms of the available soil moisture datasets, existing datasets often lack the resolution and reliability required for an effective assessment. To address this, a thorough review was conducted, various soil moisture products provide global coverage, but their coarse spatial resolution requires downscaling techniques to improve usability at local and regional scales. Since our focus is on developing a drought monitoring system with an agricultural emphasis, we prioritized products with spatial resolution 1km. We selected two high-resolution datasets: the Sentinel-1 dual-polarization SAR (DPA) with a 1 km spatial resolution (Fan et al., 2025), and downscaled SMOS soil moisture data at 1 km resolution (Escorihuela et al., 2018; Merlin et al., 2013), provides a longer temporal record. Our analysis compares these data sets across timescale to determine whether soil moisture data complement the drought monitoring approaches.

Title: Comparing how *Typhas* and ruderal vegetation drive redox heterogeneity and the fate of emerging contaminants during managed aquifer recharge

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Abstract: Managed aquifer recharge (MAR) uses infiltration ponds fed with treated wastewater to recharge groundwater, but this water still carries both conventional contaminants, such as nitrogen, and contaminants of emerging concern (CECs) such as pharmaceuticals. Whether these compounds are degraded or persist depends largely on the local redox conditions. In an infiltration pond these conditions vary strongly in space and in time, over wetting-drying recharge cycles and seasons of changing temperature and organic-carbon supply. This variability, also driven by plants vegetation, organic matter and microbes, controls contaminant fate.

We study two infiltration ponds at the Cambrils field site (Tarragona, Spain) that recharge the same treated wastewater but differ in vegetation: one is colonized by *Typha*, the other by ruderal species. Both overlie an engineered, organic-rich reactive barrier of compost, wood, and biochar. Earlier monitoring suggested that the *Typha* pond develops more oxic conditions, pointing to plant control of redox through root oxygen release and litter inputs. Over a one-year, three seasonal campaigns, we combine continuous redox, oxygen, and hydrological sensing; pore-water and sediment chemistry across depth; 16S rRNA profiling of microbial communities; plant biomass and leaf elemental analysis; and drone-based vegetation surveys.

By coupling these datasets, we aim to map how redox conditions evolve spatially and seasonally, and to understand how vegetation and the release of dissolved organic carbon (DOC) by plant litter drive the consumption of electron acceptors and establish the sequence of redox zones. By treating contaminant attenuation as an ecosystem function shaped by vegetation, this work links plant-soil-microbe interactions and carbon-redox coupling to subsurface water quality, and informs the design of nature-based MAR systems for safe water reuse.