

Trends in Biodiversity and Evolution

# Program and abstract book



**Biodiversity, Ecology and Evolution  
in Mediterranean ecosystems**  
4 - 6 December 2019 | Vairão, Portugal

**TiBE 2019**



## **ORGANIZING COMMITTEE**

Ana Perera

Antigoni Kaliontzopoulou

Arie van der Meijden

Catarina Rato

Catarina Pinho

Fernando Martínez Freiría

Gabriel Riaño

Helena Martínez

Nahla Lucchini

Paulo Célio

Pedro Coelho

Urtzi Enriquez Urzelai

Verónica Gomes

Yuri Simone

## **SCIENTIFIC COMMITTEE**

Daniele Salvi

Fernando Lima

Guillermo Velo Antón

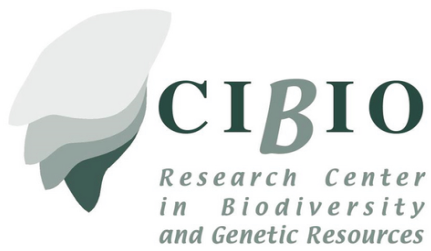
Iñigo Martínez Solano

Pierre-André Crochet

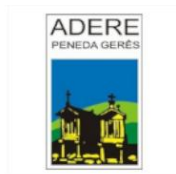
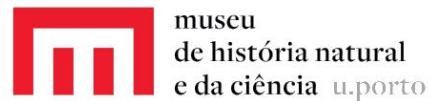
Raquel Xavier

**Photo credits:** PhenEvol research group

## ORGANIZATION



## SPONSORS AND FUNDING PARTNERS



# Contents

CONFERENCE PRESENTATION .....	5
INVITED SPEAKERS .....	6
PROGRAM .....	7
<b>Plenary talks &amp; oral presentations</b> .....	9
SESSION 1: BIODIVERSITY PATTERNS .....	10
SESSION 2: EVOLUTIONARY ECOLOGY .....	16
SESSION 3: CONSERVATION .....	22
SESSION 4: HUMAN-MEDIATED CHANGES .....	28
<b>Poster session &amp; flash talks</b> .....	34
List of participants .....	52

## CONFERENCE PRESENTATION

We are pleased to announce the 9<sup>th</sup> edition of TiBE, Trends in Biodiversity and Evolution conferences, an annual meeting organized by CIBIO-InBIO. The aim of this conference is to bring together senior researchers, post-graduate and graduate students working in the field of evolutionary biology to present and discuss cutting-edge findings in relevant topics related with speciation, molecular evolution, comparative genomics, ecology, population and conservation genetics research, among others.

TiBE2019, organized by the [PhenEvol](#) research group, is devoted to **Biodiversity, Ecology and Evolution in Mediterranean ecosystems**. Represented by the Mediterranean Basin hotspot, these ecosystems occur worldwide supporting the coexistence of a rich flora and fauna with humans. During two days, we will discuss which factors have shaped current biodiversity in Mediterranean ecosystems, evaluate their relative contribution, and analyze the impact of human activities and climate change on their biodiversity. Held in an informal but stimulating scientific atmosphere, these conferences provide an excellent opportunity for strong interaction and brainstorming between students and more experienced researchers.

The scientific program is divided into four sessions, each of which starts with a plenary talk by a leading scientists in the topic, followed by four oral communications, and flash talk sessions. In addition, there are two poster sessions at the end of each day, where participants will have the opportunity to discuss in more detail the posters presented during the flash-talk sessions.

## INVITED SPEAKERS



### Christophe Dufresnes

University of Lausanne and Hintermann  
& Weber Consulting

Switzerland

### Thomas Schmitt

Senckenberg German Entomological Institute,  
Muncheberg and Martin Luther University  
Halle-Wittenberg

Germany



### Cristina Linares

Institut de Recerca de la Biodiversitat - IRBio,  
University of Barcelona

Spain

### Allowen Evin

Institut des Sciences de l'Évolution,  
Montpellier

France)



# PROGRAM

## WEDNESDAY, DECEMBER 4

- 18:00 **Registration and joint social event** in collaboration with the seminar “Restauration and valorization of natural habitats in Peneda Gerês National Park”, organized by the Portuguese Institute for Nature and Forest Conservation (ICNF)

## THURSDAY, DECEMBER 5

### SESSION 1: BIODIVERSITY PATTERNS

- 09:00 Opening ceremony
- 09:30 Plenary talk: Dufresnes, C. Phylogeography and speciation of Mediterranean anurans in the genomic era
- 10:30 Coffee break
- 11:00 Vicent-Castelló, P. Non-congruent nuclear and mitochondrial phylogeographic patterns in *Gluvia dorsalis* (Latreille, 1817)
- 11:20 Cabezas, P. Looking into Mediterranean marine biodiversity: Amphipods (Crustacea: Amphipoda) as a model group
- 11:40 Valverde, J. Patterns and drivers of contemporary pollen flow in a generalist plant species
- 12:00 Lucchini, N. Sources of intraspecific morphological variation in *Vipera seoanei*: allometry, sex, and colour phenotype
- 12:20 Flash talks (Ferreira, S.; Marques, A.; Sánchez-Vialas, A.; Vieira, C.)

13:00 Lunch

### SESSION 2: EVOLUTIONARY ECOLOGY

- 14:30 Plenary talk: Schmitt, T. Mediterranean Biogeography and its implications for conservation
- 15:30 Cheptou, P.O. Analysing rapid evolution of plants life history traits in the face of recent environmental changes thanks to resurrection ecology in *Viola arvensis* and *Cyanus segetum*
- 15:50 Fonseca, C. Hot is worst if dry: an ecophysiological message from Cabo Verde lizards
- 16:10 Coffee break
- 16:40 Gutiérrez-López, R. Competence of Mediterranean mosquitoes for the transmission of locally circulating avian malaria parasites
- 17:00 Sanchez-Montes, G. Contrasting biogeographic responses to Pleistocene glaciations in Iberian amphibians
- 17:20 Flash talks (Bellati, A.; Giralte-Rueda, J.M.; Martínez-Gil, H.; Vieira, C.)

18:00 Poster session

## FRIDAY, DECEMBER 6

### SESSION 3: CONSERVATION

09:30 Plenary talk: Linares, C. Mediterranean marine ecosystems in the Anthropocene: emerging threats and new conservation challenges

10:30 Coffee break

11:00 Veríssimo, J. The night shift - improving the conservation assessment of nocturnal flying insects using DNA metabarcoding

11:20 Gomes-dos-Santos, A. Freshwater conservation assessments in (semi-)arid regions - Testing river intermittence and buffer strategies using freshwater mussels (*Bivalvia*, *Unionida*) in Morocco

11:40 Urošević, A. Mediterranean expats – populations of Kotschy's gecko thriving at the edge of the Pannonian plain in Serbia

12:00 Ledoux, J.-B. Eco-evolutionary processes underlying the population dynamics in the threatened Mediterranean red coral

12:20 Flash talks (Vasconcelos, R. ; Forcina, G.; Ilardo, B.S.; Martelo, J.; Veríssimo, A.)

13:00 Lunch

### SESSION 4: HUMAN-MEDIATED CHANGES

14:30 Plenary talk: Evin, A. Tracking domestication: a bioarchaeological perspective

15:30 Ramos, R. Responses of grassland birds to changing livestock management in Mediterranean grasslands

15:50 Freitas, I. Habitat selection and morphological variation across human-altered habitats in secondary contact zones - The case of Western Mediterranean vipers in northern Iberia

16:10 Coffee break

16:40 Dinis, M. Assessing the impact of habitat loss on a Palearctic relict in Morocco

17:00 Sousa, R. Anthropogenic habitats for two of the rarest freshwater species in the Mediterranean hotspot - Stable refuges or ecological traps?

17:20 Flash talks (Galán Díaz, J.; Lima, C.; Nogueira, J.; Carvalho, C.)

18:00 Closing ceremony

19:00 Farewell Dinner in Centro da Memória de Vila do Conde





***Plenary talks &  
oral communications***



## **SESSION 1**

### **BIODIVERSITY PATTERNS**

**- PLENARY TALK -**

**PHYLOGEOGRAPHY AND SPECIATION OF MEDITERRANEAN ANURANS IN  
THE GENOMIC ERA**

Christophe Dufresnes

*University of Lausanne and Hintermann & Weber Consulting, Switzerland*

Over the past decades, the improvement of molecular tools in biogeography has led to the discovery of an unsuspected amount of cryptic diversity among the herpetofauna of the Palearctic, especially in Mediterranean regions. In amphibians, detailed phylogeographic analyses have been carried on most taxonomic groups, shedding light onto the role of past geological and climatic processes in shaping species diversity and distributions. The advent of genomic resources has now initiated another leap forward, by providing enough resolution to accurately decipher young diversifications at the nuclear, chromosome and even gene levels, and thus get a more comprehensive appreciation of the evolutionary mechanisms ruling the species-population continuum. In this talk, I will present new phylogeographic results obtained by RAD-sequencing from radiations representative of the seven families of anuran amphibians inhabiting the Western Palearctic (from genera *Alytes*, *Discoglossus*, *Bombina*, *Pelodytes*, *Pelobates*, *Bufo*, *Hyla* and *Rana*), with a particular focus on how the patterns of introgression across secondary contact zones can inform on the progress and genetic architecture of speciation in space and time, with lessons for species delimitation. Integrating specific case studies into a comparative framework, this data emphasize that conventional markers had misled phylogeographic conclusions in some groups, revisit the concept of “thresholds of speciation” to delimit nascent species, and illustrate the progressive accumulation of barrier loci putatively linked to hybrid incompatibilities as post-zygotic isolation between diverging lineages builds up. These amphibian speciation genomic frameworks will allow to tackle many fascinating aspects previously out of reach on the origin and maintenance of cryptic nascent species.

# 1. NON-CONGRUENT NUCLEAR AND MITOCHONDRIAL PHYLOGEOGRAPHIC PATTERNS IN *Gluvia dorsalis* (LATREILLE, 1817)

Pablo Vicent-Castelló, Mario García-París, Ernesto Recuero

*Museo Nacional de Ciencias Naturales (MNCN-CSIC), José Gutiérrez Abascal, Madrid, Spain*

The use of phylogeographical methods in wide range species with large morphological plasticity over geographically heterogeneous areas (like the Iberian Peninsula) have frequently revealed the existence of multiple lineages leading to more or less complex patterns of genetic diversity. *Gluvia dorsalis* (Latreille, 1817), a widely distributed Iberian endemic sun-spider (Solifugae), is a perfect subject to test these assumptions. The morphological diversity exhibited by this species is considerable, and in consequence it was subdivided in multiple taxa, but, later synonymized under a single name. In this study we will try to test among contrasting taxonomic hypotheses and to evaluate the extent of morphological plasticity displayed by *Gluvia*. We obtained partial sequences of two mitochondrial (16S and *coxI*) and one nuclear (ITS2) genes from samples collected in multiple populations, covering most part of the species distribution with the aim to reconstruct the phylogeographic patterns and evolutionary history of *Gluvia dorsalis*. Bayesian phylogenetic reconstructions and Coalescence time-calibrated phylograms show two independent evolutionary lineages within *Gluvia*. Marked discrepancies between nuclear and mitochondrial topologies depict differences in the diversification processes and demographic trends along the species evolutionary history.

## 2. LOOKING INTO MEDITERRANEAN MARINE BIODIVERSITY: AMPHIPODS (CRUSTACEA: AMPHIPODA) AS A MODEL GROUP

M.Pilar Cabezas<sup>1,2</sup>, António Múrias dos Santos<sup>1,2</sup>

1. *Faculdade de Ciências, Universidade do Porto, Porto, Portugal*
2. *MarChange, CIBIO-InBIO, Universidade do Porto, Vairão, Portugal*

The Mediterranean Sea is known to harbour at least 6.3% of the world marine biodiversity. However, the existence of important gaps in taxonomic knowledge, especially for smaller invertebrate taxa, and the increasing reports on cryptic species, point out that even the most recent assessments of diversity are likely underestimated in this region. Conversely, the Mediterranean Sea is considered an important hotspot for biological invasions. The ever-increasing global maritime trade and rising seawater temperatures, associated with climatic change, are drastically accelerating the introduction of alien species, which are currently one of the most important drivers of biodiversity alteration in this area. Most of these invaders belong to marine invertebrate taxa which are often taxonomic-problematic groups, hampering our capacity to discern the role of cryptic diversity from human-driven range shifts in the Mediterranean biodiversity. In this study, we will focus on amphipods, small marine crustaceans which are an important trophic link between primary producers and higher trophic levels. Their complicated taxonomy and great intraspecific variability, the high densities they reach in artificial substrata, their high potential for introduction and establishment across many global regions, including the Mediterranean, and their limited capacity for autonomous dispersion, make them one of the most interesting groups among marine invertebrates to investigate the impact that cryptic species and biological invasions may have on our perception about the Mediterranean biodiversity.

### 3. PATTERNS AND DRIVERS OF CONTEMPORARY POLLEN FLOW IN A GENERALIST PLANT SPECIES

Javier Valverde<sup>1</sup>, José M. Gómez<sup>2</sup>, Francisco Perfectti<sup>3</sup>

1- *Department of Plant Biology, CIBIO-InBIO, Universidade do Porto, Vairão, Portugal*

2- *Department of Functional and Evolutionary Ecology, Experimental Station of Arid Zones (EEZA-CSIC), Almería, Spain*

3- *Department of Genetics, University of Granada, Granada, Spain*

Contemporary pollen flow in animal-pollinated plants results from the foraging movements of pollinators. These are influenced by pollinator's preferences on different aspects of individual plants and consequently, non-random matings may arise. Such patterns ultimately reflect the spatial genetic structure of plant populations, and therefore their determination is of great interest in understanding the importance of pollinators in the evolution of plant populations. In a population of the generalist plant *Erysimum mediohispanicum* (Brassicaceae) we characterized the phenotype and microenvironment of the plants flowering in each of two consecutive years. For each year we analyzed the mating patterns occurring among these plants, as well as the patterns of pollinator visitation and foraging movements. We found that matings mostly occurred among nearby plants presenting synchronous flowering times and growing in microenvironments with similar light availability. As a consequence, the resulting mating network showed that plants tend to mate with the most promiscuous ones and in clusters. This structure fitted the predictions of the foraging movements of most effective pollinators. Our study links individual-based plant networks with contemporary pollen flow and demonstrates that in a generalist plant species the interactions with pollinators, and thus pollen flow, can be structured.

#### **4. SOURCES OF INTRASPECIFIC MORPHOLOGICAL VARIATION IN *Vipera seoanei*: ALLOMETRY, SEX, AND COLOUR PHENOTYPE**

Nahla Lucchini, Antigoni Kaliontzopoulou, Guillermo Aguado Val, Fernando Martínez-Freiría

*CIBIO-InBIO, Universidade do Porto, Vairão, Portugal*

Snakes frequently exhibit ontogenetic and sexual variation in head dimensions, as well as the occurrence of distinct colour morphotypes which might be fitness-related. In this study, we used linear biometry and geometric morphometrics to investigate intraspecific morphological variation related to allometry and sexual dimorphism in *Vipera seoanei*, a species that exhibits five colour morphotypes, potentially subjected to distinct ecological pressures. We measured body size (SVL), tail length and head dimensions in 391 specimens, and examined variation in biometric traits with respect to allometry, sex and colour morph. In addition, we analysed head shape variation by recording the position of 29 landmarks in 123 specimens and establishing a low-error protocol for implementing geometric morphometrics to European vipers. All head dimensions exhibited significant allometry, while sexual differences occurred for SVL, relative tail length and snout height. After considering size effects, we found significant differences in body proportions between the sexes and across colour morphs, which suggests an important influence of lowland and montane habitats in shaping morphological variation. By contrast, head shape did not exhibit significant variation across sexes or colour morphs. Instead it was mainly associated to allometric variation, where the supraocular and the rear regions of the head were the areas that varied the most throughout growth and across individuals. Overall, this study provides a thorough description of morphological variability in *Vipera seoanei* and highlights the relevance of combining different tools (i.e. linear and geometric morphometrics) and analyses to evaluate the relative contribution of different factors in shaping intraspecific variation.



**SESSION 2**  
**EVOLUTIONARY ECOLOGY**



**- PLENARY TALK -**

**MEDITERRANEAN BIOGEOGRAPHY AND ITS IMPLICATIONS FOR  
CONSERVATION**

Thomas Schmitt

*Senckenberg German Entomological Institute, Müncheberg and Martin Luther University Halle-  
Wittenberg (Germany)*

The Mediterranean region is of high biogeographic complexity. Due to strong range changes and survival in different refugia during the past (mostly Pleisto- and Pliocene), a highly complex pattern of different genetic lineages has developed, even within the large Mediterranean peninsulas and in North Africa, the so-called refugia-within-refugium patterns. Consequently, the biogeographic structuring of the Mediterranean Basin is much more complicated than previously thought. Therefore, the postglacial recolonisation to the North was not the expansion of a mostly homogeneous lineage out of the different Mediterranean peninsulas, but only the respective leading edge lineages within each peninsula performed major range expansions so that the areas north of the Mediterranean region have a much simpler and younger biogeographic structure than these more southern areas. Consequently, the Mediterranean Basin is not only a hotspot in species diversity in the western Palaearctic, but also the intraspecific diversity and differentiation of Mediterranean biogeographic elements is peaking here. Therefore, the importance of the conservation of species including their regional populations in this entire region is of paramount importance for the maintenance of the genetic heritage of Europe. For addressing all these aspects, this talk gives typical examples for the patterns of Mediterranean biogeography with a focus on the western Mediterranean Basin, hereby highlighting the conservation relevance of this region.

# **1. ANALYSING RAPID EVOLUTION OF PLANT LIFE HISTORY TRAITS IN THE FACE OF RECENT ENVIRONMENTAL CHANGES THANKS TO RESURRECTION ECOLOGY IN *Viola arvensis* AND *Cyanus segetum***

Pierre-Olivier Cheptou

*Centre d'Ecologie Fonctionnelle et Evolutive (CEFE) UMR 5175, CNRS, Université de Montpellier, Université Paul-Valéry, Montpellier, France*

The comparison of past populations (thanks to *ex situ* seed collections) to current populations can shed light on the evolutionary change of traits of organisms in the face of global change. In this study, I will present empirical data on the adaptation of plant reproductive traits (flowering traits, phenology) to climate change and pollinator decline. Using seed collections (1990s vs. 2010) at the same location, I will show how floral traits and phenological traits have changed over time in two species: cornflowers (*Centaurea cyanus*, Asteraceae) and pansy (*Viola arvensis*, Violaceae). Common garden experiments have demonstrated the evolution of traits over a few decades. The comparison with neutral genetic markers allows to conclude that such evolutionary changes result from directional selection (and not drift). However, the direction of selection on traits is not always similar in the two species. I will discuss how such responses can be interpreted in the light of environmental changes, especially the decline of pollinators.

## 2. HOT IS WORST IF DRY: AN ECOPHYSIOLOGICAL MESSAGE FROM CABO VERDE LIZARDS

Carlos Fonseca<sup>1,2</sup>, Miguel Carretero<sup>1</sup>, Herculano Diniz<sup>3</sup>, Raquel Vasconcelos<sup>1</sup>

- 1- CIBIO-InBIO, Universidade do Porto, Vairão, Portugal
- 2- Universidade de Coimbra, Departamento Ciências da Vida, Coimbra, Portugal
- 3- Projecto Vitó, São Filipe, Ilha do Fogo, Cabo Verde

Climate change (CC) scenarios forecast intense environmental shifts in the Mediterranean Basin biodiversity hotspot, and sedentary ectotherms are expected to be the most affected organisms. We expected to provide clues on how species inhabiting milder climates will respond to CC analysing the physiological responses of reptiles inhabiting the most arid and warmest areas in this region. Cabo Verde Archipelago presents high numbers of endemics, some threatened by CC. On Fogo Island, two endemic viviparous skinks have contrasting sizes and distributions. While *Chioninia vaillantii* is larger and restricted to cooler/humid areas in the north, *Chioninia delalandii* is smaller and distributed across the island, even in hotter/more arid areas. This suggests that the first is more restricted in its thermal/hydric ecophysiology than the second, explaining its distribution. Additionally, pregnant females are expected to be more sensitive to CC. We experimentally tested both hypotheses by measuring evaporative water loss (EWL) rates, and determining preferred temperatures (T<sub>pref</sub>) and space use of individuals of both species, with/without water available. The species differed in EWL due to surface/volume ratio differences. *C. delalandii* kept higher T<sub>pref</sub> and was more frequently found in the hot part of the terrarium than *C. vaillantii*. As expected, lack of drinking water affected T<sub>pref</sub>, and all pregnant females selected lower T<sub>pref</sub> than conspecific males and non-pregnant females. This evidence confirms recent findings, suggesting that water ecology modulates thermoregulation in ectotherms, and that aridification will intensify CC effects. Overall, Cabo Verde lizards may be useful models of the Mediterranean Basin ectotherms for Conservation Biology.

### 3. COMPETENCE OF MEDITERRANEAN MOSQUITOES FOR THE TRANSMISSION OF LOCALLY CIRCULATING AVIAN MALARIA PARASITES

Rafael Gutiérrez-López<sup>1,2</sup>, Josué Martínez-de la Puente<sup>2,3</sup>, Laura Gangoso<sup>2</sup>,  
Jordi Figuerola<sup>2,3</sup>

- 1- Biodiversity, Ecology & Conservation Department, CIBIO-InBIO, Universidade do Porto, Vairão, Portugal
- 2- Wetland Ecology, Estación Biológica de Doñana, Seville, Spain
- 3- CIBER Epidemiología y Salud Pública, (CIBER), Seville, Spain

Avian malaria parasites are common infecting birds worldwide, including Mediterranean area. Their life cycle includes both avian hosts and mosquito vectors. Thus, it is essential to identify those factors affecting the development of avian malaria parasites in mosquitoes. We used a study model composed by two Mediterranean common mosquito species from southern Spain for the transmission of two locally circulating avian *Plasmodium* morphospecies. We tested the competence of *Culex pipiens* and *Aedes (Ochlerotatus) caspius* for the transmission of *Plasmodium relictum* and *Plasmodium cathemerium* infecting wild House sparrows (*Passer domesticus*). We assessed the effects of parasite (i.e. clade) identity and parasite load on *Plasmodium* transmission risk through its effects on mosquito survival and transmission rate. We found that *C. pipiens* was able to transmit the two *Plasmodium* species, while *A. caspius* was unable to transmit any of them. However, both the parasite transmission rate and the cost on *C. pipiens* survival differed between the two *Plasmodium* clades. Mosquitoes fed on birds infected by *P. relictum* showed a lower survival and transmission rate than those fed on birds infected by parasites related to *P. cathemerium*, whereas non-significant associations were found with intensity of infection in the birds. Our results confirm the existence of inter- and intra-specific differences in the ability of *Plasmodium* species to develop in mosquito species, which may be the result of complex evolutionary processes. In addition, their effects on mosquito longevity and development result in important differences in the transmission risk of the different parasite species by mosquitoes in Mediterranean area.

#### 4. CONTRASTING BIOGEOGRAPHIC RESPONSES TO PLEISTOCENE GLACIATIONS IN IBERIAN AMPHIBIANS

Gregorio Sánchez-Montes<sup>1</sup>, Ernesto Recuero<sup>1</sup>, A. Márcia Barbosa<sup>2</sup>, Íñigo  
Martínez-Solano<sup>1</sup>

- 1- *Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales, Madrid, Spain*
- 2- *Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO/InBIO), Universidade de Évora, Évora, Portugal*

Comparative empirical evidence from phylogeographic studies combining molecular data and species distribution modelling (SDM) suggests that Iberian amphibians responded differently to glacial-interglacial cycles during the Pleistocene. Some species, in accordance with classic hypotheses, suffered widespread extinctions across climatically unstable areas in the Iberian Peninsula, which resulted in range contractions to glacial refugia and subsequent expansion and recolonization events. This scenario is exemplified by species like *Pleurodeles waltl* and *Pelobates cultripes*, which show genetic diversity gradients across their current range, with higher genetic diversity in the south and genetically depleted areas in the north that are interpreted to result from recent colonization of areas experiencing higher turnover in climatic favorability from glacial refugia. However, other sympatric species (*Hyla molleri*) were apparently able to track climatic fluctuations via range shifts with no genetic signatures of extinction-recolonization events. The resilience of *H. molleri* seems to have been mediated by cold-tolerance and higher dispersal ability, as compared to more thermophilic species adapted to the Mediterranean realm, like *P. waltl* or *P. cultripes*. Can we reconcile these contrasting reconstructions of historical demography in Iberian amphibians with information about their population biology? In this talk, we will discuss the role of differences in demographic traits and dynamics across species in shaping range-wide phylogeographic patterns, based on the integration of molecular evidence and capture mark-recapture data from a ten-year population monitoring study of a central Iberian amphibian community.



## **SESSION 3** **CONSERVATION**

**- PLENARY TALK -**

**MEDITERRANEAN MARINE ECOSYSTEMS IN THE ANTHROPOCENE:  
EMERGING THREATS AND NEW CONSERVATION CHALLENGES**

Cristina Linares

*Institut de Recerca de la Biodiversitat (IRBio), University of Barcelona (Spain)*

Mediterranean marine ecosystems are increasingly impacted by local and global stressors including overfishing, pollution, invasive species and climate change. The cumulative effects of these multiple threats are driven important shifts in the distribution, the structure and composition of benthic ecosystems in the Mediterranean Sea. Habitat-forming species such as algae, bryozoans, sponges and corals, which provides an important structural role for the ecosystems among other ecosystem services, are increasingly threatened by these stressors and understanding how they will respond to anthropogenic pressures is key to develop sound management strategies and conservation actions. In this context, the aim of this presentation is twofold. First, to show how the combination multiple approaches such as long-term field monitoring, field and laboratory experiments, demographic and spatial modelling is crucial to identify the winners and losers at the species, population and community level in a changing world. Second, it aims to highlight that protection and restoration actions are essential components of a conservation strategy in order to halt and reverse the degradation of benthic ecosystems in the Mediterranean Sea. The contrasting responses observed among different benthic species and habitats unravel the complexity to anticipate potential changes in the future configuration of benthic ecosystems but also highlight some promising capacities to buffer global change effects, especially when conservation actions are implemented.

# 1. THE NIGHT SHIFT: IMPROVING THE CONSERVATION ASSESSMENT OF NOCTURNAL FLYING INSECTS USING DNA METABARCODING

Joana Verissimo<sup>1,2</sup>, Rebecca Mateus<sup>1,3</sup>, Vanessa Mata<sup>1,2</sup>, Sónia Ferreira<sup>1</sup>,  
Luís P. da Silva<sup>1</sup>, Pedro Beja<sup>1,4</sup>

- 1- *CIBIO-InBIO, Universidade do Porto, Vairão, Portugal*
- 2- *Department of Biology, Faculty of Sciences, University of Porto, Portugal*
- 3- *Department of Animal Biology, Faculty of Sciences, University of Lisbon, Portugal.*
- 4- *CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, Institute of Agronomy, University of Lisbon, Portugal*

There is evidence for insect population declines worldwide, putting at risk an unknown but potentially very large number of species, hindering critical ecosystem services. However, except for a few groups such as pollinators, information is still scarce on how anthropogenic drivers affect insect communities. DNA metabarcoding can help to offset these problems, providing a relatively simple tool for assessing entire insect communities. Here we provide a case study to assess the conservation value of natural (cork oak woodlands and riparian galleries) and agricultural (olive groves and vineyards) habitats for nocturnal flying insects in a Mediterranean mosaic landscape. Insect communities were described from bulk samples collected in July and September 2017 using UV light traps, aiming to quantify community variations in diversity, composition, and functional traits. We detected 1081 operational taxonomic units, most of which were Lepidoptera, Diptera, and Coleoptera but species accumulation curves suggest that many species were missed. Richness was consistently lower in vineyards, while olive groves showed comparable richness to cork oak and riparian habitats. A functional trait analysis focusing on moths showed that oak and riparian habitats had larger species, while oak habitats had more specialized diets species. We show the importance of natural habitats for insect conservation in farmed landscapes, but also the key role of extensive land uses such as traditional olive groves. More generally, we show the power of DNA metabarcoding to foster assessments covering simultaneously hundreds to thousands of species, providing much-needed information to include insects in conservation planning and management.



## 2. FRESHWATER CONSERVATION ASSESSMENTS IN (SEMI-)ARID REGIONS: TESTING RIVER INTERMITTENCE AND BUFFER STRATEGIES USING FRESHWATER MUSSELS (BIVALVIA, UNIONIDA) IN MOROCCO

André Gomes-dos-Santos<sup>1,2</sup>, Elsa Froufe<sup>1</sup>, Duarte V. Gonçalves<sup>1</sup>, Ronaldo Sousa<sup>3</sup>, Vincent Prié<sup>4</sup>, Mohamed Ghamizi<sup>5</sup>, Hassan Benaissa<sup>5</sup>, Simone Varandas<sup>6</sup>, Amílcar Teixeira<sup>7</sup>, Manuel Lopes-Lima<sup>1,8,9</sup>

- 1- CIIMAR/CIMAR — Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal
- 2- Department of Biology, Faculty of Sciences, University of Porto, Porto, Portugal
- 3- CBMA - Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Braga, Portugal
- 4- Muséum National d'Histoire Naturelle, Département Systématique et Evolution, ISyEB, Paris, France
- 5- Muséum d'Histoire Naturelle de Marrakech, Université Cadi Ayyad, Faculté des Sciences Semlalia, Marrakech, Morocco
- 6- CITAB-UTAD - Centre for Research and Technology of Agro-Environment and Biological Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal.
- 7- CIMO-ESA-IPB - Mountain Research Centre, School of Agriculture, Polytechnic Institute of Bragança, Bragança, Portugal
- 8- CIBIO-InBIO, Universidade do Porto, Vairão, Portugal
- 9- IUCN SSC Mollusc Specialist Group, c/o IUCN, Cambridge, England

The IUCN Red List assessments are essentially based on population trends and range, namely Area of Occupancy (AOO) and Extent of Occupancy (EOO). Range estimations are based on fixed grids, but this is likely inappropriate for species living in river networks. Furthermore, AOO and EOO are measured using the whole hydrographic network, therefore disregarding temporary sections, which is particularly problematic in arid and semi-arid regions. Here we mapped the permanent hydrographic network of Morocco using satellite imagery, complemented with field surveys to collect samples for molecular analyses of the five freshwater mussel species present and assess their distribution. The phylogeographic patterns are described for each species and used to identify priority areas and evolutionary significant units for conservation. Permanent hydrographic river sections represent only 18.3% of the whole hydrographic network. A north-to-south gradient of genetic diversity, species richness and distribution range was found, being coherent with water availability and river intermittence. Isolated evolutionary units were detected in southern basins that should also receive particular attention in conservation planning. We propose the mean river width multiplied by the extent of the river network as the best and the most adequate way to estimate both EOO and AOO. Given the worldwide degradation of freshwater systems and biodiversity, an accurate (re)assessment of species conservation status supported with maps of intermittent water bodies will be essential for prioritizing and guiding conservation actions and management plans, especially in arid and semi-arid regions.

### 3. MEDITERRANEAN EXPATS – POPULATIONS OF KOTSCHYI’S GECKO THRIVING AT THE EDGE OF THE PANNONIAN PLAIN IN SERBIA

Aleksandar Urošević<sup>1</sup>, Marko Maričić<sup>2</sup>, Dušan Mrkić<sup>3</sup>, Marko Anđelković<sup>1</sup>

1- *Evolutionary biology, Institute for Biological Research “Siniša Stanković”, University of Belgrade, Belgrade, Serbia*

2- *Institute of Zoology, Faculty of Biology, University of Belgrade, Belgrade, Serbia*

3- *Pančevo, Serbia*

Human activities, especially transportation and urbanization, coupled with climate change, can lead to changes in faunal compositions of some regions through range shrinking/expansion of certain species. Some lizards, particularly geckos, proved as adept colonizers, especially in urban ecosystems. The Kotschy’s gecko (*Mediodactylus kotschy* sensu lato) is a small crepuscular and nocturnal lizard characteristic for the eastern Mediterranean. Recent molecular analyses showed that it is, in fact, a species complex. In Serbia, Kotschy’s gecko naturally occurs only in Prizren, Metohia, but recently it reached the southern edges of the Pannonian plain, which are under the strong influence of continental climate (hot summers and cold winters, with long periods of frost). Recently several populations of this small, inconspicuous lizard were discovered in Novi Sad, Belgrade, Smederevo and Pančevo, and possibly Niš, further to the south. The hypothesis of introduction during historic times was proposed, but a more likely explanation is a relatively recent simultaneous introduction, probably facilitated through railroad beds as corridors. Taxonomic identity of the introduced populations is still poorly known, but according to their morphological characters, they most likely belong to the kotschy group. Involvement of citizen scientists, who shared their gecko findings with the Serbian Herpetological Society, proved invaluable in detecting the cases of introduction of this lizard. Such cooperation will further be encouraged and facilitated.

#### 4. ECO-EVOLUTIONARY PROCESSES UNDERLYING THE POPULATION DYNAMICS IN THE THREATENED MEDITERRANEAN RED CORAL

Jean-Baptiste Ledoux<sup>1,2</sup>, Sunčica Stipoljev<sup>2</sup>, Silvia Frias<sup>2</sup>, Paula López-Sendino<sup>2</sup>, Ignasi Montero-Serra<sup>3</sup>, Agostinho Antunes<sup>1</sup>, Cristina Linares<sup>3</sup>, Jean-Philip Royer<sup>4</sup>, Pierre Drap<sup>4</sup>, Joaquim Garrabou<sup>2</sup>

- 1- CIIMAR/CIMAR, Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, Porto, Portugal.
- 2- Institut de Ciències del Mar, CSIC, Barcelona, Spain.
- 3- Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Institut de Recerca de la Biodiversitat (IRBIO), Universitat de Barcelona, Barcelona, Spain.
- 4- Aix Marseille Université, CNRS, ENSAM, Université de Toulon, LIS UMR 7020, Domaine Universitaire de Saint-Jérôme, Bâtiment Polytech, Marseille, France

Characterizing the eco-evolutionary processes underlying the dynamics of natural populations is a crucial task for evolutionary ecologists with important conservation implications. The red coral, *Corallium rubrum*, is a patrimonial species from the Mediterranean Sea characterized by low population dynamics and restricted dispersal capacities. This long-lived octocoral is affected by overfishing (for its use in jewelry) and warming-induced mortality events, which induced dramatic shifts in population demographic structure. How these demographic changes impact the population dynamics remains to be fully understood. Here, we combined population genetics (microsatellites), demographic surveys and photogrammetric methods to explore the interaction among population decline, genetic drift and gene dispersal within red coral populations. First, we hypothesized that density decrease should increase genetic drift within populations. To test this hypothesis, we conducted sibship and progeny arrays analyses in a pristine-like and a declining population. Surprisingly, the two populations showed similar mating patterns and effective population sizes. We thus hypothesized that higher gene dispersal within population may buffer the increase of genetic drift expected in declining populations. To address this issue, we compared the patterns of fine-scale spatial genetic structure in three populations with contrasted demographic structures. While a pattern of isolation by distance among individuals was observed in the three populations, the inferred demographic parameters (neighborhood size and effective dispersal) suggested that lower mate density may be compensated by higher gene flow. This study sheds new light on the dynamics of the red coral with implications for its restoration.



## **SESSION 4**

### **HUMAN-MEDIATED CHANGES**

## - PLENARY TALK -

### TRACKING DOMESTICATION: A BIOARCHAEOLOGICAL PERSPECTIVE

Allowen Evin

*Institut des Sciences de l'Evolution, Montpellier (France)*

The domestication of plants and animals marks a major transition in human history and a key element in the development of modern societies. On the other hand, domestication can be seen as the longest lasting experiment of artificial selection. Observations of domestic mammals reveal that the most significant morphological changes linked with domestication include decreasing brain size, changes in the proportions, and modifications of external characters such as floppy ears, rolled tails and piebald coloration. Most of these characters are not, or not easily, accessible in archaeological remains due to fragmentation resulting from taphonomic processes (before and after being deposited). In archaeological contexts, available morphological criteria are often scarce and the number of characters available to quantify the phenotype is limited but provide irreplaceable information to understand the spatio-temporal evolution of the domesticates and the diversity that we see today. I will discuss the use of geometric morphometrics to study the size and shape of the teeth and crania of archaeological and modern domestic species (dogs and pigs). I will challenge the well established ideas of paedomorphism (retention of ancestral (wild) juvenile characteristics into adulthood) and size reduction during domestication. Finally, I will demonstrate the benefit of integrative approaches combining geometric morphometrics with other approaches such as ancient DNA or isotopic analyses, that led us to a much better understanding of the complex, continuous and still ongoing process that is domestication. Special attention will be given to the Mediterranean basin, from its oriental extremity that has seen the beginning of the Neolithic farming spread into Europe to its more occidental distribution at the end of the Mediterranean Neolithic pathway.

# 1. RESPONSES OF GRASSLAND BIRDS TO CHANGING LIVESTOCK MANAGEMENT IN MEDITERRANEAN GRASSLANDS

Rita F. Ramos<sup>1,2</sup>, João Diogo<sup>1,2</sup>, Joana Santana<sup>1,2</sup>, João P. Silva<sup>1</sup>, Luís Reino<sup>1,2</sup>, Stefan Schindler<sup>2,3</sup>, Pedro Beja<sup>1,2,4</sup>, Francisco Moreira<sup>1,5</sup>

- 1- CIBIO-InBIO, Universidade do Porto, Vairão, Portugal
- 2- CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Laboratório Associado, Instituto Superior de Agronomia, Universidade de Lisboa, Lisbon, Portugal
- 3- EAA, Environment Agency Austria, Vienna, Austria
- 4- Cátedra EDP Biodiversidade/EDP Chair in Biodiversity, CIBIO/InBIO-Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto
- 5- Cátedra REN em Biodiversidade, CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Laboratório Associado, Universidade do Porto, Portugal

Due to changes in the European Union Common Agricultural Policy (CAP), there has been a shift in the management of many Mediterranean pastures, involving increases in grazing intensity and a replacement of traditional sheep grazing by cattle grazing. This study aimed at comparing effects of different grazing systems and vegetation structure on ground nesting bird populations in Mediterranean grasslands of Southern Portugal. In the spring of 2019, bird, vegetation (height, NDVI and composition) and grazing management data were collected from 50 parcels, with 54% grazed by sheep and 46% grazed by cattle. Vegetation was higher in cattle grazing pastures with higher percentages of forbs plants. However, overall, grazing pressure was lower in sheep grazing pastures, with more pronounced differences during spring months. From the most common (six) bird species, Zitting Cisticola (*Cisticola juncidis*) and Little Bustard (*Tetrax tetrax*) were more prevalent and abundant in parcels managed for sheep and cattle, respectively. Zitting Cisticola, Corn Bunting (*Emberiza calandra*) and Calandra Lark (*Melanocorypha calandra*) were related to at least one vegetation variable (height, NDVI or cover by forbs), irrespective of livestock type. Calandra Lark and Little Bustard abundances were related positively and negatively, respectively, to grazing intensity. Our results show that the management of Mediterranean grasslands are reflected in vegetation structure and grazing pressure during the breeding season of ground nesting birds. This management drives different responses across different species, eg. Little Bustard beneficiates from cattle grazed parcels with low grazing pressure while Calandra Lark prefers higher grazing pressures during spring.

## 2. HABITAT SELECTION AND MORPHOLOGICAL VARIATION ACROSS HUMAN-ALTERED HABITATS IN SECONDARY CONTACT ZONES: THE CASE OF WESTERN MEDITERRANEAN VIPERS IN NORTHERN IBERIA

Inês Freitas<sup>1</sup>, Óscar Zuazo, Pedro Tarroso<sup>1</sup>, Antigoni Kaliontzopoulou<sup>1</sup>,  
Fernando Martínez-Freiría<sup>1</sup>

*CIBIO-InBIO, Universidade do Porto, Vairão, Portugal*

Anthropogenic landscape transformation imposes novel selective forces on natural populations, potentially causing changes in species requirements, behaviour and morphology. Yet, its impact over species dynamics and how it shapes trait evolution in coexistent species remain poorly explored. Here, we investigate the role of landscape transformation in shaping patterns of habitat selection and morphological variability of Western Mediterranean vipers (*Vipera aspis* and *Vipera latastei*), across two contact zones in Northern Iberia characterized by contrasting levels of human disturbance: the High Ebro (a natural landscape) and Oja-Tirón (an intensive cereal culture landscape). Ecological niche models (ENM) were performed for both species in each contact zone (1037 1x1km records), using a set of climatic and habitat related variables. Multivariate analyses (discriminant, variation and trajectory analyses) were performed over ten phenotypic traits for ca. 1000 specimens from both species and contact zones. ENMs showed climate as the main distributional driver in both contact zones, allowing a sharp transition between the predicted suitable areas of both species. Landscape change, on the other hand, is shaping distributional patterns in Oja-Tirón, forcing species to inhabit the same structural areas. Discriminant analyses showed higher power to differentiate species in Oja-Tirón, suggesting that increased competition may have promoted higher species differentiation (i.e. character displacement). Additionally, ANOVA and trajectory analyses show clear differences between species and sexes in the patterns of morphological variation, suggesting different responses to human disturbance. Overall, our results provide evidence for the influence of human disturbance on the patterns of phenotypic variation and habitat selection of these vipers.

### 3. ASSESSING THE IMPACT OF HABITAT LOSS ON A PALEARCTIC RELICT IN MOROCCO

Marco Dinis, João C. Campos, Fernando Martínez-Freiría, Guillermo Velo-  
Antón

*CIBIO-InBIO, Universidade do Porto, Vairão, Portugal*

Habitat loss and degradation are the most pervasive threats to biodiversity. Understanding their dynamics is particularly urgent in developing countries as they are characterized by ongoing expansion of human populations, infrastructure development and agricultural intensification. While information on landscape characterization and biodiversity distributions is often limited in such regions, remote sensing techniques and predictive distribution modelling can help to circumvent these issues. Morocco is part of the Mediterranean Basin Global Biodiversity Hotspot, characterized by high vertebrate endemic richness, and ranked medium in the Human Development Index (123th out of 180 countries). Several endemic Palearctic relicts occur in this country, closely associated with high altitude and humid Mediterranean forest habitats. We analyzed a time series (2000-2018) of remotely sensed NDVI (Normalized Difference Vegetation Index) data to quantify recent dynamics of vegetation in northern Morocco. Distribution modelling was used to predict the distribution of suitable habitats for the Palearctic relict *Salamandra algira*, and changes in vegetation productivity were quantified within the predicted suitable habitat for the species. Vegetation loss was identified in 31% of the study area, and in 45-49% of the suitable area of *S. algira*. Vegetation loss was concentrated in coastal areas of the Tingitana Peninsula and in the Middle Atlas Mountains, and predominately associated with expansion of agriculture, urbanization, and resource extraction. These results show that areas of importance for the persistence of Palearctic taxa are currently threatened by vegetation loss, which may be of particular concern for taxa with high allopatric diversification, such as *S. algira*.



#### 4. ANTHROPOGENIC HABITATS FOR TWO OF THE RAREST FRESHWATER SPECIES IN THE MEDITERRANEAN HOTSPOT: STABLE REFUGES OR ECOLOGICAL TRAPS?

Ronaldo Sousa<sup>1</sup>, Joana Garrido Nogueira<sup>1,2</sup>, Hassan Benaissa<sup>3</sup>, Mohamed Ghamizi<sup>3</sup>, Simone Varandas<sup>4</sup>, Amílcar Teixeira<sup>5</sup>, Manuel Lopes-Lima<sup>2</sup>

- 1- CBMA Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Braga, Portugal.
- 2- CIBIO-InBIO, Universidade do Porto, Vairão, Portugal
- 3- Muséum d'Histoire Naturelle de Marrakech, Université Cadi Ayyad, Faculté des Sciences, Marrakech, Morocco.
- 4- CITAB-UTAD - Centre for Research and Technology of Agro-Environment and Biological Sciences, University of Trás-os-Montes and Alto Douro, Forestry Department, Vila Real, Portugal.
- 5- Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança, Bragança, Portugal.

Anthropogenic habitats may serve as a refuge for aquatic species, including freshwater mussels (*Bivalvia*, *Unionida*). Evaluating the role of anthropogenic habitats is a fundamental, but still ignored, conservation issue given the pace at which humans have been converting natural ecosystems. In this study, possible differences in abundance, size and condition index of two of the rarest freshwater species (*Margaritifera margaritifera* and *Pseudunio marocanus*) in the Mediterranean hotspot colonizing anthropogenic (water mill and irrigation canals) and natural habitats (rivers) were assessed in Portugal and Morocco. For *M. margaritifera* no differences were found in the abundance colonizing both habitats, but individuals present in water mill canals had a significantly higher condition index and size. For *P. marocanus* results showed that the individuals colonizing the irrigation canal had a significantly higher density and condition index when compared to natural conditions, but no differences were found regarding size. Since both species are listed as endangered or critically endangered by the IUCN, their presence in anthropogenic habitats has high conservation importance as the canals seem to provide stable conditions for the settlement, growth and survival of freshwater mussels. However, the occurrence of an exceptional drought during the late summer of 2017 in the case of *M. margaritifera* and dredging operations of the irrigation canal in the case of *P. marocanus* were responsible for high mortalities. Therefore, these anthropogenic structures may also function as an ecological trap. Overall, this study can be used by managers to promote future actions that enhance freshwater mussel protection and guarantee their survival, including on anthropogenic habitats.



***Poster session &  
flash talks***

## INBIO BARCODING INITIATIVE: DNA BARCODING PORTUGUESE TERRESTRIAL INVERTEBRATE BIODIVERSITY

Sónia Ferreira<sup>1</sup>, Joana Paupério<sup>1</sup>, Filipa Martins<sup>1,2</sup>, Joana Veríssimo<sup>1,2</sup>, Cátia Chaves<sup>1</sup>, Joana Pinto<sup>1</sup>, Pedro Sousa<sup>1</sup>, Catarina Pinho<sup>1</sup>, Martin Corley<sup>1,3</sup>, Daniel Oliveira<sup>1,2</sup>, Silvia Pina<sup>4</sup>, Vanessa Mata<sup>1,2</sup>, Hugo Rebelo<sup>1,4,5</sup>, Ana Filipa Filipe<sup>1,4</sup>, Nuno Fonseca<sup>1</sup>, Pedro Beja<sup>1,4</sup>

- 1- *CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Portugal*
- 2- *Department of Biology, Faculty of Sciences, University of Porto, Portugal*
- 3- *Pucketty Farm Cottage, Faringdon, Great Britain.*
- 4- *CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, Institute of Agronomy, University of Lisbon, Portugal*
- 5- *School of Biological Sciences, University of Bristol, Bristol, UK.*

DNA barcoding is an essential tool for biodiversity monitoring and conservation studies. However, its applicability is hindered by the lack of comprehensive reference collections, particularly of invertebrates that are underrepresented in reference databases. In the northwest of the Mediterranean Basin biodiversity hotspot, Portugal holds a unique and diverse fauna. Nevertheless, the vast majority of species remains understudied and underrepresented in DNA barcoding databases. InBIO Barcoding Initiative (IBI) aims to fill the gap regarding Portuguese terrestrial invertebrate taxa. By combining fieldwork and networking with taxonomists and ecologists, more than 8000 specimens have already been collected and over 6000 sequenced, covering over 150 families of insects from more than 20 orders. During the development of the IBI reference collection of DNA sequences, many relevant findings on the Portuguese fauna were made. For several groups, a reasonable representation has already been achieved. Major challenges are the hyperdiverse orders such as Coleoptera, Diptera, and Hymenoptera, which represent an enormous part of the invertebrate diversity and have remarkable ecological relevance but are poorly studied in Portugal. DNA barcodes of Portuguese invertebrates facilitated the correct identification of enigmatic specimens, namely undocumented species in the region, pinpointed the existence of undescribed species, and allowed linking males and females of sexually dimorphic species. Cryptic diversity was found in several insect groups. The use of high-throughput sequencing to produce the DNA barcodes also allowed us to tackle challenges posed by the existence of nuclear copies. Overall, IBI is expected to become a fundamental tool for biodiversity monitoring in Portugal.

## COMPARING TESTS FOR SELECTION IN A GENOME SCAN OF AN IBERIAN AMPHIBIAN, *Pelobates cultripes*

Adam Marques<sup>1</sup>, Jeff Hanson<sup>1</sup>, Miguel Camacho<sup>1</sup>, Craig Moritz<sup>2</sup>, Pedro Tarroso<sup>1</sup>, Guillermo Velo-Anton<sup>1</sup>, Ana Verissimo<sup>1,3</sup>, Silvia Carvalho<sup>1</sup>

1- BIODESERTS, CIBIO-InBIO, Vairao, PT

2- Biology, The Australian National University, Canberra, AU

3- Virginia Institute of Marine Science, Gloucester Point, US

Developments in landscape genomics have facilitated a proliferation in tests for selection to identify candidate adaptive (non-neutral) markers in natural populations. Method assumptions and suitability vary, so researchers often compare results between tests to identify concurrent markers as a correction for false positives. However, challenges remain in resolving disagreements between multiple methods to achieve suitable false-negative and false-positive rates. Here we applied eight tests for selection, representing three methodological approaches, and compared the candidate markers among tests obtained in an amphibian case-study species, *Pelobates cultripes*, in a natural system. Cluster analyses performed on concurrent candidate markers showed spatial patterns differing from neutral ones, as well as between methods. While the proportion of concurrent markers was not influenced by comparisons within or between methodologies, concurrent markers identified by comparisons within a common methodology were more clearly described non-neutral patterns. Depending on the assumed model of selection, non-neutral markers may present differing spatial genetic diversity patterns. Concurrence between methodological consistent tests is an effective means to describe non-neutral genetic variation in exploratory genome-wide scans for selection.

**IS ECOLOGICAL NICHE EVOLUTION INFLUENCING DISTRIBUTION  
BOUNDARIES ACROSS SPECIES OF THE GIANT BLISTER BEETLE  
*Berberomeloe*?**

Alberto Sánchez-Vialas<sup>1</sup>, Javier Lobón-Rovira<sup>2</sup>, Urtzi Enriquez-Urzelai<sup>2</sup>,  
Mario García-París<sup>1</sup>, Ernesto Recuero<sup>1</sup>

1- Museo Nacional de Ciencias Naturales, Madrid, Spain.

2- CIBIO Research Centre in Biodiversity and Genetic Resources, InBIO, Universidade do Porto, Campus Agrário de Vairão, Portugal.

*Berberomeloe* (Coleoptera: Meloidae) is an endemic genus of the western Mediterranean Basin, distributed across the Iberian Peninsula and Northwestern Africa. Until recently, this genus included only two morphologically distinct species: *B. majalis* (Linnaeus, 1758) and *B. insignis* (Charpentier, 1818). A recent molecular phylogeny supported by morphological evidences, however, has shown an unexpected taxonomic diversity within *Berberomeloe*, raising the current species composition to 10 species. Most species originated in the Pleistocene, except for the close relatives *B. insignis* and *B. tenebrosus*, which split in the Pliocene. Several contemporaneous geographic barriers have been identified within some of the species ranges (e.g. Sistema Central mountains, and Guadalquivir and Tajo river basins). However, no geographical barrier is apparently responsible for distribution boundaries across species. In addition, we investigated whether ecological niche evolution influenced the current distributions of *Berberomeloe* species. We found low levels of niche overlap (Schoener's D: 0.048, 95% CI: 0.023–0.073), with support for niche divergence between species. Altogether, our results suggest that niche differentiation, rather than geographic barriers, are influencing the distribution boundaries among the species of *Berberomeloe*.

## MEDITERRANEAN COLLECTIONS ON THE NATURAL HISTORY AND SCIENCE MUSEUM OF THE UNIVERSITY OF PORTO (MHNC-UP): DIVERSITY AND POTENTIAL

Cristiana Vieira<sup>1,2</sup>, Francisco Álvares<sup>1,2</sup>, Constança Vieira de Andrade<sup>1</sup>, Luís M. P. Ceríaco<sup>1,3</sup>, Paulo Farinha-Marques<sup>4,5</sup>, Paulo Gusmão<sup>1</sup>, Iúri Frias<sup>4</sup>, Maria João Fonseca<sup>1</sup>, Rita Gaspar<sup>1,2,6</sup>, Helena Gonçalves<sup>1,2</sup>, José Manuel Grosso-Silva<sup>1</sup>, João Muchagata<sup>1,7</sup>, Joana Salgueiro<sup>1</sup>, João Pedro Tereso<sup>1,2,8</sup>, Joana Tinoco<sup>1</sup>, Joana Torres<sup>1</sup>, Ricardo Jorge Lopes<sup>1,2</sup>, Nuno Ferrand<sup>1,2</sup>

- 1- *Museu de História Natural e da Ciência da Universidade do Porto (MHNC-UP/Uporto/PRISC)*
- 2- *Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto (CIBIO-InBIO)*
- 3- *Departamento de Zoologia e Antropologia (Museu Bocage), Museu Nacional de História Natural e da Ciência (MUHNAC)*
- 4- *Jardim Botânico do Porto (Museu de História Natural e da Ciência da Universidade do Porto (MHNC-UP/Uporto/PRISC)*
- 5- *Departamento de Geociências, Ambiente e Ordenamento do Território, Faculdade de Ciências da Universidade do Porto*
- 6- *Universidade de Santiago de Compostela*
- 7- *Museu da Lourinhã*
- 8- *Uniarq- Centro de Arqueologia da Universidade de Lisboa*

The Natural History and Science Museum of the University of Porto (MHNC-UP) inherited most of the natural and scientific collections of several older museums of this University. MHNC-UP is currently undergoing an extensive refurbishment process, from infrastructures to museographic discourse, curating and restoring all extant collections, promoting the incorporation of new specimens and supporting research and preparing new exhibitions and educational programs. Collections cover an array of topics within the fields of natural sciences (geology, paleontology, zoology, botany) and humanities (archaeology, anthropology, ethnobotany, ethnography, history of science), while the adjoined Botanical Garden hosts living collections of plants of several Mediterranean regions. Within these collections there are specimens of particular importance for the study of Mediterranean biodiversity, including type material of several botanical and zoological taxa, representatives of rare and elusive taxa, important historical specimens from the 19<sup>th</sup> and 20<sup>th</sup> century, as well as paleontological specimens contemporaneous of major events that shaped present-day environment and biodiversity of Mediterranean ecosystems. The archaeobotanical and zooarchaeological collections provide invaluable testimonies on the evolution of Mediterranean ecosystems in the last 10,000 years. These collections are complemented by metadata with a wide array of anthropological and ethnographic information providing cultural contexts to understand the historical relations between humans and nature, as well as how these relations have been shaping the Mediterranean basin. Here we present an overview on the diversity of collections and discuss its importance to present-day research, education and dissemination activities for promotion of scientific culture concerning Mediterranean ecosystems.

## MOLECULAR ASSESSMENT OF WATER FROG POPULATIONS IN THE WESTERN MEDITERRANEAN

Adriana Bellati<sup>1</sup>, Ivan Mirabella<sup>1</sup>, Michele Maglia<sup>1</sup>, Jean-Michel Delaugerre<sup>2</sup>, Claudia Corti<sup>3</sup>

- 1- Department of Earth and Environmental Sciences , University of Pavia, Pavia, Italy
- 2- Conservatoire du littoral, Bastia, France
- 3- Museo di Storia Naturale dell'Università di Firenze, Sezione di Zoologia "La Specola", Firenze, Italy

The amphibian genus *Pelophylax* (Fitzinger, 1843) is native to Eurasia and Northern Africa and it encompasses approximately 20 taxa commonly known as water frogs. Among them are included natural hybrids (kleptons) which reproduce via hybridogenesis, i.e. they discard one parental genome and backcross with the parental species whose genome has been eliminated to restore the hybrid condition. Kleptons are morphologically difficult to distinguish from their parental taxa, but can be easily recognized on a molecular basis. In Central Italy, the native hybridogenetic system of *P. bergeri* and *P. kl. hispanicus* (the B-H system) occurs. Members of this system also occur in three Western Mediterranean islands: Corsica, Elba and Sardinia. We collected and analysed biological samples from a large dataset of water frogs from central Italy and Western Mediterranean islands, in order to characterize populations of the northern Tyrrhenian basin. A multilocus approach was adopted to ascribe individuals to the correct taxon, and infer the evolutionary history of insular populations. According to the results, insular individuals showed mtDNA haplotypes (cytb) identical or only slightly differentiated from peninsular populations, but only pure populations of the parental species *P. bergeri* were detected on islands by a diagnostic nuclear marker (SAI-1). Furthermore, microsatellites (9 loci) revealed higher differentiation of insular populations from the mainland, possibly due to local adaptation and/or distinct evolutionary history. Overall, this study clarifies the previously unknown genetic composition of insular populations of water frogs inhabiting Western Mediterranean islands.

# COMPLEMENTARITY OF VEGETATION RESPONSES TO RAINFALL INCREASES RESILIENCE OF UNGULATE POPULATIONS IN DOÑANA NATIONAL PARK

Juan M. Giralt-Rueda, Francisco Carro, Ramón C. Soriguer, Luis Santamaría

*Department of wetland Ecology, Doñana Biological Station - CSIC, Seville, Spain*

Mediterranean environments are characterized by intra- and inter-annual fluctuations in plant primary production which are likely to regulate the carrying capacity and density-dependent responses of ungulate populations. These effects may, however, vary across spatial and temporal scales. Habitat heterogeneity, particularly when associated to differentiated phenological responses, may allow wild ungulates to mitigate temporal fluctuations by using different resources along the year. In this work, we use a 30 – years dataset (namely rainfall, satellite data and total counts of ungulate populations) to assess how temporal variability in rainfall affects plant primary production in two different habitats (Mediterranean sclerophyllous forest and marshland) of the Doñana National Park; and how this variation in primary production influences, in turn, the population dynamics of different species of ungulates. Remote-sensing data indicate a temporal alternation in the phenological cycles of both vegetation types, which lengthened the period of food availability within each year. Furthermore, the two types of vegetation showed complementary responses to variation in the amount and timing of rainfall, which increases the predictability of food availability across years. Ungulate surveys indicate that red and fallow deer populations respond differently to the inter-annual variation in primary production of the two vegetation types. These differences mitigate the negative impact of droughts on ungulate populations, inasmuch as the spatial subdivision of the area allows access to both vegetation types. Our findings deepen the knowledge on vegetation-ungulate interactions in Mediterranean areas, potentially contributing to develop better management strategies of ungulate populations and adapt them to ongoing climate change.



## SEXUAL SELECTION AND BREEDING SUCCESS IN THE NATTERJACK TOAD (*Epidalea calamita*)

Helena Martínez-Gil<sup>1</sup>, Gregorio Sánchez-Montes<sup>2</sup>, Iñigo Martínez-Solano<sup>2</sup>

1- *CIBIO-InBIO, University of Porto, Vairão, Portugal*

2- *Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain*

Individual breeding success is a key component of fitness. Both phenotypic traits and behavioural strategies are potentially involved in mating performance. Unravelling the relative leverage of phenotype and behaviour on the probability of mating therefore provides insights on the strength and direction of sexual selection. We tested the association between two phenotypic traits (body size and body condition) and a variable describing individual breeding behaviour (the number of captures of individuals during the breeding season, used as a proxy of the time spent at the breeding site) and reproductive success. We obtained biometric data from males and females in a natterjack toad (*Epidalea calamita*) population in sierra de Guadarrama (Madrid, Spain) during the breeding season of 2018 and recorded mating pairs observed in breeding ponds to estimate the probability of mating and the number of mating partners in both sexes. Both the body size of individuals and the number of captures during the breeding season were significantly associated with the probability of mating in males and females. Furthermore, the number of captures of individuals of both sexes was associated with the number of mating partners during the breeding season. These results highlight the combined role of phenotype and behaviour in shaping individual breeding success and fitness.

## THE MEDITERRANEAN IN A CLOSET: BOTANY COLLECTIONS ON THE HERBARIUM OF THE NATURAL HISTORY AND SCIENCE MUSEUM OF THE UNIVERSITY OF PORTO (MHNC-UP)

Cristiana Vieira<sup>1,2</sup>, Helena Hespanhol<sup>2</sup>, Paula Portela<sup>2,3</sup>, Joana Marques<sup>2</sup>,  
Carlos Vila-Viçosa<sup>2</sup>

- 1- *Museu de História Natural e da Ciência da Universidade do Porto (MHNC UP/UPorto/PRISC)*
- 2- *Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto (CIBIO-InBIO)*
- 3- *Faculdade de Ciências da Universidade do Porto (FCUP)*

The Herbarium of the Natural History and Science Museum of the University of Porto (MHNC-UP) (registered in the *Index Herbariorum* as PO) is an active collection in continuous growth that contains about 120,000 herbarium specimens of fungi, lichens, algae, bryophytes, pteridophytes and vascular plants. The story of botany in Porto is inseparable from the origins of the first specimens of bryophytes and lichens collected by Isaac Newton in 1848, in mainland Portugal. The majority of specimens were collected in Portugal, but PO also includes a General Herbarium with specimens from Portugal's former African colonies and many other countries worldwide obtained through a versatile exchange policy. PO botanical collections have been used in the context of systematics, taxonomy and chorology studies, but also within the framework of applied science such as bioindication, biomonitoring, and biodeterioration, or in-depth studies of ecophysiology and molecular genetics. These collections were considered in many publications, including the first Portuguese and Iberian Floras, dating back to 1914. Because of ongoing research collaborations, several case-studies will be presented, highlighting specimen types, collections and collectors, in order to give an overview of the possible applications of the PO botanical collections, particularly the ones from Mediterranean. We aim to reveal the uniqueness of these collections and invite researchers to contribute to its potential future use, including both physical and digital access.

**CABO VERDE GIANT GECKO: HOW MANY UNITS FOR CONSERVATION?**

Katelene Delgado<sup>1</sup>, Evandor P. Lopes<sup>1,2</sup>, Raquel Vasconcelos<sup>1,2</sup>

- 1- FECM-UniCV, Faculdade de Engenharia e Ciências do Mar, Universidade de Cabo Verde, Campus da Ribeira de Julião, Cabo Verde
- 2- CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto, Campus de Vairão, Portugal

Cabo Verde Islands are the southernmost area within the Mediterranean Basin biodiversity hotspot. *Tarentola gigas* (Bocage 1875) is the largest gecko found in that Archipelago. It is subdivided into two subspecies, one confined to the Branco Islet, *Tarentola gigas brancoensis* Schleich 1984, and another to the Raso Islet, *Tarentola gigas gigas* (Bocage 1875). These arid islets were classified as Integral Natural Reserves and further studies on the species are needed to outline more assertive conservation measures. Thus, this study aims to integrate for the first time genetic analyses, based on mitochondrial markers, with morphological analyses, based on morphometric and meristic data to test if there are relevant differences between the two subspecies. The results indicated that they are two closely related subspecies, with some visible differences in size and head shape, possibly related to habitat or drift. Given the conservation status of the species, this should be further investigated, aiming at adequate management of these two evolutionarily significant units.

## THE RED-LEGGED PARTRIDGE (*Alectoris rufa*) FROM ELBA ISLAND: CONSERVATION PERSPECTIVES FOR A LAST RESORT RESOURCE IN ITALY

Giovanni Forcina<sup>1,2</sup>, Monica Guerrini<sup>2</sup>, Filippo Barbanera<sup>2</sup>

1- CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos,  
Universidade do Porto, Vairão, Portugal

2- Department of Biology, University of Pisa, Pisa, Italy

The red-legged partridge (*Alectoris rufa*, Galliformes) is listed as Species of European Conservation Concern (SPEC 2) and evaluated as threatened under the European legislation. Although introgressed with the exotic chukar partridge (*A. chukar*), the conservation value of the Elba Island population (Tuscan Archipelago National Park, central Italy) is not under question, as it represents the ultimate wild repository of at least part of the otherwise extinct Italian *A. r. rufa* genome. Moreover, its comparatively long natural history, self-sustainability and lack of restocking over the last 25 years represent additional valuable features. Nevertheless, the alleged affiliation of this population to the nominal subspecies has not been investigated yet, though it would provide key information for its management within an adaptive conservation framework. In this study, we collected 113 fecal samples across Elba and genotyped the joint Cytochrome-b and Control Region genes (ca. 2,250 nucleotides) for comparison with 149 conspecifics from all over the species distribution range. Other than confirming extensive *A. chukar* mitochondrial DNA introgression in Elba partridges, their assignment to the nominal subspecies from Italy and France was disproved by haplotypes ascribed to its Iberian counterpart. Moreover, after 30 years of steady demographic decrease of local partridges, our analyses show very limited connectivity between western and eastern subpopulations due to conifer reforestation, which made the habitat in central Elba unsuitable for the species. These data call for the creation of ecological corridors to restore connectivity and evaluate the possible adaptive introgression in this overtly admixed yet irreplaceable landbird island population.

## CONSERVATION GENOMICS OF *Esox flaviae* (ITALIAN PIKE)

Barbara Sofia Ilardo<sup>1,3</sup>, Richard Brown<sup>1</sup>, Hazel Nichols<sup>2</sup>, Diego Micheletti<sup>3</sup>,  
Andrea Gandolfi<sup>3</sup>

1- *Liverpool John Moores University, Faculty of Science, School of Natural Sciences and Psychology, Liverpool, United Kingdom*

2- *Swansea University, Department of Biosciences, Swansea, United Kingdom*

3- *Fondazione Edmund Mach, San Michele all'Adige, Italy*

The recent discovery of a novel pike species naturally distributed in the Alpine region, *Esox flaviae* (“Italian pike”), has fuelled debate on the conservation status of this prized game fish and apex predator. For decades, allochthonous Northern pike (*E. lucius*, here “European pike”) have been widely used in stocking practices to sustain angling activities. Although the two species differ phenotypically, hybrids are often indistinguishable, and patterns of introgression are becoming increasingly complex to unravel with traditional genetic markers, namely microsatellites. We aim to bypass this obstacle by using Whole Genome Sequence data (WGS) to study population structure and genomic adaptation in the Italian pike, and, ultimately, develop a genotyping tool to aid its conservation. Samples were previously categorized as either Italian ( $n = 16$ ), European ( $n = 6$ ) or hybrid ( $n = 6$ ) based on microsatellites. In this study, the European pike genome was used as reference to align reads, yielding 7.3 million quality-filtered SNPs. Our SNP dataset allowed for successful clustering of individuals at species and subpopulation levels using Principal Component Analysis, as well as a more thorough analysis of hybridization as opposed to microsatellites, using FastSTRUCTURE. Genome-wide selection scans (GWSS) were carried out, which involved calculation of per-locus statistics such as  $F_{ST}$ ,  $\pi$  and  $\alpha$  (the rate of adaptive molecular evolution as described by the McDonald-Kreitman test). Several chromosomal regions were identified as candidates for selection. Ongoing analyses will shed further light on the patterns of adaptive variation and the functional consequences of introgressive hybridization.

## LINKING MICROHABITAT USE WITH MODELS OF FORAGING SUCCESS IN AN IMPERILLED MEDITERRANEAN STREAM FISH

Joana Martelo<sup>1,2</sup>, Gary D. Grossman<sup>3</sup>, M. Filomena Magalhães<sup>1</sup>

- 1- *cE3c, Centre for Ecology, Evolution and Environmental Changes, Faculty of Sciences, University of Lisbon, Lisbon, Portugal*
- 2- *MARE, Marine and Environmental Sciences Centre, Faculty of Sciences, University of Lisbon, Lisbon, Portugal*
- 3- *Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA*

Little is known about the habitat requirements of endangered cyprinids in Europe and especially on the Iberian Peninsula. Here, we relate microhabitat use by an imperilled Mediterranean fish, *Squalius torgalensis*, to foraging success-based models. Specifically, we quantified i) variation in focal microhabitat use in the Torgal stream during two dry years, testing differences among reaches, years and length classes, and ii) assessed the effects of velocity, individual length and group composition on per capita prey capture rate and reactive distance in groups of two, four and six fish. Length-related variation in microhabitat use was low, with small and large chub tending to favour areas with boulders, roots and aquatic vegetation or displaying random microhabitat use. The percentage of prey captured decreased with velocity and was higher than randomly expected for dominant individuals in groups of six fish. These results indicate that, in dry years, microhabitat use by chub may be driven by factors other than velocity, because foraging success is high under the range of low velocities prevailing in streams. Moreover, group size influences foraging success and most likely, microhabitat use of chub. Maintenance of microhabitats that enable high foraging success, and fish densities that facilitate social foraging, should be considered when developing conservation strategies that deal with the increase in intensity and frequency of drought in Mediterranean streams.

## GENETIC STOCK STRUCTURE AND CONNECTIVITY IN MEDITERRANEAN AND BLACK SEAS SPINY DOGFISH *Squalus acanthias*

Ana Veríssimo<sup>1</sup>, Carlotta Mazzoldi<sup>2</sup>, Lorenzo Zane<sup>2</sup>, Natalia Gordeeva<sup>3</sup>,  
Sergii Snigirov<sup>4</sup>, Yuriy Kvach<sup>5</sup>

1- CIBIO-InBIO, Vairao, Portugal,

2- Department of Biology, University of Padova, Padova, Italy

3- Vavilov Institute of General Genetics, Moscow, Russia

4- Odessa National I. I. Mechnikov University, Odessa, Ukraine

5- Institute of Vertebrate Biology, Brno, Czech Republic

The spiny dogfish or piked dogfish *Squalus acanthias* is taken in demersal and pelagic fisheries in the Mediterranean and Black seas, where it is currently considered an Endangered and Vulnerable species, respectively, due to declining population trends attributed to overfishing. Initially thought to be widespread in the Mediterranean Sea, the species suffers from common misidentification basin-wide and may in fact be restricted to a few regions, such as the Gulf of Lion and the Adriatic Sea. Beyond issues in species identification, little is known about the stock structure and level of connectivity among stocks in the Mediterranean and Black seas, despite the relevance of such information for adequate fisheries management. This study aims at clarifying the genetic stock structure of *S. acanthias* and estimate current connectivity levels among stocks in the Mediterranean and Black seas. Mitochondrial ND2 and 16 nuclear microsatellite loci genotypes were obtained for Adriatic and Black seas collections, as well as from adjacent Atlantic population from around the British Isles. Results show the existence of distinct genetic stocks in the Adriatic and Black Seas with little connectivity between them, as well as with the Atlantic counterparts. Moreover, the Black Sea population exhibits much lower genetic diversity than the Adriatic and Atlantic populations, both at the mitochondrial and nuclear markers. These results have direct application to fisheries management, highlighting the need for urgent adequate management of these unique stocks.

## PERCEPTION OF THE VALUE OF ECOSYSTEM SERVICES TO THE INTERMUNICIPAL SCALE IN THE TÂMEGA E SOUSA REGION

Cristiana Carvalho<sup>1</sup>, João P. Honrado<sup>2</sup>, Ana Sofia Vaz<sup>2</sup>

1- *Economics and Environmental Management, Faculty of Economy, University of Porto*

2- *Research Network in Biodiversity and Evolutionary Biology, Research Centre in Biodiversity and Genetic Resources (InBIO-CIBIO), University of Porto*

The unsustainable management of natural resources has motivated a rapid degradation of ecosystems, negatively affecting their capacity to provide services. This reduction of ecosystem services is an important barrier to human well-being, so a paradigm shift is needed. The aim of this study is to assess the perception of local administration agents regarding ecosystem services, their dynamics of offer and demand, and their determinant factors at an inter-municipal scale. For this a participatory workshop with local administration agents was held at the “Comunidade Intermunicipal do Tâmega e Sousa”, in the context of the elaboration of its climate change adaptation plan. A questionnaire was used to inquire the perceptions of those agents concerning ecosystem services in the territory. According to the respondents, the demand of ecosystem services is higher than their offer in the territory. Provisioning services (food and water for consumption) are the most valued, followed by regulation services (protection against wildfires and water cycle regulation). Recreation and landscape aesthetics are the cultural services holding the highest offer, but environmental education and existence values are the ones with the highest demand. Considering the projected future climate change, wildfires, heat waves and cold waves will be the most important determinants of service production, especially of regulating services. The perception of local administration agents is a crucial element for the valuation and valorization of ecosystem services, not only in the context of climate change adaptation, but more broadly considering their contributions for the well-being of local citizens.



## COMMUNITY PLANT STRUCTURE IN INVADED RECIPIENT CALIFORNIAN GRASSLANDS AND PUTATIVE DONOR COMMUNITIES IN SPAIN

Javier Galán Díaz<sup>1</sup>, Enrique G. de la Riva<sup>2</sup>, Montserrat Vilà<sup>1</sup>

1- *Ecología Integrativa, Estación Biológica de Doñana (EBD-CSIC), Sevilla, Spain*

2- *Department of Ecology, Brandenburg University of Technology, Cottbus, Germany*

The introduction of exotic plant species over new regions is causing the homogenization of recipient communities. Invasion of Californian Mediterranean grasslands by Eurasian herbs constitutes one of the best examples, where more than two-thirds out of the 975 exotic plant species registered are originally European. The success of European grasses and forbs was facilitated by a great propagule pressure during the first Spanish settlements in the 18th century, followed by deliberate introductions. Currently, this pool of Eurasian plants dominates Californian grasslands, altering their diversity and functioning. The unidirectional introduction of such a big pool of species from Europe to North America allows to explore some questions considering the whole community, and avoids to focus on single invasive species that are known in advance to cause great impacts across the introduced range. For example, in a scenario with similar climatic regimes and grazing pressures, do these novel communities assemble in a similar way to the native range? Previous studies on exotic herbaceous species suggest that the abundance at home predicts the abundance in the new range, and that only a small proportion of exotic species become more dominant over the introduced range in terms of cover and occurrence. Also, exploring how exotic species assemble in the native and introduced ranges allows assessing how exotic species richness and abundance impact the pool of native species. In this project, we compare how the pool of exotic species assembles in native and exotic ranges, and how it impacts the rest of species in the community at both ranges, in terms of abundance and beta-diversity.

## THE INVASION OF *Vespa velutina* AROUND THE WORLD: A REVIEW WITHIN THE DPSIR FRAMEWORK

Cristina Lima<sup>1,2</sup>, Ana Sofia Vaz<sup>1,3</sup>, João Honrado<sup>1,2</sup>, José Aranha<sup>4,5</sup>, Nazaret Crespo<sup>4</sup>, Joana R.Vicente<sup>1</sup>

- 1- *InBIO/Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO), Campus Agrário de Vairão, Portugal*
- 2- *Department of Biology, Faculty of Sciences, University of Porto, Portugal.*
- 3- *Laboratorio de Ecología (iEcolab), Instituto Interuniversitario de Investigación del Sistema Tierra en Andalucía (IISTA-CEAMA), and Departamento de Botánica, Facultad de Ciencias, Universidad de Granada, Campus Fuentenueva, Spain*
- 4- *Department of Forestry Sciences and Landscape Architecture (CIFAP), University of Trás-os-Montes and Alto Douro, Vila Real, Portugal*
- 5- *Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal*

The yellow-legged hornet (*Vespa velutina*; native to Asia) has become established and invasive in several regions worldwide, including Europe, Japan, Kyushu and Republic of Korea. In this study we aim to review the invasion status of this species at the global scale. We performed a systematic literature search using Scopus, Google Scholar and ISI Web of Knowledge engines, to gather all indexed scientific publications on the yellow-legged hornet. The search was done considering standardised protocols, resulting in a total of 207 documents. The selection of relevant documents was done by applying a series of inclusion and exclusion criteria based on the title, keywords and abstract of each document. From the set of documents concerning *V. velutina*, 98.15% analysed the hornet from an invasion perspective, whereas the remaining 1.85% developed studies under a native scope. A final set of 101 documents was considered for the literature review. Considering the set of studies presenting the hornet as an invasive species, we collected information about the main Drivers, Pressures, State, Impacts, and Responses (i.e. DPSIR framework) associated to *V. velutina* at different spatio-temporal contexts. Specifically, our results provide answers for the following questions: Which are the most acknowledged drivers of the species distribution? Which are the most recognised ecological preferences of the hornet? What are the known impacts caused by the species? Which have been the most efficient methods for its prevention, control and management? We finally discuss potential ways forward for the research and management of *V. velutina* across social-ecological settings.

## EFFECTS OF AN EXTREME CLIMATIC EVENT ON THE ENDANGERED PEARL MUSSEL *Margaritifera margaritifera*

Joana Garrido Nogueira<sup>1,2</sup>, Manuel Lopes-Lima<sup>2</sup>, Simone Varandas<sup>3</sup>,  
Amílcar Teixeira<sup>4</sup>, Ronaldo Sousa<sup>1</sup>

- 1- CBMA - Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Braga, Portugal.
- 2- CIBIO/InBIO - Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal.
- 3- CITAB-UTAD - Centre for Research and Technology of Agro-Environment and Biological Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal.
- 4- Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança, Bragança, Portugal.

Droughts can change the distribution and alter the behaviour, phenology and physiology of many species, leading in extreme cases to high mortalities or even extirpation. In this study, a before/after comparison was performed in two Portuguese river basins (Rabaçal and Tuela) to assess the possible effects of an extreme drought on the abundance and size structure of two pearl mussel *Margaritifera margaritifera* populations, a Critically Endangered species in Europe. The hydrological year of 2017 was extremely dry in Portugal and this situation was responsible for a major reduction of the river flow and rapid decrease in the water levels during summer. One year after the drought, a significant reduction in abundance was observed (i.e. 27.6% for the Rabaçal and 38.7% for the Tuela basin populations). However, no differences were detected in the size structure of the two pearl mussel populations. Droughts are predicted to increase in number and intensity and it is crucial to monitor *M. margaritifera* populations, given the low resistance (and possibly low resilience) of this species to these extreme conditions. Management measures that could help the conservation of pearl mussels are discussed.

## List of participants

<b>NAME</b>	<b>AFFILIATION</b>	<b>COUNTRY</b>	<b>CONTACT</b>
Jéssica Abrantes	FCUP	Portugal	jgoncalves.abrantes@gmail.com
Lurdes Alves	Câmara Municipal de Vila do Conde	Portugal	lurdes.alves@cm-viladoconde.pt
Beatriz Amorim	CIBIO/InBIO	Portugal	bia.silvamorim@gmail.com
Margarida Andrade	CIBIO/InBIO	Portugal	margarida.andrade.22@gmail.com
Adriana Bellati	University of Pavia	Italy	adriana.bellati@unipv.it
Patrícia Beltrão	FCUP - CIBIO/InBIO	Portugal	pbsantospt@gmail.com
Ana Benvindo	CIBIO/InBIO	Portugal	anamargaridabenvindo@gmail.com
Giacomo Bruni	ECOISTITUTO delle CERBAIE SNC	Italy	giacomobruni90@gmail.com
Sofiya Bryukhova	FCUP	Portugal	sbryukhova@gmail.com
M. Pilar Cabezas Rodriguez	CIBIO/InBIO	Portugal	pilarcabezas@cibio.up.pt
João Carneiro	CIIMAR	Portugal	joamiguelsov@gmail.com
Miguel A. Carretero	CIBIO/InBIO	Portugal	carretero@cibio.up.pt
Paulo Celio	CIBIO/InBIO	Portugal	pcalves@cibio.up.pt
Pierre-Olivier Cheptou	CEFE CNRS (UMR 5175)	France	pierre-olivier.cheptou@cefe.cnrs.fr
Pedro Coelho	CIBIO/InBIO	Portugal	plobocoelho@gmail.com
Tiago Costa	FCUP	Portugal	tmoc1991@gmail.com
Nazaret Crespo	Universidade de Trás-os-Montes e Alto Douro	Portugal	nazareth.forestal@gmail.com
Angelica Crottini	CIBIO/InBIO	Portugal	acrottini@cibio.up.pt
Ivo da Costa	CIBIO/InBIO	Portugal	ivodacosta11@gmail.com
Prem Alberto Daswani Aguilar	CIBIO/InBIO	Portugal	premalb.96@gmail.com

<b>NAME</b>	<b>AFFILIATION</b>	<b>COUNTRY</b>	<b>CONTACT</b>
Lucas De Meira Chaves	Universidade do Porto	Portugal	lucasdemeirachaves@hotmail.com
Marco Dinis	CIBIO/InBIO	Portugal	dinismarco6@gmail.com
João Diogo	CIBIO/InBIO	Portugal	joamadiogo@hotmail.com
Celso Domingos de Souza Filho	CIBIO/InBIO	Portugal	bio.celso.domingos@gmail.com
Christophe Dufresnes	University of Laussane and Hintermann	Switzerland	Christophe.Dufresnes@hotmail.fr
Urtzi Enriquez-Urzelai	CIBIO/InBIO	Portugal	urtzi.enriquez@gmail.com
Allowen Evin	Institut des Sciences de l'Evolution	France	allowen.evin@univ-montp2.fr
Gonçalo Ferraz	FCUP - CIBIO/InBIO	Portugal	goncalo.ferraz@outlook.com
Ana Ferreira	FCUP - CIBIO/InBIO	Portugal	isabelferreira98@hotmail.com
Sonia Ferreira	CIBIO/InBIO	Portugal	hiporame@gmail.com
Clara Figueiredo Vázquez	FCUP - CIBIO/InBIO	Portugal	clarafigueiredob1a@gmail.com
Carlos Fonseca	University of Coimbra	Portugal	cfonseca285@gmail.com
Giovanni Forcina	CIBIO/InBIO	Portugal	giovanni.forcina@cibio.up.pt
Bárbara Freitas	FCUP - CIBIO/InBIO	Portugal	barbarabfreitas6@gmail.com
Inês Freitas	CIBIO/InBIO	Portugal	ifinesfreitas@hotmail.com
Joana Freitas	FCUP - CIBIO/InBIO	Portugal	joanafreitas0596@gmail.com
Javier Galán Díaz	EBD-CSIC	Spain	javiergalandiaz@gmail.com
Juan Miguel Giralt Rueda	Estación Biológica de Doñana - CSIC	Portugal	giralt@ebd.csic.es
Célia Gomes	CIBIO/InBIO	Portugal	celtic.nature@gmail.com
Verónica Gomes	CIBIO/InBIO	Portugal	veronica.a.s.g@gmail.com
Sandra Gonçalves	FCUP	Portugal	sandraisabel1996@hotmail.com
Rafael Gutiérrez López	CIBIO/InBIO	Portugal	rgutierrez@cibio.up.pt
Barbara Sofia Ilardo	Liverpool John Moores University	UK	B.S.Ilardo@2018.ljmu.ac.uk
Diogo Jesus	FCUP - CIBIO/InBIO	Portugal	diogoepjesus@gmail.com

<b>NAME</b>	<b>AFFILIATION</b>	<b>COUNTRY</b>	<b>CONTACT</b>
Antigoni Kaliontzopoulou	CIBIO/InBIO	Portugal	antigoni@cibio.up.pt
jean-baptiste ledoux	CIIMAR	Portugal	jbaptiste.ledoux@gmail.com
Cristina Lima	FCUP	Portugal	cristinalima@live.com
João Lima	FCUP - CIBIO/InBIO	Portugal	joaolemoslima@gmail.com
Cristina Linares	Institut de Recerca de la Biodiversitat	Spain	cristinalinares@ub.edu
Manuel Lopes Lima	CIBIO/InBIO	Portugal	mlopeslima@cibio.up.pt
Nahla Lucchini	CIBIO/InBIO	Portugal	nany_91ts@hotmail.it
Nahla Lucchini	CIBIO/InBIO	Portugal	lucchini.nahla@gmail.com
Francisco Tarcísio Moraes Mady	Universidade de Trás os Montes e Alto Douro	Portugal	madyftm@gmail.com
Adam Marques	CIBIO/InBIO	Portugal	adam.marques@cibio.up.pt
Cristiana Marques	CIBIO/InBIO	Portugal	cristiana.ij.marques@gmail.com
Valéria Marques	FCUP - CIBIO/InBIO	Portugal	valeria.vscm@hotmail.com
Joana Martelo	MARE Marine and Environmental Sciences Centre	Portugal	jmmartelo@fc.ul.pt
Helena Martinez	CIBIO/InBIO	Portugal	Helenamartg95@gmail.com
Helena Martínez	CIBIO/InBIO	Portugal	helenamartg95@gmail.com
Fernando Martínez-Freiría	CIBIO/InBIO	Portugal	fmartinez-freiria@cibio.up.pt
Iñigo Martinez-Solano	MNCN-CSIC - CIBIO/InBIO	Spain	inigomsolano@gmail.com
Beatriz Martins	FCUP - CIBIO/InBIO	Portugal	bia_triz88@hotmail.com
José Melo-Ferreira	CIBIO/InBIO	Portugal	jmeloferreira@cibio.up.pt
Inês Miranda	CIBIO/InBIO	Portugal	inesmiranda@cibio.up.pt
Mónia Nakamura	CIBIO/InBIO	Portugal	moniayui@gmail.com
Joana Nogueira	CIBIO/InBIO	Portugal	joanafgnogueira93@gmail.com
Daniel Oliveira	CIBIO/InBIO	Portugal	daniel.jet100@gmail.com

<b>NAME</b>	<b>AFFILIATION</b>	<b>COUNTRY</b>	<b>CONTACT</b>
Lucas Pacheco	FCUP	Portugal	Lucaspacheco97@gmail.com
Ana Pereira	CIBIO/InBIO	Portugal	anantunespereira@gmail.com
Joana Pereira	FCUP - CIBIO/InBIO	Portugal	up201606645@fc.up.pt
Maria Pereira	FCUP - CIBIO/InBIO	Portugal	isabel.pereira12@hotmail.com
Ana Perera	CIBIO/InBIO	Portugal	perara@cibio.up.pt
Costanza Piccoli	CIBIO/InBIO	Portugal	costanza.piccoli.92@gmail.com
Libânia Pinheiro	CIBIO/InBIO	Portugal	libaniapinheiro@gmail.com
Catarina Pinho	CIBIO/InBIO	Portugal	catarina@cibio.up.pt
Catarina J. Pinho	CIBIO/InBIO	Portugal	cpinho541@gmail.com
Rita Ramos	CIBIO/InBIO	Portugal	ritaafamos@cibio.up.pt
Catarina Rato	CIBIO/InBIO	Portugal	catarina.rato@cibio.up.pt
Gabriel Riaño	CIBIO/InBIO	Portugal	gabri.mochales@gmail.com
Cláudia Ribeiro	FCUP	Portugal	lippa@live.com.pt
Guilherme Roxo	FCUP	Portugal	roxoguilherme@gmail.com
Beatriz Saldanha	FCUP - CIBIO/InBIO	Portugal	beatrizsaldanha5@gmail.com
Sara Sampaio	FCUP - CIBIO/InBIO	Portugal	sara.r.n.s.sampaio@gmail.com
Alberto Sánchez Vialas	MNCN-CSIC	Spain	alberto.alytes@gmail.com
Gregorio Sánchez-Montes	MNCN-CSIC	Spain	gregorio.sanchezmontes@mncn.csic.es
André Santos	CIIMAR	Portugal	andrepousa64@gmail.com
Thomas Schmitt	Senckenberg German Entomological Institute	Germany	thomas.schmitt@senckenberg.de
Yuri Simone	CIBIO/InBIO	Portugal	yurisimone1@gmail.com
Pedro Sousa	CIBIO/InBIO	Portugal	prsousa@gmail.com
Ronaldo Sousa	Universidade do Minho	Portugal	rg.eco.sousa@gmail.com
Roman Straňanek	CIBIO/InBIO	Portugal	strananek.roman@gmail.com

<b>NAME</b>	<b>AFFILIATION</b>	<b>COUNTRY</b>	<b>CONTACT</b>
Jordana Teixeira	CIBIO/InBIO	Portugal	jordana_mileny_ce@hotmail.com
Cátia Torres	FCUP - CIBIO/InBIO	Portugal	catia.filipa.torres@gmail.com
Aleksandar Urošević	Institute for Biological Research "Siniša Stanković", National Institute of Republic of Serbia, University of Belgrade	Serbia	aurosevic@ibiss.bg.ac.rs
Javier Valverde	CIBIO/InBIO	Portugal	jvalverde@cibio.up.pt
Arie van der Meijden	CIBIO/InBIO	Portugal	mail@arievandermeijden.nl
Diana Vasconcelos	FCUP - CIBIO/InBIO	Portugal	dianasilvav2005@gmail.com
Raquel Vasconcelos	CIBIO/InBIO	Portugal	raquel.vasconcelos@cibio.up.pt
Daniel Velarde Garcez	Universidade de Porto	Portugal	danielv1rd1@gmail.com
Ana Verissimo	CIBIO/InBIO	Portugal	averissimo@cibio.up.pt
Joana Veríssimo	CIBIO/InBIO	Portugal	joana.filipa.verissimo@gmail.com
Pablo Vicent	MNCN-CSIC	Spain	pablovicent0000@gmail.com
Cristiana Vieira	MNHC - UP	Portugal	cvieira@mhnc.up.pt
Raquel Xavier	CIBIO/InBIO	Portugal	raq.xavier@gmail.com