BOOK OF ABSTRACTS

Biodiv

Annual Meeting 2025

Welcome

Hi BIODIVers!

It is with great pleasure that we welcome you to the 6th edition of the BIODIV Annual Meeting. This edition is taking place from the 27th to the 29th of April 2025 at Biological Station of Mértola, in the heart of the stunning Alentejo region, Portugal.

The BIODIV Annual Meeting gathers all BIODIV students from Lisbon and Porto with the intention of promoting the exchange of scientific ideas, giving students the opportunity to present and discuss their work.

This year, our motto is "**Bridging Science and Society - From Discovery to Impact**".

Building on the 2024 edition, which examined career paths after completing a PhD—whether within academia or transitioning to industry—this year's meeting will tackle the more complex challenge of translating scientific research from the lab bench to the broader public. Many discoveries face challenges long before they reach the greater public and understanding how to navigate these waters is key to creating science that truly resonates.

The meeting will showcase successful case studies and innovative strategies, aiming to inspire students to bridge the ever-widening divide between science and society. Through captivating testimonials from leading researchers, hands-on workshops, and dynamic open discussions, participants will explore practical ways to turn their discoveries into meaningful contributions to biodiversity conservation and societal well-being.

This book of abstracts will hopefully provide you with all you need to know about this year's Meeting, but if you have any questions, do not hesitate to ask.

We wish you a fantastic meeting!

The Organizing Committee,

Beatriz Portinha
Diana Vasconcelos
Diogo Coutinho-Lima
Isabel Ferreira
Joana Freitas
João Rosa
Mariya Kozak
Sharath Thota

Activities

Plenary talks

This year, the three plenary talks will be focused on the motto of our meeting, “Bridging Science and Society - From Discovery to Impact”. We have invited four speakers that will tell us about their work and career paths, demonstrating how research goes beyond academic boundaries, focusing not only on its impact on society but also on its contribution to the future of science itself. We hope these talks will help you to reflect on your own career path.

BIODIV student talks and posters

One of the main goals of the Annual Meeting is to foster the exchange of ideas and knowledge with each other. As such, presentations by the students are one of the main aspects of our programme! During the talks and poster session, BIODIV students will have the opportunity to present their PhD project to the BIODIV community, promoting scientific discussion and the exchange of ideas.

Workshop

Within the scope of this year’s motto, we will have an activity organised by João Palma, entitled “PYP - Pursue Your Passion - enjoying an adventure in research”.

Social activities

We want to make sure you will have plenty of opportunities to hang out with your PhD colleagues, get to know each other, and foster new and meaningful connections. Thus, social events will include:
Welcome reception: On the 27th of April we will have an informal get together in Mértola City Center. You will be able to enjoy the beginning of the conference, getting to know your colleagues accompanied by delicious pizzas and snacks.

Ice-breaking activities: Throughout the meeting, we will have various activities to encourage interaction with your fellow PhD colleagues, making the meeting more dynamic and fun.

Social dinner: On the 29th of April we will have a group dinner at “Restaurante – Casa Amarela” to celebrate the 6th BIODIV Annual Meeting with style.

Outdoor activity: On the 29th of April we will have a guided visit to the Biological Station of mértola (EBM) and Mértola.

Important information

Where is it?

Welcome Reception

Largo do Rossio do Carmo,
7750-369 Mértola

Accommodations

Clube Náutico (here)
Flor do Guadiana (here)
Beira Rio's Apartments (here)

Venue BIODIVmeeting 2025

Cine-teatro Marques Duque
Rua Dr. Afonso Costa 56 78, 7750-352
Mértola

Social Dinner

Restaurante – Casa Amarela
Estrada dos Celeiros, 7750-301
Mértola

🏡 Accommodation in Mértola:
You'll be assigned specific accommodation, and we'll guide you to it upon arrival on the 27th. If you're arriving on your own, your accommodation will be at one of the following locations:

📍 Important Note:
Although the event is hosted by the Mértola Biological Station, all sessions will take place at the municipality theatre, Cineteatro Duque Marques.

If you have any questions or need help with logistics, feel free to reach out.

Looking forward to seeing you all soon in beautiful Mértola!

Emergency contacts

BIODIV Organizing Committee

Mariya Kozak	+ 351 925 202 862
João Rosa	+ 351 965 145 545
Isabel Ferreira	+ 351 913 228 606

Local emergency numbers
GNR Mertola: + 351 286 612 127
Bombeiros V. Mertola: + 351 286 610 010

Schedule

Sunday, 27th April

10:00 – 18:00 Porto -> Lisbon -> Mértola

18:00 – 20:00 **WELCOME RECEPTION**

Monday, 28th April

09:00 – 09:30 **REGISTRATION**

09:30 – 10:00 **OPENING SESSION**

10:00 – 11:00 Plenary I - **Paulo Célio Alves**

11:00 – 11:30 **COFFEE BREAK**

Student session I - BEHAVIOURAL ECOLOGY

11:30 – 11:45 Alexandre Silva
11:45 – 12:00 Sofia Costa
12:00 – 12:15 Helga Babette
12:15 – 12:30 Pedro Santos

12:30 – 14:00 **LUNCH**

14:00 – 15:00 Plenary II - **Martina Panisi**

Student session II - GENOMICS

15:00 – 15:15 Marcela Alvarenga
15:15 – 15:30. José Costa
15:30 – 15:45 Sofia Alves

15:45 – 16:15 **COFFEE BREAK**

Student session III - VENOMICS

16:15 – 16:45 Margareta Lakušić

Student session IV – FLASH TALKS

16:45 – 16:50 Joana Ferreira e Silva
16:50 – 16:55 Mario Saez
16:55 – 17:00 Marisa Naia
17:00 – 17:05 Maryam Mostajeran
17:05 – 17:10 Carolina Baptista
17:10 – 17:15 João Rosa
17:15 – 17:20 Nellia F. Nyoni

17:20 – 17:30 **BREAK**

17:30 – 18:30 **POSTER SESSION**

Tuesday, 29th April

09:30 – 12:30 Guided visit to **BIOLOGICAL STATION OF MÉRTOLA (EBM)** and **MÉRTOLA**

12:30 – 14:00 **LUNCH**

14:00 – 15:00 Plenary III - **João Marques**

Student session V - GENOMICS

15:00 – 15:15 Sara Sampaio
15:15 – 15:30 Ludmilla Blaschikoff
15:30 – 15:45 Rita Afonso

15:45 – 16:15 **COFFEE BREAK**

Student session VI - MICROBIOTES

16:15 – 16:30 A. Isabel Ferreira
16:30 – 16:45 Sofia Coimbra
16:45 – 17:00 Diana Vasconcelos

17:00 – 17:15 **BREAK**

Student session VII - ECOLOGY

17:15 – 17:30 Vasco Valdez
17:30 – 17:45 Luca Di Giorgio
17:45 – 18:00 Eva Malta-Pinto
18:00 – 18:15 Joana Freitas

20:00 – 23:00 **SOCIAL DINNER**

Wednesday, 30th April

9:00 – 10:00 Plenary V - **Alice Nunes**

10:00 – 10:30 **COFFEE BREAK**

10:30 – 11:30 Workshop - **João Palma**

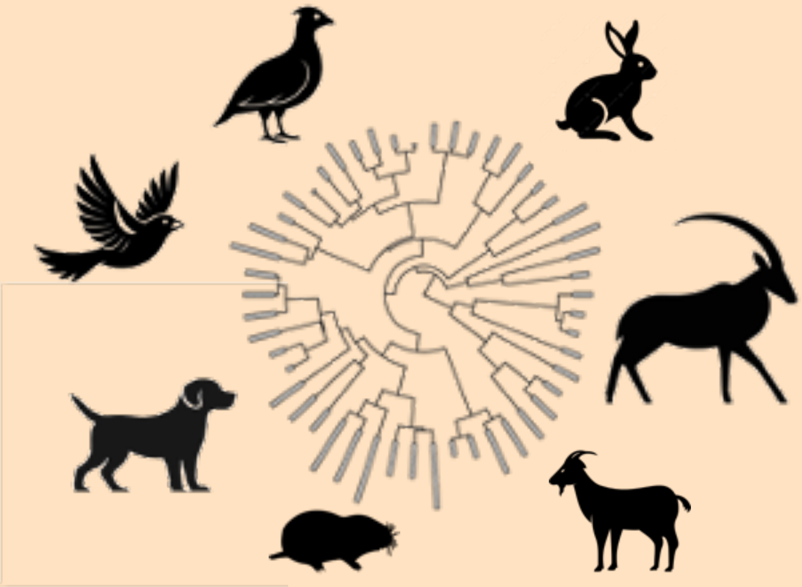
11:30 – 12:30 **CLOSING SESSION**

12:30 – 14:00 **LUNCH**

14:00 – 20:00 Mértola -> Lisbon -> Porto

Posters

1. Beatriz C. Saldanha
2. Eugénio Silva
3. Mariya Kozak
4. Diogo Coutinho-Lima
5. Nellia F. Nyoni
6. Mariana Ribeiro
7. Sara Sampaio
8. Gonçalo Ferraz
9. João Rosa
10. Carolina Baptista



Speakers

João Palma

PYP - Pursue Your Passion - enjoying an adventure in research

Date: 30th April
Time: 10:30 – 11:30

In this presentation, João Palma, originally a biologist with a PhD in Production Ecology and Resource Conservation from Wageningen University, and recognized among the world's top 2% of cited researchers in forestry and agroforestry, will discuss his shift from academic research to independent pursuits. Living near Mértola, João skillfully combines hands-on agricultural tasks—such as repairing tractor tire punctures and replacing diesel pumps—with the establishment of hydrologically efficient landscapes, like keyline designs. His high-level research spans from programming for high-performance computing, forest ecosystem modeling, developing web-based sustainability tools for farmers, GIS, promoting open-source tools and FAIRess or soil metabarcoding analysis. The session will also feature a demonstration of his work on extracting essential oils from an underutilized native species, Rockrose (Cistus ladanifer), contextualized within current policies, including discussions on the "sunk cost fallacy". João will highlight the importance of adhering to best practices in scientific research and maintaining a legacy, regardless of the research environment, be it within or outside traditional academic frameworks.

Martina Panisi

Whose voices are shaping conservation research?

Date: 28th April
Time: 14:00 – 15:00

Can we truly capture the full story of biodiversity change without integrating people into our research and engaging them in future conservation actions? Research that overlooks social dimensions often risks producing conservation recommendations that are impractical or disconnected from real-world challenges. My journey as a researcher began with ecological assessments, but over time, I observed a parallel decline: as species declined, local knowledge about them also changed. If biodiversity knowledge is not passed down, who will safeguard these species locally in the future? Moreover, local conservation priorities do not always align with international agendas, further complicating the path to effective action. How can we, as researchers, integrate social and ecological factors into our work and move beyond data collection to generate actionable, context-specific strategies that bridge science and society? Drawing on my experiences in Saudi Arabia, São Tomé, and Tanzania, I will illustrate how participatory research - by integrating community members, such as students, resource users, and traditional knowledge holders - strengthens conservation recommendations, informs IUCN assessments, and enhances the likelihood of long-term success, ensuring that our findings not only advance science but also lead to meaningful local change.

João Marques

Exploring how genomics and science education can help strengthen the link between Science and Society

Date: 29th April
Time: 14:00 – 15:00

Scientific research is essential to understand the natural world, but its impact on society depends on how well knowledge is shared and communicated. In this talk, I will present two projects that show different ways to bring science and society closer together. First, I will talk about Myxohares, a genomic research initiative aimed at uncovering the genetic basis of myxomatosis susceptibility in Iberian hares. By leveraging high-quality reference genomes and cutting-edge genomic tools, this project seeks to inform disease control strategies, species conservation, and biodiversity management. It also exemplifies how large-scale genomic initiatives such as ERGA and BGE contribute to advancing our ability to monitor and mitigate wildlife diseases. In the second part, I will focus on a long-standing collaboration with a secondary school, where we have developed project-based learning (PBL) initiatives that actively engage students in STEM research. These initiatives have led to scientific publications, conference presentations, and public exhibitions, but most importantly, they have helped foster scientific literacy and critical thinking among students—some of whom have pursued scientific careers as a direct result. This case study highlights the impact of small-scale, hands-on scientific engagement in shaping future generations of informed citizens and researchers. Through these examples, I hope to show how research and education can work together to make science more relevant to society and have a real impact beyond academia.

Alice Nunes

Science-based ecological restoration to inform national and European restoration policies

Date: 30th April
Time: 09:00 – 10:00

Recent global political initiatives on nature restoration by the United Nations and the European Union highlight the urgency of restoring ecosystems to halt biodiversity loss, reverse ecosystem degradation, address the climate crisis, and ensure human security and well-being on a global scale. Scientific support, along with the monitoring and management of restoration projects in the medium and long term, are key factors for the success and cost-effectiveness of restoration efforts. This communication will provide examples of restoration projects implemented in Portugal under different contexts. It will focus in particular on restoration projects that have been monitored for more than 10 years, especially those carried out in semi-arid Mediterranean areas. Agroforestry systems, such as the oak woodlands (montado) that dominate Portuguese drylands, are currently in decline due to multiple interacting environmental factors, including climate change and unsustainable land use. Over the past decades, several projects have been implemented to restore and adapt these systems to climate change. These projects have primarily focused on promoting both natural and assisted regeneration of oaks, as well as pasture restoration, through oak seeding and/or planting and grazing management. Their long-term scientific monitoring has contributed to better predicting climate change impacts and informing land management strategies and decision-making, to combat desertification and enhance the resilience of these vital dryland agroforestry systems to climate change.

Students

Assessing climate change effects on steppe bird reproduction: integrating movement with microclimate and biophysical modelling

Saldanha, B. C. (1,2,3); Marques, A. T. (1,2,4); Rubalcaba, J. G. (5); Silva, J. P. (1,2,4,6)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Instituto Superior de Agronomia, Universidade de Lisboa, Lisboa, Portugal;
(5) Department of Biodiversity, Ecology and Evolution, Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain;
(6) IUCN SSC Bustard Specialist Group.

Steppe birds are facing significant population declines aggravated by climate change. Adapted to arid environments, these birds exert a combination of physiological and behavioural responses to buffer the impacts of elevated temperature. However, behavioural thermoregulation has its limits, as extreme temperatures can restrict activity windows for essential behaviors like breeding and foraging. Recent studies have documented the use of microrefugia by steppe birds, yet our understanding of how microclimates buffer the impacts of climate change on thermoregulation and breeding success are still limited. This gap is partly due to the challenges in collecting data on breeding biology and phenological patterns, as these birds are elusive and highly sensitive to manipulation. Our project will combine high-resolution GPS tracking, 3D accelerometers and field monitoring data from 5 threatened ground nesting steppe birds in Iberia: Little Bustard, Black-bellied and Pintail sandgrouses, Stone Curlew and Montagu's Harrier, with microclimate and biophysical models. Specifically, we will 1) develop biophysical and microclimate models to assess the availability of microclimates and predict how these buffer bird's energy requirements for thermoregulation; 2) explore the causes of the observed sex ratio differential by investigating differences in energy expenditure between sexes during breeding; 3) examine the influence of ambient temperature, incubation and nest temperature on hatching success and the potential of adults to buffer these impacts; and 4) outline a multi-species conservation guideline on habitat management aiming for improved breeding success. Thus, inferring, in a non-invasive manner, the mechanisms underlying climate warming impacts on breeding success of steppe birds.

Keywords: Conservation, Ecology, Behaviour

Protecting what we cannot see: A multidisciplinar approach to uncover the movement dynamics and fishing risk of tiger sharks (*Galeocerdo cuvier*) off western Africa

Torralba Sáez, M. (1,2,3); Queiroz, N. (1,2); Godinho, R. (1,2,3,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Zoology, Faculty of Sciences, University of Johannesburg, Johannesburg, South Africa.

Understanding the movements of large, highly migratory pelagic sharks, many of which are overexploited, is paramount for their conservation. One such species, the tiger shark (*Galeocerdo cuvier*), occurs circumglobally in tropical and warm temperate waters. Tiger sharks exhibit remarkable versatility in feeding habits, habitat-use (from nearshore to pelagic), and movement patterns (from local-resident to highly migratory), making them a keystone marine top predator that provides important ecosystem services across disparate environments. However, the abundance of tiger sharks has declined by ~30% due to fishery overexploitation and shark control programs, with current signs of fragmented and some extinct populations. Knowledge on tiger shark population trends, structure, and migratory behaviour has been mostly centred around developed countries, leading to some protection initiatives. Conversely, the lack of research and unregulated fisheries in developing regions, like Africa, hinders effective large-scale management. My PhD thesis project proposes to fill this knowledge gap and, through the implementation of multiple techniques spanning from satellite tracking to genetic analysis, obtain critical information on the population status, movement dynamics, and fishing risk of tiger sharks off western Africa with which to propose robust, science-based conservation measures.

Keywords: Ecology, Behaviour, Genetics

The role of infectious diseases on Iberian wolf conservation in human-dominated landscapes: addressing the neglected domestic-wild canid interface

Ferreira-e-Silva, J. (1,2,3); Nakamura M. (1,2); López-Bao, J. V. (4); Santos, N. (1,2)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) BRI - Biodiversity Research Institute (CSIC – Oviedo University – Principality of Asturias), Oviedo University, Mieres, Spain.

The Iberian wolf is a grey wolf subspecies exclusively found in the Iberian Peninsula that nearly faced extinction in the 20th century. Despite the generalized wolf expansion observed across Europe in the last decades, in Portugal, the number of packs decreased by 8% and their range contracted by 23%, between 2003 and 2019.

Pathogens are one of the drivers of the current global biodiversity decline. While rarely identified as the sole cause of extinctions, they can act synergistically with other threats. The current gap of knowledge on disease ecology for most pathogens, hampers quantifying their role in wildlife population declines.

Distemper, parvovirosis and sarcoptic mange have been associated to wolf mortality and demographic impacts in endangered canid populations. Studies showed the circulation of these pathogens between the three Iberian canids: Iberian wolf, red fox and dog. This research plan will: 1) quantify the demographic effects of the aforementioned pathogens on Iberian wild canids; 2) estimate the species-specific basic reproduction number (R0) for each host-pathogen system. We will use PCR techniques to isolate the pathogens’ nucleic acids from non-invasively sampled faeces, previously submitted to individual genetic identification. The data of each species’ abundance, pathogen prevalence and shedding will be incorporated to estimate the R0 under a Bayesian framework.

This will be a pioneer study into the disease ecology of the Iberian canid community by aiming to estimate the accurate contributions of each host to pathogens’ maintenance. It will help to inform conservation plans and open the dialogue between conservationists and stakeholders.

Keywords: Conservation, Epidemiology; Carnivores

The effects of climate change on meso- and small carnivores: a review and meta-analysis

Valdez, V. (1); Ferreras, P. (2); Rosalino, L.M. (1)

(1) CE3C - Centre for Ecology, Evolution and Environmental Changes & CHANGE - Institute for Global Change and Sustainability, FCUL University of Lisbon, Lisbon, Portugal;
(2) IREC - Instituto de Investigación en Recursos Cinegéticos, Ciudad Real, Spain.

Climate change is a major threat to biodiversity. Higher trophic-level species, as mesocarnivores, are especially affected due to bottom-up cascading effects. The scale of the effects of climate change on mesocarnivores may differ between regions and taxonomic groups, but such variation is still less known. We reviewed 119 articles and detected an increase in studies on climate change effects, with canids and mustelids being the most studied carnivores, while herpestids, procyonids, viverrids, and ailurids were the least studied. Most of the detected studies were from Europe, followed by North and South America. Africa and Oceania presented less studies. The most common approach in assessing the impact of climate change on carnivores was based on the study of the species' spatial ecology and habitat use, but also on population and community ecology. We used 21 articles targeting 54 carnivore species in a meta-analysis. Our results show that, although some habitat generalist species, mainly canids and procyonids, with a wide range of habitats might benefit from climate change, most meso- and small carnivores will likely experience range contraction. This pattern differs between the carnivore families. Species from arid environments, as well as those that are specialists in montane and tropical forests, are likely to experience the greatest declines in their distributional range. Our study highlights that climate change affects carnivores differently and there is also a regional variation in the effects; therefore, conservation actions targeting the mitigation of climate change effects should be tailored to each continent and species.

Keywords: Conservation, Biodiversity, Ecology

Exploring Ecosystem Services and Disservices of Free-ranging Garrano Ponies

Freitas, J. (1,2,3); Lagos, L. (4); Vaz, A. S. (1,5); Álvares, F. (1,2)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Universidade da Coruña, BIOCOST group, Facultade de Ciencias e Centro de Investigación Interuniversitario das Paisaxes Atlánticas Culturais. Universidade da Coruña. Edificio Fontán, Cidade da Cultura de Galicia, Monte Gaiás, s/n. 15707 Santiago de Compostela, España;
(5) NBI, Natural Business Intelligence, Tec Labs 1.2.1, Campus da Faculdade de Ciências da Universidade de Lisboa, Portugal.

Understanding ecological, sociocultural and economic contributions of large herbivores is pivotal for biodiversity conservation and sustainable land management. Garranos are an endangered autochthonous breed of mountain ponies from northwest Portugal, which play a crucial role in ecosystem functioning and hold high sociocultural value for rural communities. However, rural abandonment, land use changes, wolf predation and administrative requirements threaten their survival and traditional free-ranging system.

We aim to examine the ecosystem services (ES) and disservices (EDS) associated with Garranos, exploring their roles in biodiversity conservation, wildfire mitigation and sociocultural significance, through a multidisciplinary approach. This includes a systematic literature review, ecological field assessments, stakeholder interviews and questionnaires, and benchmarking analyses.

Regarding biodiversity conservation, the role of Garrano ponies in wolf diet was assessed using a meta-analysis based on data collected from a systematic literature review. Preliminary results showed Garranos are a preferred prey of Iberian wolves, with higher consumption rates than domestic and wild ungulates in areas where these ponies are free-ranging. This highlights Garranos' role as a buffer species, potentially reducing predation on economically valuable livestock.

Regarding habitat conservation and wildfire mitigation assessment, currently we have GPS-tagged 9 Garrano ponies to assess habitat use and collected 240 faecal samples for dietary analysis. The sociocultural and economic roles of Garranos are analysed using online surveys on general public's perception towards this breed and interviews with horse owners. The results will support a cost-benefit analysis, assessing synergies and trade-offs between ES and EDS to develop sustainable management and conservation strategies for Garranos.

Keywords: Conservation, Ecology

The Legacy of Ancient Introgression in Hares

Costa, J. (1,2,3,4); Marques, J. P. (1,2,3); Farelo, L. (1,2,3); Boursot, P (4); Melo-Ferreira, J (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(5) Institut des Sciences de l'Évolution Montpellier (ISEM), Université de Montpellier, CNRS, IRD, Montpellier, France.

Introgression is now recognized as a widespread phenomenon, playing a significant role in shaping both species evolution and genetic diversity. Hares provide an excellent model for studying introgression dynamics due to frequent inter-species contacts and historical range shifts during the Ice Ages. A particularly intriguing case involves the broom hare (*Lepus castroviejoi*) and the Italian hare (*Lepus corsicanus*), two closely related species that exhibit traces of mountain hare (*Lepus timidus*) introgression. This event is hypothesized to have occurred in their common ancestor.

In this study, we identified candidate regions of ancient introgression among the three species by detecting genomic regions with local phylogenies that clustered them together. To determine whether these regions resulted from introgression events, we used demographic models to simulate Dxy distributions under a scenario without gene flow.

Future research will focus on examining these regions for genes potentially associated with adaptive processes as well as refining the timing of these introgression events through an extensive dataset of mitogenomes from all European hare species.

Genomics is a powerful tool for addressing broader ecological and evolutionary questions, and our work highlights how historical hybridization events have shaped present-day biodiversity. Understanding species interactions, particularly in the face of climatic changes, not only enables us to reconstruct evolutionary histories but also helps in informing conservation efforts.

Keywords: Evolution, Biodiversity, Genetics

Amphibian ecology, landscape dynamics and citizen engagement for freshwater conservation

Naia, M. (1,2,3,4); Vasconcelos, C. (3,4); Arenas-Castro, S. (5); Crottini, A. (1,2,6)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) CIIMAR – Interdisciplinary Centre of Marine and Environmental Research of the University of Porto, Matosinhos, Portugal;
(5) Department of Botany, Ecology and Plant Physiology , University of Códoba, Córdoba, Spain;
(6) Department of Biology, University of Florence, Via Madonna del Piano 6, I-50019 Sesto Fiorentino, Florence, Italy.

Freshwater ecosystems provide essential services and the highest degree of species diversity of any other habitat. They are in sharp deterioration, paralleled by a decline in freshwater species (e.g., amphibians). Wetlands and amphibians suffer from a negative public perception that limits the impact that conservation measures can have on this habitat and animal group. The Regional Protected Landscape of Vila do Conde Coast and Mindelo Ornithological Reserve as numerous wetlands, and it is renowned for its international herpetological value. However, drastic habitat alterations are underway and management actions can be needed. This region represents an excellent model for developing an approach to bridge the research implementation gap by implementing long-term effective conservation measures. This presentation aims to present preliminary results on the amphibian community composition in the Reserve and on the local communities’ knowledge and perception of freshwater ecosystems. Ultimately, this research project aims to integrate landscape changes analysis and amphibian community characterisation, with the development of citizen engagement activities, through science communication research, to develop science-based measures for freshwater conservation.

Keywords: Conservation, Biodiversity, Ecology

Microgeographic genomic variation and connectivity in an endangered semiaquatic mammal

Sampaio, S. (1,2,3); Barbosa, S. (1,2); Andrés, J. A. (4); Quaglietta, L. (5) ; Bogdanowicz, S. (4); Barros, P. (6) ; Horníková, M. (7); Paupério, J. (8); Alves, P. C. (1,2,3,9); Searle, J. B. (1,2,3,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY, USA;
(5) CIBIO/InBIO, Research Center in Biodiversity and Genetic Resources, Institute of Agronomy, University of Lisbon, Lisbon, Portugal;
(6) Fluvial and Terrestrial Ecology Laboratory, University of Trás-os-Montes and Alto Douro, 5000-801 Vila Real, Portugal;
(7) Laboratory of Molecular Ecology, Institute of Animal Physiology and Genetics, Czech Academy of Sciences, Liběchov, Czechia;
(8) EMBL-EBI, European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, Cambridge, UK;
(9) EBM, Biological Station of Mértola, Mértola, Portugal.

The Iberian desman (*Galemys pyrenaicus*), a semiaquatic mammal endemic to southwestern Europe, is listed as Endangered by the IUCN due to significant range and population decline. Its restriction into headwaters highlights the importance of understanding its genetic variation and connectivity for effective conservation strategies. While previous studies identified five major genetic units across its range, gaps remain in the microgeographic dynamics that shape genetic exchange within specific regions.

This study combines newly generated SNP data with previously available datasets to explore genetic structure in the Iberian desman at a regional scale using a set of 110 SNPs on 115 individuals, confirming the presence of five major phylogeographic units. Focusing on the newly generated data, we explored the microgeographic dynamics of the Occidental unit with a higher-resolution dataset (7,604 SNPs, 14 individuals). This analysis revealed evidence of isolation by distance (IBD), indicating limited dispersal at short spatial scales. Additionally, within the Douro river system, we identified overland dispersal between adjacent headwaters from closely located watersheds, highlighting the importance of both aquatic and terrestrial corridors in maintaining connectivity.

Our findings emphasize the critical role of headwater regions in supporting gene flow and preserving genetic diversity in this species. Conservation efforts should prioritize the protection and restoration of riparian and terrestrial corridors, particularly in fragmented landscapes, to mitigate isolation and preserve genetic health. This study underscores the value of genomic approaches in conservation and contributes to a deeper understanding of the ecological and evolutionary processes that maintain population connectivity in endangered species.

Keywords: Conservation, Genetics

Data mining for new markers: finding parasites in host genome sequences

Ferreira, A. I. (1,2,3,4); Harris, D. J. (1,2)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) E2S - Escola Superior de Saúde

Species of the genus *Hepatozoon* are apicomplexan parasites that infect a wide range of vertebrates, including reptiles, amphibians, birds, and mammals. In reptiles, this is one of the most commonly identified blood parasites, but prevalence and intensity vary significantly across geographic regions and host species. Despite their broad host range, mitochondrial and apicoplast sequences for *Hepatozoon* remain scarce, with most phylogenetic studies relying on the highly conserved 18S rRNA gene, which limits species differentiation.

This study aimed to expand knowledge of diversity within *Hepatozoon* by screening mitochondrial and apicoplast sequences against available whole genome datasets. We used the complete mitochondrial genome of *Hepatozoon catesbianae* from an amphibian, and then only the COI, COIII, and CytB regions, along with additional sequences for the mitochondria and apicoplast from *Hepatozoon canis* from a dog. BLAST searches were performed against WGS from Lepidosauria, Amphibia, Aves, Mammalia, Rodents, Lagomorphs, and Carnivora. Significant matches were aligned, and phylogenetic relationships were inferred. Various gene sequences could be identified apparently belonging to these parasites within whole genome datasets from birds, mammals and snakes. Preliminary phylogenetic comparisons using nuclear, mitochondrial and apicoplast gene sequences indicate a lack of congruence between markers, and highlight various issues in current taxonomy. The additional data may be useful in the development of additional primers for organelle sequences that can be used to better understand the evolutionary history of this ancient parasite group.

Keywords: Evolution, Biodiversity, Genetics

Tracing the origin of a 2000-year-old biological invasion

Silva, E. (1,2,3); Alves, J. (1,2,4,5), Carneiro, M. (1,2), Larson, G. (5)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, UK;
(5) Palaeogenomics and Bio-Archaeology Research Network, School of Archaeology, University of Oxford, Oxford, OX1 3QY, UK.

Biological invasions occur when species spread beyond their native ranges, often causing ecological and economic harm. While globalization has accelerated invasions, little is known about their occurrence in ancient times. To address this, we investigated one of the earliest documented cases: the introduction of the European rabbit (*Oryctolagus cuniculus*) to the Balearic Islands. Originally from the Iberian Peninsula, rabbits are now among the most widespread invasive mammals, mainly due to human-mediated introductions in modern times. The Balearic introduction is an exception, recorded by Strabo and Pliny the Elder about 2,000 years ago. They described a rabbit infestation that damaged agriculture, prompting locals to seek help from the Roman Emperor. This parallels modern rabbit-driven ecological disasters, such as in Australia, making it one of the earliest well-documented invasions. To better understand this ancient biological invasion, we have generated 38 exomes and 51 mitochondria of ancient and modern rabbits from three different Balearic islands (Mallorca, Menorca and Ibiza), spanning 2,400 years. We were able to date and sequence the oldest translocated rabbit up to date and our findings reveal independent introductions across the different Balearic Islands, demonstrating complex translocation events linked to human movement unique to each island. We also detected striking changes across different time periods, likely stemming from recent introductions. This research offers a long-term perspective on biological invasions, showing how human activity has shaped ecosystems for millennia by facilitating species dispersal and demonstrating the lasting ecological impacts of invasive species.

Keywords: Evolution, Biodiversity, Genetics

Evolutionary policy for biological invasions: diversifying action pathways and bridging science and society through Living Labs

Malta-Pinto, E. (1,2,3), Vicente, J. R. (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;

Biological invasions are a major driver of global environmental change and biodiversity loss. Globalisation, international trade and long-distance transport continue to facilitate the spread of invasive alien species and amplify their ecological and socio-economic impacts. While policy goals and targets have been established, implementation often relies on rigid governance structures that struggle to succeed, as they are unable to address the challenges posed by the complexity and uncertainty of invasion processes.

In this presentation, I introduce the concept of Evolutionary Policy - a framework for thinking about policy under dynamic and continuously evolving conditions. Using biological invasions as a case study, I explore how the evolutionary principles of variation, selection, renewal, and retention can be leveraged to enhance the adaptability and resilience of governance systems. I discuss practical ways to achieve this, particularly through the diversification of action pathways (i.e., promotion of functional redundancy within policy systems) and the establishment of Living Laboratories (i.e., real-world platforms that foster collaboration, dialogue, experimentation, knowledge exchange, and capacity building). Finally, I highlight my role in establishing a Living Lab in northern Portugal, aimed at enhancing the capacity of local actors to manage biological invasions. This Living Lab will be one of several established across Europe as part of the Horizon project OneSTOP.

Keywords: Conservation, Biodiversity, Ecology

Effects of Artificial Canopy Gaps on Holm Oak Regeneration in Dryland Afforestations

Rosa J. N. (1,2,3,5,6); Moreira F. (1,2,4,6); Ceia R. S. (1,2,4,6); Pesendorfer M. B. (5,7)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) CIBIO – Research Center in Biodiversity and Genetic Resources,InBIO Associated Laboratory, Instituto Superior de Agronomia, Universidade de Lisboa, Lisboa, Portugal;
(5) BOKU, University of Natural Resources and Life Sciences, Vienna, Austria;
(6) Biological Station of Mértola, Praça Luís de Camões, Mértola, Portugal;
(7) Migratory Bird Center, Smithsonian Conservation Biology Institute, USA.

Holm oak (*Quercus rotundifolia*) naturally regenerates in the understory of Pinus pinea and Eucalyptus plantations in southern Portugal, presenting an opportunity to recover degraded forest patches and to enhance diversity and structural complexity of such sites. To assess the impact of artificial canopy gaps on holm oak regeneration, we implemented a Before-After Control-Impact (BACI) experimental design in 2023, creating openings through different thinning treatments in stone pine and eucalypt plantations. Over three years, we monitored the survival and growth of holm oak individuals under varying light availability. Our results reveal how different gap sizes influence regeneration dynamics, and which thinning treatments optimize light conditions while mitigating environmental stress. This study provides insights into assisted natural regeneration as a strategy for restoring afforested landscapes in semi-arid regions.

Keywords: Convervation; Ecology; Restoration

Global review on the effects of roads on felids: knowledge gaps, patterns, and mitigation measures

Grilo, C. (1); Revilla, E. (2)

(1) BIOPOLIS | CIBIO-InBIO - Research Centre in Biodiversity and Genetic Resources | Associate Laboratory / Infrastructure Ecology, Lisboa, Portugal;
(2) EBD-CSIC - Estación Biologica de Doñana - Consejo Superior de Investigaciones Científicas / Biodiversidad y Cambio Global, Sevilla, España.

Felids are particularly vulnerable to transport infrastructure due to negative impacts such as barrier effects and mortality. However, there is limited knowledge on which species are most affected and how these impacts influence their population dynamics. This knowledge gap can limit the development of effective conservation strategies when planning or upgrading roads. The first chapter of my thesis is a systematic review examining: (1) geographical distribution of studies on the effects of roads on felids, (2) knowledge gaps regarding the species studied and the types of road effects assessed, (3) which road effects impact each felid species and, (4) which mitigation measures are effective. I identified N = 748 studies on the effects of roads on felids. Preliminary results indicate that the least-studied aspect of road impacts on felids are indirect conflicts with humans (e.g. cattle depredation near roads; N = 54), while the species with the least available knowledge are *Leopardus braccatus* (N = 1), *Felis nigripes* (N = 1), and *Catopuma badia* (N = 2). The species where data was available with the highest mortality rates are *Prionailurus bengalensis*, *Felis chaus*, and *Leopardus colocolo*. Additionally, I will compare my findings with the IUCN Red List to identify felid species potentially underrepresented in road-related threat assessments. Finally, I will present a table summarizing the effectiveness of various mitigation measures in reducing road impacts on felids.

Keywords: Conservation, Ecology, Behaviour

Wild vs. Captive: a comparative study of genetic and genomic approaches across continents

Meneses_Ribeiro, M (1,2,3); Koepfli, K. P. (4,5); Jansen van Vuuren, B. (6); Godinho, R. (1,2,7)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Smithsonian-Mason School of Conservation, George Mason University, Front Royal, VA 22630, USA;
(5) Center for Species Survival, Smithsonian's National Zoo and Conservation Biology Institute, Front Royal, VA 22630, USA;
(6) Centre for Evolutionary Genomics and Wildlife Conservation, University of Johannesburg, South Africa;
(7) Department of Zoology, Faculty of Sciences, University of Johannesburg, Auckland Park, South Africa.

As defined by the IUCN, a species' conservation status considers population numbers in both wild and ex-situ captive populations. While genetic diversity is not formally included in these assessments, it plays a critical role in maintaining evolutionary potential and effective conservation management. Robust genetic monitoring in captive breeding programs is essential for sustaining biodiversity, particularly for species of economic relevance and conservation concerns. Traditional microsatellite analysis provides valuable insights into genetic structure, but advanced genomic techniques could offer deeper understanding of genetic diversity, inbreeding, and admixture in both captive and wild populations. The sable antelope (*Hippotragus niger*), a large African antelope with five distinct phylogroups, exemplifies the need for such thorough genetic assessments. Despite a decline in wild populations, the species is classified as "least concern" due to increasing numbers in captivity, driven primarily by its economic value for trophy hunting and farming in Southern Africa and North America.

This study examines the genetic diversity and structure of sable antelope populations in South African and North American game farms compared to their wild counterparts. Previous microsatellite data indicated a low prevalence of genetically pure individuals in South African farms, with only two of the five phylogroups represented in captivity, while the wild ancestry of North American stock remains largely unknown. We assessed whether North American farms might retain lineages now scarce in South Africa and compared traditional microsatellite analysis with a species-specific panel of 5,000 single nucleotide polymorphisms (SNPs). Our dataset included 54 wild samples, 85 from South African farms, and 76 from North America.

Our findings show that North American farms primarily house individuals from a single wild phylogroup, yet they exhibit greater genetic diversity than both South African captive and wild populations. Structure and differentiation analyses reveal that North American individuals form a distinct genetic group, separate from South African populations. SNPs and microsatellites demonstrated equally reliable assignments to wild groups and structure patterns, though SNP markers provided enhanced resolution. These results highlight how geographic isolation and management strategies influence genetic diversity and structure in captive populations. Incorporating comprehensive genetic analyses is crucial to preserve genetic health and ensure that reintroduction efforts support the long-term evolutionary potential and adaptability of species.

Keywords: Ecology,

A genetic overview of the evolutionary potential of understudied wolf populations

Mostajeran, M. (1,2,3); Godinho, R. (1,2,3,4); Lobo, D. (1,2); Khalatbari, L. (1,2)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Zoology, Faculty of Sciences, University of Johannesburg, Johannesburg, South Africa.

The Arabian wolf (*Canis lupus arabs*) is a unique canid native to the fragmented landscapes of the Arabian Peninsula. Once widespread, these wolves now face significant challenges from habitat loss, human pressures, and increased contact with free-roaming domestic dogs. These interactions raise important questions about hybridization and its role in shaping the evolutionary path of the species. Exploring hybridization and speciation in the Arabian wolf is crucial to understanding how human-driven environmental changes are reshaping natural populations. This study aims to examine the genetic structure of the Arabian wolf and assess the extent of wolf-dog hybridization.

In the field, non-invasive samples are collected from several nature reserves in the AlUla region. Microsatellite analysis is then used to build a detailed genetic database that allows for individual identification and the detection of hybridization events. Alongside these efforts, whole-genome sequencing of select individuals provides high-resolution data on genetic diversity and helps trace historical gene flow between wolves and dogs.

Population genetic analyses, including Bayesian clustering and demographic modeling such as the Pairwise Sequentially Markovian Coalescent (PSMC) approach, are applied to reconstruct the population's genetic history. These methods offer insights into past admixture events and reveal trends in population dynamics over time. The main goals of this research are to determine the current genetic status of the Arabian wolf, quantify the level of past and present hybridization with domestic dogs, and understand how these genetic interactions may affect the long-term survival of the species.

Keywords: Evolution, Conservation, Genetics

The Dairy Microbiome: A Reservoir of Antibiotic Resistance Genes

Duarte-Coimbra, S. (1,2,3); Pérez-Pardal, L.(1,2,3); Beja-Pereira,A.(1,2,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) DGAOT - Faculdade de Ciências, Universidade do Porto, Porto.

The dairy holobiome refers to the community of microorganisms present in the ecosystem of a dairy farm, incorporating the animal, cohabiting human, and environmental microbiomes. Integrated into the MICRODAI project, this study aims to characterize the dairy farm ecosystem and assess its potential as a reservoir for antibiotic resistance genes. This knowledge can be used as a biosafety indicator, contributing to the well-being of animals and humans on dairy farms. Fecal samples were collected from eigtheen dairy farms in the Northern region of Portugal, selected based on biosafety surveys and with equitable representation of small, medium, and large farms. Total DNA was extracted and sequenced using long-read Nanopore technology. Bioinformatic analysis identified 15485 taxa, with larger dairy farms with a lower diverse microbiome. The most abundant phyla are Pseudomonadota, Bacillota, and Uroviricota, and the species are *Escherichia Coli, Caudoviricetes sp.,* and *Oscillospiraceae bacterium*. *Caudoviricetes sp.* are bacteriophages that can play a crucial role in maintaining animal health by controlling pathogens. Tet40, TetQ, and InuC genes were identified in higher prevalence in our samples, which confer resistance to tetracycline and lincosamide. Both antibiotics are commonly used in bacterial infections in animals. These findings highlight the dairy farm environment as a significant reservoir for antibiotic resistance, highlighting the need for improved biosecurity measures to mitigate public health risks. While these results are preliminary, they demonstrate evidence of the potential of third-generation sequencing for identifying bacterial genomes, including genomic regions associated with resistance to antibiotics, disinfectants, and detergents.

Keywords: Biodiversity, Genetics

Ecological and social impacts of Asian Toad invasion in Madagascar: past, present, and future perspectives.

Di Giorgio, L. (1,2,3); Licata, F. (1,2); Porcel, X. (1,2,3); Crottini, A. (1,2,4).

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Biology, University of Florence, Via Madonna del Piano 6, I-50019 Sesto Fiorentino, Florence, Italy.

The invasion of the Asian common toad (*Duttaphrynus melanostictus*) in Madagascar, first detected in 2014, represents an ecological and socio-economic concern. Its toxicity, accelerated lifecycle, and adaptability threaten both biodiversity and local livelihoods.

Since the scientific community has become aware of the spread of the toad, scientific investigations have been developed to investigate the toad's invasion from different perspectives. Early studies focused on mapping its spread, movement patterns, and habitat preferences, providing a foundation for targeted monitoring efforts. Current research aims to examine the toad's larval ecology—an overlooked yet crucial aspect of its life cycle. Looking ahead, other research is investigating the species' physiological tolerances and potential distribution shifts under climate change scenarios, informing long-term mitigation efforts.

Effective invasive species management must bridge the gap between research and real-world action. The spread of *D. melanostictus* not only threatens Madagascar's unique biodiversity but also carries significant socio-economic implications. The loss of native species, hence, could disrupt ecosystem services, negatively affecting ecotourism. Additionally, declines in predator populations due to toad toxicity may lead to trophic cascade, potentially increasing rodent populations and their associated risks.

Understanding these ecological and socio-economic dynamics is crucial for developing science-based management strategies. Strengthening collaborations between researchers, policymakers, and local communities will be key to mitigating the impacts of this invasion and preventing similar threats in the future.

Keywords: Ecology, Invasive species

Contribution of neutral and adaptive evolutionary processes in venom diversification across species distribution

Lakušić, M. (1,2,3); Slagboom, J. (4); Dugmedijev, A. (5); Antonov, K. (5); Smith, L. (6); Burić, I. (7); Merdan, S. (8); Tzoras, E. (9); Anđelković, M. (10); Florian-Hempel, B. (11); Kool, J. (4); Martínez-Freiría, F. (1,2)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) AIMMS - Amsterdam Institute of Molecular and Life Sciences, Vrije Universiteit Amsterdam, Amsterdam, the Netherlands;
(5) IBER-BAS - Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria;
(6) IOME - Institute of Organismic and Molecular Evolution, Johannes Gutenberg University, Mainz, Germany;
(7) Hyla - Association Hyla, Zagreb, Croatia;
(8) ATRA - Herpetological Association in Bosnia and Hercegovina ATRA, Sarajevo, Bosnia and Hercegovina;
(9) Unaffiliated, Patras, Greece;
(10) IBISS - Institute for Biological Research “Siniša Stanković”, University of Belgrade, Belgrade, Serbia;
(11) TZR - Veterinary Center for Resistance Research, Freie Universität Berlin, Berlin, Germany.

Venomous species with complex evolutionary histories occuring under a diverse range of biotic and abiotic conditions offer an excellent model system to investigate the contribution of neutral and adaptive factors underlying intraspecific venom variation. In this study, 90 venom samples of *Vipera ammodytes* from 32 localities covering its distribution in the Balkan Peninsula were analysed to identify venom phenotypes and their distribution, evaluate the influence of neutral and adaptive processes on venom variation and determine environmental factors associated with specific venom components. Individual venoms were characterised using a high-throughput proteomic approach, and multivariate analyses of environmental variables were performed to evaluate relationships with neutral and adaptive processes. Two main venom phenotypes, designated Balkan and Euxine, were identified. The Balkan phenotype is widespread across central and western regions, whereas the Euxine phenotype is restricted to the Black Sea coast. Further analyses revealed finer-scale subgroups within these phenotypes, highlighting complex patterns of geographic venom variation, including regions of admixture. Notably, no significant relationships were found between venom composition and phylogenetic groups, suggesting a limited role of neutral processes in shaping venom variation. Instead, adaptive processes, reflected by significant correlations with biogeographic features such as ecoregions and phytoprovinces, emerged as important drivers of venom variation. Environmental variables, specifically aridity, temperature seasonality, and annual precipitation, were significantly correlated with toxin abundances. Although certain variation patterns remain unexplained, particularly in the less extensively sampled Euxine region, the overall geographic variation in venom phenotypes likely reflects regional selective pressures, such as prey availability and climatic conditions.

Keywords: Evolution, Ecology, Venomics

Characterizing the impact of a sub-lethal high temperature on spider mite reproduction

Costa, S. G. (1); Magalhães, S. (1,2); Rodrigues, L. R. (1)

(1) CE3C - Centre for Ecology, Evolution and Environmental Changes & CHANGE - Institute for Global Change and Sustainability, FCUL University of Lisbon, Lisbon, Portugal;
(2) Wissenschaftskolleg zu Berlin, Institute for Advanced Study, Berlin, Germany.

Reproduction is generally more sensitive to high temperatures than survival and arguably a better predictor of the response of populations to climate change. Still, how temperature simultaneously impacts male and female reproductive traits is still not fully understood. Here, we addressed how a sublethal high temperature affects the reproduction of the spider mite *Tetranychus cinnabarinus*, a species where only the first mate sires the offspring of a female. Males and females maintained at 25 or 36°C during development were paired and the fertility of both sexes, their mating rate, mating and remating eagerness, and the paternity of the offspring of females with different mating histories were measured. Female and male fertility declined at 36°C, resulting in lower offspring production and a male-biased sex ratio, respectively, because of haplodiploidy. However, when females remated, a shift in paternity share was observed, with more than one male contributing to the offspring. Mating behaviour accompanied this change, as female mating eagerness decreased in pairs with heat-stressed males, while remating eagerness increased when at least one sex was heat-stressed during the first mating. Interestingly, mating rate decreased in heat-stressed females, possibly due to worse body condition. The observed temperature-induced changes allowed restoring the offspring sex ratio, but did not recover the offspring number. These shifts in mating behaviour and mating system should alter the interactions within and between the sexes, potentially affecting sexual selection and sexual conflict in this species. Whether such changes suffice to prevent population extinction remains an open question.

Keywords: Evolution, Behaviour

Shaped by Fire: Unraveling the Impact of Fire on Lizard Gut Microbiome

Vasconcelos, D. S. (1,2,3); Xavier, R. (1,3); Santos, X. (1,3); Harris, D J. (1,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;

The increasing frequency and intensity of forest fires have significantly altered ecosystems, creating open spaces with early successional vegetation. In these environments, species adapted to mature habitats may decline, while those suited to disturbed areas can find new opportunities. In northern Portugal, where fire activity is frequent, the native species *Podarcis lusitanicus*, may thrive in fire-altered landscapes due to the increased presence of rocks and boulders.

Host-microbiota interactions play a crucial role in the ecology and evolution of species, influenced by factors such as diet, phylogeny, and environmental conditions. This study examined how fire affects the gut microbiota of *P. lusitanicus*. Lizards were sampled from four locations, each with areas burned in 2022 and 2016, along with nearby unburned regions, totaling 12 sites. Cloacal swabs were collected, and bacterial communities were analyzed through metabarcoding of the V4 hypervariable region of the 16S rRNA gene.

Results revealed fire regimes were significantly influenced the bacterial community. Sex seemingly impacted microbial diversity, with females exhibiting higher richness. Additionally, the interaction between sex and individual size affected bacterial composition. And, lastly, diet also influenced bacterial composition, thought its effect was not consistent across all the metrics analyzed.

These findings highlight the ecological resilience of *P. lusitanicus* in fire-prone regions, shedding light on how wildfires shape host-microbe interactions. Understanding these dynamics is essential for predicting how lizard populations and their microbiota adapt to changing fire regimes, offering valuable insights into species survival and ecosystem adaptation in fire-affected landscapes.

Keywords: Biodiversity, Ecology, Genetics

Pawprints in the Genome: Unraveling the DNA of the Portuguese Native Dog Breeds

Blaschikoff, L. (1,2,3); Serra, O. (4); Dreger, D. (5); Spatola, G. J. (5); Simões, F. (4); Parker, H. G. (5), Ostrander, E. A. (5); Ginja, C. (1,2,6); Pires, A. E. (1,2,7)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) INIAV, Instituto Nacional de Investigação Agrária e Veterinária - Unidade de Biotecnologia e recursos Genéticos, Oeiras, Portugal;
(5) Cancer Genetics and Comparative Genomics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda MD, USA;
(6) CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa, Av. Universidade Técnica, 1300-477 Lisboa, Portugal;
(7) Faculdade de Medicina Veterinária, Universidade Lusófona-Centro Universitário de Lisboa; I-MVET Investigação Medicina Veterinária; CECAV - Centro de Ciência Animal e Veterinária. Portugal.

The presence of dogs in Portugal dates to, at least, 7,600 years ago, supported by zooarchaeogenetic evidence. Nowadays, 11 native dog breeds are recognized and are the result of a complex and long evolutionary process.

This study characterises the genomic diversity, population structure and phylogeny of the Portuguese native dog breeds, based on 46 newly generated genomes (4-6 per breed, 9-16x coverage) and 170K SNPs from published data on other 1,781 individuals across 215 worldwide dog breeds for a comprehensive population genomics analysis.

The results revealed new maternal haplotypes distributed across haplogroups A-D, high autosomal diversity within breeds, low to moderate inbreeding levels, shallow genetic differentiation between breeds and distinct population structure patterns - from greater homogeneity to within-breed sub-structure. Runs of Homozygosity analysis revealed that most breeds have a high frequency of short ROH segments (≤1.7 Mb), suggesting little recent inbreeding. These results reflect the diversity of the demographic history of Portuguese dog breeds, such as geographical isolation as in the Castro Laboreiro Watchdog, recent admixture in the Algarve Barrocal and Portuguese Warren Hound, shared ancestry in the Alentejo Mastiff, Transmontano Mastiff and Estrela Mountain Dog breeds and a severe bottleneck in the Portuguese Water Dog.

These outcomes highlight the importance of the Portuguese native dog breeds as a source of genetic variation and their utility and cultural relevance, providing the basis to guide conservation and management actions towards these locally well-adapted and resilient dog breeds.

Keywords: Conservation, Biodiversity, Genetics

Museomics reveals the evolution of alternative genetic basis of winter coat color polymorphism in long-tailed weasels (*Neogale frenata*)

Alvarenga, M. (1,2,3); Pimenta, J. (1,2); Miranda, I. (1,2,3); Farelo, L. (1,2); Mills, L. S. (4); Good, J. M. (4,5); Melo-Ferreira, J. (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Division of Biological Sciences, University of Montana, Missoula, USA;
(5) Wildlife Biology Program, College of Forestry and Conservation, University of Montana, Missoula, USA.

Human-driven environmental changes are reshaping ecosystems at an unprecedented pace, questioning whether species will be able to adapt or face extinction. Understanding how standing genetic variation may promote species' response to changing environments is crucial for conservation efforts. Seasonal traits provide a powerful framework for studying climate-driven evolution, and seasonal coat color (SCC) change – the ability of some species to transition from brown in summer to white in winter to keep camouflage year-round – is a striking model system. This adaptation allows animals avoiding detection in environments with seasonal snow, but as snow cover is dramatically reducing due to climate change, winter-white individuals will tend to become mismatched and more visible, facing predation and reduced fitness. However, variation in winter color exists, with some individuals keeping brown coats year-round in regions with less or no winter snow. Winter coat color polymorphism (WCCP) could thus be key to population persistence in changing environments. Here, we investigated the genetic basis, origin, and evolutionary history of WCCP in the long-tailed weasel (*Neogale frenata*), one of the 21 SCC species. Using whole-genome and targeted enrichment sequencing from natural history museum specimens, we analyzed two coat color transition zones in the Western and Eastern United States. Our genome-wide association scans identified a single gene associated with WCCP in both regions, yet distinct candidate deletions were found in each population. Using population genomic and phylogenomic approaches, we explored the origin of these variants and the evolutionary mechanisms maintaining adaptive genetic variation over time. Our findings shed light on the evolution of WCCP and underscore the value of SCC as a model for understanding how species adapt to rapid environmental change.

Keywords: Evolution, Conservation Genomics; Climate Change

Experimentally increased foraging interactions facilitates new social bonds in a cooperatively breeding bird

Fourie, H. B. (1, 2,3); Doutrelant, C. (4,5); Depalle, Y. ; Ferreira, A. C. (1,2,5,6); Covas, R. (1,2,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) FitzPatrick Institute of African Ornithology, DST-NRF Centre of Excellence, University of Cape Town, Rondebosch 7701, South Africa;
(5) CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France;
(6) Department of Evolutionary Biology and Environmental Science, University of Zurich, Zurich 8057, Switzerland.

Preference in social partner choice is often attributed to kinship, as associations among kin provide indirect benefits via shared genes which can enhance inclusive fitness. However, repeated interactions across spatial and temporal proximity can increase social associations and promotes social partner choice independent of kinship. In social environments that are largely kin based, interaction frequency and relatedness can be intertwined.

In this study, we tested if experimentally increasing the number of feeding associations at one set-up can facilitate the formation of new and stronger associations among less-related individuals at another set up. We studied the sociable weaver (*Philetairus socius*) a bird that lives in colonies with a highly kin-based social environment that naturally prefers to forage with related individuals. However, whether relatedness is the only possible driver of this social feeding preference is unknown.

We built RFID-based systems to detect individuals and create “restrictive feeders” that prevented birds from foraging with their kin and instead encouraged interactions with less related individuals. We monitored subsequent associations at unrestricted feeders where birds can forage with who they want. Our results show that this manipulation led to new and stronger associations among those less related birds that were forced to interact more often. This suggests that proximity can promote social partner choice even in a predominantly kin-based context. These findings show the frequency of social encounters can act as a mechanism of social partner selection and has implications for understanding how group cohesion is maintained animal societies.

Keywords: Evolution, Behaviour, Social Network

Birds’ structural coloration diversity explained by changes in feather keratinization

Afonso, R. O. (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal.

Coloration is a fascinating aspect of avian biology. The vast diversity of hues and patterns observed among birds is shaped by natural and sexual selection as a result of its high ecological impact, in particular for sexual attractiveness, communication and camouflage. Bird colors can emerge from the deposition of pigments throughout feather development and/or from the interaction of light with nanostructures within the feathers. Among the latter are colors such as opaque blues and violets, known as non-iridescent structural colors. This mechanism of color production occurs within feather barbs and relies on two principles: absorption of light by a proximal layer of melanin; and refraction of short wavelengths by interaction with a “spongy-like” matrix formed by keratin and air spaces. While this is well established, the genetic bases of non-iridescent structural coloration in birds and how it is formed during feather development have remained poorly understood. Many avian species have been domesticated along Human history, which led to the emergence of numerous varieties, introducing novel color combinations and hues. Here, we combine photonics, microscopy, genomics and gene expression analyses to investigate an artificially selected mutation resulting in different shades of blue in lovebirds, which is representative of the natural variation in non-iridescent structural coloration observed among birds. This research uncovers a novel molecular mechanism based on protein cross-linking that can explain both the formation of opaque blue feathers, as well as the fine tuning of its hue, bringing a relevant advance in the field.

Keywords: Evolution, Biodiversity, Genetics

The adaptive potential of sharks in a changing ocean: insights from comparative and population genomics

Alves, J. S. (1,2,3,4); Queiroz, N. (1,2), Arnaud-Haond, S. (4); Marques, J. P. (1,2); Melo-Ferreira, J. (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) MARBEC, Univ Montpellier, Ifremer, IRD, CNRS, Sète, France.

The impacts of climate change on the oceans are intensifying, with rising temperatures and declining oxygen levels, posing significant challenges to ectothermic species like sharks that rely on external conditions for temperature regulation. These high-energy predators are vulnerable to both climate change and overfishing, resulting in the loss of millions of individuals annually. However, the combined effects of fishing pressure and climate-driven environmental changes on the genetic diversity of marine species remain largely unexplored. The blue shark (*Prionace glauca*), a heavily fished migratory predator, is an ideal model for investigating genetic diversity patterns and resilience to these pressures. Early studies suggested a homogeneous genetic structure, likely due to its high mobility, while more recent SNP analyses detected subtle genetic differentiation between the North Atlantic and the Mediterranean. However, the resolution of these methods is limited. Whole-genome sequencing offers a higher-resolution approach to clarify these genetic signals.

The project's primary objective is to generate a high-quality genome assembly of the Atlantic blue shark, which will anchor subsequent analyses. It will also explore shark lineage evolution from a macroevolutionary perspective, considering adaptive traits across the evolutionary tree of these species. Fine-scale patterns of genetic diversity in blue sharks, particularly across the Atlantic, will be studied using population genomics, with integration of movement ecology data to explore species behavior. Preliminary results from population structure analyses, utilizing whole-genome sequencing for the first time in this species, will be presented. This project aims to provide conservation guidelines for blue sharks and other pelagic marine predators.

Keywords: Evolution, Conservation, Genetics

Traffic reductions benefited species already tolerant of noise pollution

Santos, P. M. (1,2,3) Mennill, D. J. (4), Koper, N. (5), Cardoso, G. C. (1,2)

1. CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
2. BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
3. Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
4. Department of Integrative Biology, University of Windsor, Windsor, Ontario, N9B3P4, Canada;
5. Faculty of Environment, University of Northern British Columbia, Prince George, BC V2N 4Z9, Canada.

Anthropogenic noise is a highly pervasive but many times neglected pollutant worldwide. Noise from human activities is known to affect communication in wild animals, increase physiological stress and impact important biological dynamics such as breeding, space orientation and predator-prey dynamics. Because noise is most intense at lower frequencies of the power spectrum, species that communicate using lower frequencies and within narrower bandwidths are expected to be severely impacted because of “energetic masking” (i.e. the overlap of noise and vocalization frequencies). During the COVID-19 pandemic, anthropogenic activities were severely halted for many months worldwide, and reductions of human traffic were connected to increases in abundance of many bird species in North America. Because songbirds are a group of highly communicative species known to be impacted by current high levels of noise pollution, we tested if the verified abundance changes from pre-pandemic to pandemic periods were related with the frequency characteristics of species’ songs. Surprisingly, species expected to be more acoustically resistant to noise (i.e. vocalizing at high frequencies and within wider frequency bandwidths) were the ones that presented stronger abundance changes in counties/states of USA and Canada where traffic reductions were greater. Such results seem to indicate that current levels of noise pollution can also be negative towards so called "noise-tolerant" species and how traffic reductions verified during the COVID-19 pandemic were potentially not severe enough to impact counts of less-tolerant species.

Keywords: Biodiversity, Ecology, Behaviour

Inducible tomato defences persist in detached leaves, but are differentially affected by plant integrity and genotype

Kozak, M. (1), Godinho, D. P. (1,2), Yayla E. (3), Fragata, I. (1), Magalhães, S. (1,4), Leonor Rodrigues, L. (1)

(1) CE3C - Centre for Ecology, Evolution and Environmental Changes & CHANGE - Institute for Global Change and Sustainability, FCUL University of Lisbon, Lisbon, Portugal;
(2) Gulbenkian Institute for Molecular Medicine, Oeiras, Portugal;
(3) Istanbul Technical University, İstanbul, Turkey;
(4) Wissenschaftskolleg zu Berlin, Institute for Advanced Study, Berlin, Germany.

Herbivore and pathogen attacks often lead to the induction of plant defences. Given the intricate nature of such response, plant integrity is assumed to be a pre-requisite for the successful mounting of defences, a hypothesis supported by work done in plant-pathogen interactions. However, the relevance of plant integrity in plant-herbivore interactions, particularly in direct plant defences, is unclear and lacks empirical molecular validation. To test this, we measured gene expression of plant defence-related genes (PPO-D, PI-IIc and PR-1a) in intact plants or detached leaves of two tomato varieties (Castlemart and Moneymaker) infested with the herbivorous spider mite *Tetranychus urticae*. We also tested whether defences persisted in leaves after one, four, seven or fourteen days of infestation of detached leaves. We found that tomato defences were induced in both intact plants and detached leaves. Moreover, the expression of all three genes in detached leaves increased over time, with the two late-expression genes, PI-IIc and PR-1a, displaying a higher increase. However, differences in induction levels between intact plants and detached leaves varied with plant variety and the gene assessed. Our results indicate that detached leaves mount a persistent defensive response, which suggests that both intact plants and detached leaves can be used in studies addressing herbivore interactions with plant defences and herbivore interaction. However, studies aiming at identifying the role of specific genes should account for the differential, variety-dependent, role of plant integrity in their expression.

Keywords: Ecology, Genetics

European Rabbits as Undocumented Hosts of CCHFV in Portugal

Baptista, C. (1,2,3); Santos, N. (1,2); Vial, L. (4); Jori, F. (4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) UMR ASTRE, CIRAD, Campus International de Baillarguet, Montpellier 34398, France.

Crimean-Congo Hemorrhagic Fever virus (CCHFV) has emerged in Southwestern Europe since 2013, posing a significant public health risk. European rabbits are considered potential hosts for the immature stages of *Hyalomma lusitanicum*, a main CCHFV vector in Iberian wildlife. However, their role in CCHFV life cycle remained undocumented. To address this, 667 samples were collected from wild rabbits from 20 different sites in Portugal (2018-2023) and tested for antibodies against CCHFV. Overall seroprevalence was of 0.60% (CI95 0.23%-1.53%). However, in an active focus of CCHFV circulation in Southern Portugal seroprevalence rised to 5.77% (CI95 1.98 – 15.64%) in 2022 (CI95 1.98 – 15.64%). This study provides evidence of the circulation of CCHFV among lagomorphs in Europe, confirming the role of rabbits as hosts for infective Hyalomma ticks in areas of enzootic circulation in the Iberian Peninsula.

Keywords: Conservation, Biodiversity, Ecology

The acoustics of mobbing behaviour in a highly cooperative bird

Marmelo, M. (1,2,3); Rybak, F. (4); Covas, R. (1,2,6); Doutrelant, C. (5,6)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Université Paris-Saclay, CNRS, Institut des Neurosciences Paris-Saclay, Saclay, France;
(5) CEFE-UMR5175 CNRS - Université de Montpellier, Montpellier, France;
(6) FitzPatrick Institute of African Ornithology, DST-NRF Centre of Excellence, University of Cape Town, Rondebosch, South Africa.

Mobbing behaviour is “an anti-predator behaviour where preyed-upon species approach and/or harass a predator while displaying conspicuous, stereotyped movements and/or vocalizations” (Carlson & Griesser, 2022). It is widespread in nature, and identifying mobbing is generally straightforward. However, being a collective response, mobbing is often difficult to measure, especially in species that mob in large groups. The most common method of quantifying mobbing, presence or intensity, is recording the calling behaviour of the mobbing species (Carlson & Griesser, 2022).

This project aims to describe mobbing behaviour of the sociable weaver (Philetairus socius), a colonial, cooperatively breeding passerine endemic to southern Africa, by analysing their acoustic reaction to different threats. Twenty-two sociable weaver colonies were presented with models of two type of predators, Pygmy Falcon, Polihierax semitorquatus, and Cape Cobra, Naja nivea, as well as decoys of two non-predators, the Leopard Tortoise (Stigmochelys pardalis) and Common Scimitarbill (Rhinopomastus cyanomelas). We collected acoustic data during the 3-minute presentation of the models in each colony, of which we used 10-second segments to examine if sound parameters change in response to predators versus non-predators, and among predator types, like in other species (Kalb et al., 2019). We predict that parameters such as maximum frequency, silence, and energy distribution will be different in presence of predator versus control, to encode information not only to the conspecifics but also to the predator. However, general sound parameters may not specify the type of predator if it does not improve efficiency in deterring them.

Keywords: Behaviour

A tale of Guardians and Herders: how historical human practices have shaped the genomic landscape of Iberian livestock dogs

Coutinho-Lima, D. (1,2,3); Doadrio, I. (5); Godinho, R. (1,2,3,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Zoology, Faculty of Sciences, University of Johannesburg, Johannesburg, South Africa;
(5) Museo Nacional de Ciencias Naturales, Consejo Superior de Investigaciones Científicas, Madrid, Spain.

In Iberia, where livestock practices have long been essential to the people's livelihood, genetic diversity and relationships between native livestock guarding and herding dogs remain poorly understood. We genotyped over 300 Iberian dogs to address this gap using 39 autosomal, 6 Y-chromosome microsatellite markers, and over 100k SNPs. Our findings reveal high levels of genetic diversity, without substantial differences between the two dog types. This likely reflects the long history of pastoralism in Iberia and the absence of modern breed management in working dogs. We also identified pervasive signals of historical gene flow and a clear absence of genomic differentiation between functionally distinct breeds. We attribute this to human and livestock practices, particularly transhumance, a powerful driver of gene flow in the past. Overall, this work highlights the complex interplay between livestock practices and breeding dynamics in shaping functionally distinct dogs.

Keywords: Evolution, Genetics, Population genomics

Mucosal surfaces characterization of the genital microbiota in portuguese native goats

Nyoni, N. F. (1,2,3); Duarte-Coimbra, S. (1,2,3); Forcina, G. (1,2); Pérez-Pardal, L.(1,2,3); Beja-Pereira,A.(1,2,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal;
(2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal;
(3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal;
(4) Department of Zoology, Faculty of Sciences, University of Johannesburg, Johannesburg, South Africa;
(5) Museo Nacional de Ciencias Naturales, Consejo Superior de Investigaciones Científicas, Madrid, Spain.

Assessing the reproductive microbiome in small ruminant livestock is vital for enhancing reproductive efficiency, maintaining animal health, and optimizing pregnancy outcomes. A balanced microbiome in the reproductive tract suppresses infections, regulates immune activity, and reduces the risk of microbial imbalances that negatively affect pregnancy. Understanding this microbiome also supports better disease control, informs advanced animal husbandry practices for sheep and goats, and contributes to global food security by improving breeding success. This study aimed to characterize the genitalia microbiome - vaginal and preputial - in native goat breeds using metagenomics sequencing. This study focused on three local Portuguese goat breeds - Preta, Serrana, and Serpentine. Samples were collected from 39 goats and, for comparison, seven sheep from a local breed - Serra Estrela. Microbiome differences were obtained when combining breed and sex factors ($p=0.01$). The predominant genera in both vaginal and preputial samples included Fusobacterium, Aerococcus, Corynebacterium, Sediminibacterium, Campylobacter and Ralstonia. This contributes to the limited understanding of reproductive microbiota in Portuguese native goats, which is essential for animal husbandry and disease control.

Keywords: Microbiome; Goats; 16S rRNA, Metagenomics; Reproductive success.

Biodiv

Annual Meeting 2025

THE ORGANIZING COMMITTEE

- Beatriz Portinha
- Diana Vasconcelos
- Diogo Coutinho-Lima
- Isabel Ferreira
- Joana Freitas
- João Rosa
- Mariya Kozak
- Sharath Thota

THE SCIENTIFIC COMMITTEE

- Prof. Margarida Matos
- Prof. Paulo Célio Alves
- Prof. Rui Rebelo

THANK YOU FOR ATTENDING

U.PORTO FACULDADE DE CIÊNCIAS UNIVERSIDADE DO PORTO · BIOPOLIS · cibio · InBIO · Ciências ULisboa · ce3c centre for ecology, evolution and environmental changes · EBM ESTAÇÃO BIOLÓGICA DE MÉRTOLA · MÉRTOLA CÂMARA MUNICIPAL · Vila do Conde

fct Fundação para a Ciência e a Tecnologia · PD+F FCT PhD PROGRAMMES · GOVERNO DE PORTUGAL · NORTE 2030 Programa Regional do Norte · PORTUGAL 2030 · UNIÃO EUROPEIA Fundo Social Europeu

gradiva · CHANGE Global Change and Sustainability Institute · Biotecnómica soluções para biotecnologia e genómica · STAB vida Your easy genetics laboratory · Porto Editora · Balanches · Bee natura · A PARAGEM restaurante pizzaria