X REUNIÓN ANUAL DE ESTUDIANTES DE DOCTORADO EN BIODIVERSIDAD Y BIOLOGÍA EVOLUTIVA

Inaugura Nicolás Pérez-Hidalgo

03 de julio
08:30 am -17:15 pm

Salón de Grados,
Facultad de Farmacia

VNIVERSITAT DE VALÈNCIA

Programa de Doctorado en
Biodiversidad y Biología Evolutiva

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Paula Ruiz Rodriguez

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UBICACIÓN

UBICACIÓ / VENUE

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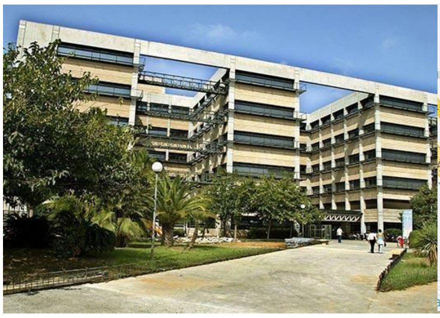

PROGRAMA

PROGRAMA / PROGRAM

08:30-09:00 Recepción

09:00-09:15 Presentación X Reunión Anual de estudiantes
Maria Antonia Rodrigo Alacreu

09:15-10:00 Ciclos biológicos complejos: el caso de los Fordinos (Hemiptera: Aphididae)
Nicolás Pérez-Hidalgo (Sesión inaugural)

BLOQUE I. GENÉTICA Y MICROBIOLOGÍA

10:00-10:15 **The gene that was not there: Hemocyanin in Podocopa**
Ximena Aurora Altonar-Gómez

10:15-10:30 **Diapause-related strategies in rotifers: adapting to environmental unpredictability**
Carlota Solano-Udina

10:30-10:45 **Differences in virulence of *M. tuberculosis* ecotypes based on host specificity**
Marta Caballer Gual

10:45-11:00 **Syncytia induction is a viral social trait**
Marc Carrascosa-Sàez

11:00-11:15 **Unlocking data in *Klebsiella* lysogens to predict phage tropism based on depolymerase sequence with machine learning**
Robby Concha-Eloko

11:15-11:45 **PAUSA CAFÉ**

11:45-12:00 **Evolutionary strategies of *Klebsiella* phages in a host-diverse environment**
Celia Ferriol-González

12:00-12:15 **Study of host-symbiont communication mediated by extracellular vesicles in Blattella germanica**
David Saiz-Martínez

12:15-12:30 **Deep mutational scanning of a model picornavirus: a deep dive into the role of mutations in interferon sensitivity and resistance**
Sebastian Velandia-Álvarez

BLOQUE II. BIODIVERSIDAD, ECOLOGÍA Y CONSERVACIÓN DE ECOSISTEMAS TERRESTRES

12:30-12:45 **Unravelling the link between productivity and climate of two sympatric *Acrocephalus* warblers across Spain**
Pau Lucio-Puig

12:45-13:00 **Unmasking the diversity of genus *Ulota* (Orthotrichaceae, Bryophyta) in Australasia**
Nikolay Matanov

13:00-13:15 **Blowing hot and cold: intralocus sexual conflict and temperature in *Drosophila melanogaster***
Soumya Panyam

13:15-13:30 **Systematics of the ornithischian dinosaurs from the Upper Jurassic of the eastern Iberian Peninsula**
Sergio Sánchez-Fenollosa

13:30-13:45 **Chromatic intrasexual signals show positive allometry in lizards**
Yujie Yang

13:45-14:00 **Effect of multiple ecological process on the co-occurrence of species in the mediterranean vegetation community: multilayer network**
Patricia Moreno-Colom – Online

14:00-14:15 **Spatial patterns and density variations of dwarf palm (*Chamaerops humilis*) across habitats in Doñana National Park, southwestern Spain**
Brayan Morera – Online

14:15-15:15 **COMIDA**

BLOQUE III. BIODIVERSIDAD, ECOLOGÍA Y EVOLUCIÓN DE ECOSISTEMAS ACUÁTICOS

15:15-15:30 **Dynamics and interaction of three humpback whale (*Megaptera novaeangliae*) populations in Mexico**
Paula Cabanilles Benito - Online

15:30-15:45 **Chondrichthyans and actynopterigians remains from upper pennsylvanian of Peru**
Leonardo Zevallos Valdivia - Online

15:45-16:00 **Study of oospores to assess the restoration potential for populations of *Chara canescens*, a bisexual-parthenogenetic charophyte species**
Adriana Arnal

16:00-16:15 **Decline of epiphytic lichens across the eastern Spain: biomonitoring and genomic techniques applied to biodiversity conservation**
Tamara Pazos

16:15-16:30 **Using environmental DNA analysis as a monitoring tool for cetacean and other marine vertebrates in the Mediterranean Cetacean Corridor**
Chloé Fernández

16:30-16:45 **Assessing the spatiotemporal variability of cumulative impacts on cetaceans in the Western Mediterranean**
Greta Jankauskaite

16:45-17:00 ***Phyllodistomum umblae* and *Crepidostomum* spp. (Digenea) differentiation in the recent radiation of European whitefish**
Mar Llaberia-Robledillo

17:00-17:15 **Monitoring of marine megafauna and its interaction with anthropogenic pressures in the western Mediterranean**
Javier Menéndez-Blázquez

CONFERENCIA PLENARIA / Conferència plenaria / Plenary talk

Ciclos biológicos complejos: el caso de los Fordinos (Hemiptera: Aphididae)

Nicolás Pérez-Hidalgo

La tribu Fordini agrupa especies de pulgones con holociclos muy complejos en los que suelen alternar la formación de agallas en sus hospedadores primarios (especies de *Pistacia*), con la vida subterránea en sus hospedadores secundarios (principalmente raíces de poáceas). Sin embargo, sus formas radicícolas, probablemente ayudadas por sus relaciones mirmecófilas, pueden desarrollar anholociclos en territorios muy alejados de la distribución natural de sus hospedadores primarios.

La mirmecofilia es el término aplicado a la asociación entre hormigas y una variedad de organismos como plantas, artrópodos y hongos. Numerosas especies de insectos han sido catalogadas como mimecófilas. Dentro de los hemípteros, especialmente en los subórdenes Sternorrhyncha (pulgones, cochinillas y moscas blancas) y Cicadomorpha (cigarras y membrácidos), muchas especies exhiben algún grado de mirmecofilia. Muchos de estos mutualismos son facultativos y no especializados, pero todos tienen un denominador común: la interacción se basa principalmente en la producción por parte de estos insectos de excreciones azucaradas que son consumidas por las hormigas que, a cambio, les proporcionan protección contra depredadores y servicios de limpieza. Este tipo de asociación se conoce como trofobiosis y alrededor del 40% de las especies de pulgones participan de manera obligada o facultativa en este tipo de asociación con diferentes especies de hormigas.

La plasticidad que presentan algunas especies de pulgones, hace que presenten adaptaciones morfológicas y biológicas para vivir tanto en sus hospedadores primarios como secundarios y adaptarse así a condiciones ambientales muy cambiantes.

RESÚMENES – Bloque I. Genética y microbiología

The gene that was not there: Hemocyanin in Podocopa

Altonar-Gómez, Ximena Aurora[1]; Ortells, Raquel[1]; Mestre, Alexandre[1]; Palero, Ferran[1]
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Keywords: Ostracoda, respiration, hemocyanin, hypoxia, phylogenetics

Hemocyanin, a functionally diverse protein superfamily, plays a crucial role in oxygen transport across arthropods. Despite extensive study within Malacostraca, information regarding its presence in Copepoda and Thecostraca, and particularly within the Podocopa order of Ostracoda, remains scarce. In this research, we utilize innovative sequencing technologies to search the hemocyanin gene in Cyprideis torosa, a small ostracod from the Podocopida order, and characterize its genetic architecture. Sediment samples were collected from the Salinas de Santa Pola Natural Park, and DNA was extracted from *Cyprideis torosa* specimens using the MagAttract DNA kit. PacBio sequencing was performed to analyze full-length hemocyanin transcripts, allowing for comprehensive identification and characterization. Additionally, Iso-Seq transcriptome sequencing was employed to identify novel isoforms and genes. Phylogenetic analysis revealed the evolutionary relationship of *Cyprideis torosa* hemocyanin with homologous genes from other crustacean species. Our findings demonstrate, for the first time, the presence of hemocyanin in Podocopa, filling a critical gap in our understanding of its distribution and evolution within Pancrustacea. The discovery of hemocyanin in this organism sheds light on its respiratory physiology and evolutionary history, providing valuable insights into the adaptation of ostracods to diverse aquatic environments

Diapause-related strategies in rotifers: adapting to environmental unpredictability

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[1] Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Universitat de València, Spain

Keywords: environmental unpredictability, life-history traits, diapause, cyclical parthenogens

Unpredictable fluctuating, natural environments drive organisms to exhibit adaptive responses. To mitigate the impact of unexpected adverse conditions, various traits may be potentially subject to selection. In many zooplankters, such traits are related to their ability to survive adverse conditions, such as desiccation, via diapausing eggs. These diapause-related traits include (1) the timing of hatching, (2) the variation in the timing of hatching, (3) the egg hatching fraction and (4) the timing of diapausing-egg production. Here, we examined a set of nine populations of the rotifer *Brachionus plicatilis* and explored the interplay between these traits and the predictability and hydroperiod they experience in their habitats. Furthermore, we addressed how these traits interact, considering the potential counterbalancing effects of certain trait responses. We found some traits combinations exhibit stronger correlations with environmental unpredictability. The significance of these findings in the ecological context of the studied system is discussed.

Differences in virulence of *M. tuberculosis* ecotypes based on host specificity

M. Caballer-Gual[1], P. Ruiz-Rodriguez[1], G. Santamaria[1], H. Hiza[1], and M. Coscolla[1]
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Keywords: *Mycobacterium tuberculosis*, *in vitro* infection, host-pathogen interactions, virulence, host specificity

Tuberculosis is one of the leading causes of death from infectious agents worldwide. It is caused by the Mycobacterium tuberculosis complex (MTBC) which is composed of 13 lineages or ecotypes. MTBC lineages can be broadly divided into animal and human-associated lineages. MTBC ecotypes possess a genomic similarity higher than 99%. However, the ecotypes differ among them in the host range they can infect. Knowing the host-pathogen interactions and their compatibility will allow us to decipher the factors that influence M. tuberculosis virulence. We hypothesize that virulence is influenced by host compatibility and that M. tuberculosis strains show higher virulence phenotypes when infecting their favored host. To test this, we have used an in vitro infection system to explore the virulence between different hosts by infecting human and bovine macrophages with two strains of M. tuberculosis from human-associated lineages (Lineages L5 and L6) and two strains associated with animals Mycobacterium bovis (Lineage A1) and Chimpanzee bacillus (Lineage A4). Our analysis revealed that the infection ratio is increased when cells are infected with their favorite strain. Additionally, these preferred host-lineage combinations resulted in decreased cell viability and higher cell death levels, in contrast to bacterial-host combinations that were not preferred. Finally, our preliminary results suggest that in high virulence combinations, upregulated gene expression pathway were associated with cellular and molecular pathways to facilitate bacterial survival, while in low virulence combinations pathways suggested activation of early immune response and recruitment of immune cell for bacterial control.

Syncytia induction is a viral social trait

Marc Carrascosa-Sàez[1], Iván Andreu-Moreno[1], Jérémy Dufloo[1], and Rafael Sanjuán[1]

[1] Institute for Integrative Systems Biology (I2SysBio). University of Valencia – CSIC

Keywords: Enveloped virus, viral entry pathways, syncytia, sociovirology

Enveloped viruses can enter cells directly by fusion with the plasma membrane or via the endocytic pathway. A property of viruses using the former route is that their receptor-binding proteins, when expressed at the plasma membrane of infected cells, can induce cell-cell fusion, leading to the formation of multinucleated cells called syncytia. It has been speculated that syncytia increase the efficiency of viral spread compared to cell-free propagation and protect virions from neutralising antibodies. However, syncytia also induce premature cytopathic effects that may interfere with the production of viral progeny. Therefore, the impact of viral entry pathways and syncytia formation remains poorly understood. Here we show that syncytia induction functions as a social trait. This is because syncytia can fuse with neighbouring cells infected with the same or a different virus variant, even if the latter does not induce syncytia. To better understand this process, we first performed simulations based on diffusion-reaction models. This showed that the dominant nature of syncytia induction leads to virus-virus interactions, co-infections and frequency-dependent selection. We then tested these findings experimentally using two SARS-CoV-2 spike variants that differ in their entry routes and syncytia induction. This confirms that syncytia facilitate virus spread at early time points at the expense of premature cell death, whereas cell-free virus transmission provides greater fitness over longer infection times. Analysing viral entry pathways through the prism of social evolution may help to improve our understanding of certain aspects of virus biology and pathogenesis.

Unlocking data in Klebsiella lysogens to predict phage tropism based on depolymerase sequence with machine learning

Robby Concha-Eloko[1], Pilar Domingo-Calap[1], Rafael Sanjuan[1*]

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Keywords: phage-bacteria interaction, prophage, depolymerase, *Klebsiella* capsule, machine learning, graph neural network

Phage therapy holds great potential to combat bacterial infections. The first contact between a phage and a bacterium is considered the most critical step of the infection process. Important pathogens express a capsule (CPS), a complex polysaccharide layer acting as a barrier that the phage has to overcome for a successful infection. Recent studies suggest depolymerase enzymes encoded by phages play a key role in this process. However, modeling these interactions at the sub-specie level remains challenging due to limited data and complex biological processes. This study addresses this challenge for the pathogen *Klebsiella* by leveraging the information encoded within its prophages. The interplay between the bacteria, the prophages, and the encoded depolymerases has been modeled using two approaches: (i) a graph neural network (ii) a sequence clustering-based method. Both approaches demonstrated significant predictive abilities for prophages and, importantly, transferred successfully to lytic phages. Additionally, a comprehensive database was compiled linking depolymerase sequences to their specific target. This study presents an innovative approach for predicting phage-host interactions at the sub-specie level, offering new insights into phage-CPS recognition and paving the way for improved phage therapies and industrial applications.

Evolutionary strategies of *Klebsiella* phages in a host-diverse environment

Celia Ferriol-González[1], Pilar Domingo-Calap[1]
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Keywords: *Klebsiella*, bacteriophage, directed evolution, host range

Klebsiella is a gram negative, capsular bacterium that is considered a major health pathogen worldwide. It exhibits enormous capsular variability which is the main determinant of the host tropism of Klebsiella phages. The aim of our work is to evaluate the ability of a phage cocktail to expand the host range over a capsule-diverse bacterial panel through directed evolution. We performed 69 passages in 3 parallel lines using a bacterial pool containing both susceptible and resistant strains to the phage cocktail. The cocktail consisted of 12 phages, some specialists (host range <=2 capsular types), and generalists (host range >2 capsular types). Metagenomic analyses were performed on several passages to understand the molecular mechanisms underlying viral adaptation. In addition, 93 single evolved phage plaques were isolated and sequenced. Our results suggest that phages can use different strategies to survive in a host-diverse environment. Generalist phages appeared to adapt by parallel evolution, accumulating mutations in their receptor binding proteins. In contrast, specialist phages tended to optimise their infection cycle within the same host. Regarding phages included in the cocktail that had sufficient intergenomic similarity, they tended to recombine. Interestingly, some phages were lost during the evolution, showing that ecological interactions between phages and bacteria determine phage survival. Finally, metagenomic data suggested that some prophages were activated during the evolution experiment. Our work is a step forward in the understanding of the molecular mechanisms of phage adaptation in an encapsulated host.

Study of host-symbiont communication mediated by extracellular vesicles in Blattella germanica

Saiz-Martínez, David[1,2]; Marcilla-Díaz[1], Antonio and Gil-García, Rosario[2]

[1] Parasitology Unit, Department of Pharmacy and Pharmaceutical Technology and Parasitology, Faculty of Pharmacy, University of Valencia, Burjassot (Valencia), Spain.

[2] Institute for Integrative Systems Biology (I2SysBio), University ofValencia CSIC, Paterna, Spain.

Keywords: Extracellular vesicles, Symbiosis, Blattella germanica, miRNA

Given the importance of symbiosis in the evolution of organisms, especially the mutualistic relationship between bacteria and different species of insects, it is important to understand how communication occurs between the symbiont and the host. The symbiont-host interaction goes beyond nutrient exchange, with molecules such as antimicrobial peptides and small non-coding RNAs playing roles in regulating symbiont population and facilitating bidirectional communication between symbiont and host, respectively. The selected model organism is the cockroach Blattella germanica, as it harbors two symbiotic systems: Blattabacterium cuenoti, an obligate endosymbiont essential for the host's survival and reproduction, and the gut microbiota, a group of organisms residing in the digestive tract performing various functions.

In recent years, extracellular vesicles (EVs) have been studied as a key component in intracellular communication, not only between different cells of the same organism but also between different organisms. Building on this knowledge, the objective of this study is to determine if EVs play a role in communication between the different symbiotic systems and the host (or between them). Such information could be used to design sustainable and safe pest control methods by targeting the endosymbiont.

Deep mutational scanning of a model picornavirus: a deep dive into the role of mutations in interferon sensitivity and resistance

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Keywords: Coxsackievirus B3 (CVB3), innate immunity, interferon, Deep Mutational Scanning (DMS).

RNA viruses have the highest mutation rate in nature. This, combined with their rapid replication and relatively large population sizes, allows them to rapidly evolve and adapt to new environments. However, while the high mutation rate is key to successful adaptation, it also plays an important role in the generation of non-viable viruses, as most mutations tend to be deleterious for protein functions. How the viruses and their proteins contend with this process and adapt under different selective pressures, such as immune responses is unclear. Deep Mutational Scanning (DMS) can help answer such questions, as it assesses the effect of all possible single amino acid mutations in a protein. This method, combined with the application of a selective pressure, can reveal crital mutations for counteracting the effects of this force. We used DMS to define single amino acid mutations across the full proteome of a model picornavirus, Coxsackievirus B3, that confer resistance or sensitivity to interferon. Several mutations with these phenotypes were identified and validation was carried out by individually constructing mutant viruses. To determine the step of the viral cycle that was affected by the interferon effector pathway, we assessed entry, replication, and translation of the mutants individually. Additionally, 20 ISGs known to affect enteroviruses were overexpressed using a lentiviral system to determine the mechanisms by which these mutants are more sensitive or resistant than the wildtype virus. Further analyses are being carried out to couple the data of different DMS selections to develop a novel live-attenuated vaccine candidate.

RESÚMENES – Bloque II. Biodiversidad, ecología y conservación de ecosistemas terrestres

Unravelling the link between productivity and climate of two sympatric *Acrocephalus* warblers across Spain

Pau Lucio-Puig[a,b]*, Rafael Muñoz-Mas[a,c], Eduardo Belda[a], Jaime Gómez[d], Francesco Ceresa[b,e], Virginia Garófano-Gómez[a,f], José Pahissa[c] and Juan S. Monrós[b]

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Keywords: bird conservation, climate change, passerines, population dynamics, population trends, wetlands

We use data from a breeding bird monitoring ringing scheme in Spain (PASER; 1995 - 2021) to investigate the effects of seasonal rainfall and temperature patterns on the productivity of two sympatric warblers: the resident/short-distance migrant Moustached Warbler (*Acrocephalus melanopogon*), and the generalist long-distance migrant Reed Warbler (*Acrocephalus scirpaceus*). Analyses were performed using Multi-Adaptive Regression Splines (MARS). Our results indicated that, between 1995 and 2021, geographic and site-specific factors drove annual productivity for both species, in combination with rainfall and temperature. For Moustached Warbler, geographic and site-related variables, together with temporal changes and trend (year), were more critical than rainfall and temperature. An accumulated rainfall of 100 mm favoured productivity, but temperature had a negative effect. By contrast, for Reed Warbler temperature was more important than trend but less than site and longitude and had a positive effect on the productivity. Contrary, rainfall had almost no effect, although it also peaked when it approached 100 mm. The increase in temperatures and a higher frequency of torrential rainfall events may compromise the conservation of the vulnerable Moustached Warbler in Spain due to their adverse effect on its productivity. On the contrary, the ongoing increase in temperatures across Spain may benefit the widely distributed Reed Warbler. Thus, Moustached Warbler populations are likely to decrease, whereas Reed Warbler populations might increase. However, further research is needed to establish climate change's impact on survival and its implication in the population trends and dynamics of these two sympatric warbler species.

Unmasking the diversity of genus *Ulota* (Orthotrichaceae, Bryophyta) in Australasia

Nikolay Matanov[1], Isabel Draper[2,3], Juan A. Calleja[2,3], Francisco Lara[2,3] & Ricardo Garilleti[1]
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Keywords: Biogeography, Integrative taxonomy, Morphology, Orthotrichoideae, Systematics

Orthotrichoideae is a complex group of mosses, both taxonomically and biogeographically, which plays an important role in epiphytic communities in temperate regions and high tropical mountains worldwide. Four genera notably contribute to the subfamily's diversity: *Orthotrichum*, *Zygodon*, *Lewinskya* and *Ulota*. The current diversity of *Ulota* s.l. (including *Atlantichella*, *Rehubryum* and *Plenogemma*) encompasses 70 taxa mostly found in temperate and temperate-cold regions. In the southern hemisphere, the genus *Ulota* has two major centers of diversity with endemism rates of 100%: Patagonia (predominantly Chile) and Australasia (New Zealand and SE Australia). In the latter, 13 taxa have been reported. Indeed, although there have been several taxonomic revisions conducted on this group on these areas, its true diversity remains not fully understood. New taxa have been recently discovered, emphasizing the challenging nature of its understanding. The morphological complexity and high taxonomic diversity within *Ulota* and its close relatives make this group one of the most taxonomically intriguing. An integrative taxonomy approach is being employed. This approach combines morphological, ecological, and molecular analyses to ascertain the true biodiversity of the genus *Ulota* and its relationships with the ulotoid genera (morphologically cryptic genera). Additionally, we also aim to understand the genetic diversity, biogeographic patterns, and the adaptive and evolutionary history that have led to the current diversity in the southern hemisphere.

The aim of this presentation is to unveil the cryptic diversity of this group in Australasia through integrative taxonomy, taking into consideration morphology, ecology, and biogeography, along with phylogenetic reconstructions.

Effect of multiple ecological process on the co-occurrence of species in the mediterranean vegetation community: multilayer network

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Keywords: Multilayer network, Co-ocurrence of fleshy-fruit species, plant-plant interactions and plant-animal interactions

Spatial distribution of species mold biodiversity, and viceversa. Co-occurrence of plant is caused for ecological process that affect the association between plant species across different ontogenetic stages and with different magnitude of effect. Usually, those ecological process are interspecific interactions, such as pollination, recruitment or herbivory. However, those process had been largely studied isolated, missing their joint effect on plant co-occurrence, but multilayer network could be a tool to study several interactions at the same time and their effect along the life of individuals, as they allow to study interaction within and between networks. We studied Mediterranean fleshy-fruit species and their co-occurrence pattern through the co-dispersión, recruitment, herbivory, and competition in six different sites of C. Valenciana to assess the relative contribution of each process (i.e. each network), in the formation of community and how it changes between sites with a contrasted frequency of herbivory and dispersion. We studied 2500m2 in every site, in which we quantified the juveniles of our focal species growing below canopy species, the cover of the canopy species, quantify the herbivory and the co-occurrence pattern. Also, we recollected mammals' excrement to study the dispersion and germination effect. Thus, plant and animal species will convert in nodes and the links connecting them will indicate the presence or lack of interaction and the magnitude of it, also, studying the properties of the network we would understand the role of the species on the assemblage of the community.

Spatial patterns and density variations of dwarf palm (*Chamaerops humilis*) across habitats in Doñana National Park, southwestern Spain

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Keywords: cluster characteristics, habitat effect, Mediterranean ecosystem, point pattern

Understanding how plant distribution and density vary across habitat types is necessary to accurately model their distribution, and it also helps to identify the underlying mechanisms of such variations. We examine the spatial patterns, density, cluster characteristics and individual traits of a keystone Mediterranean dwarf palm (*Chamaerops humilis*) in four different habitat types (marsh island, pine forest, prairie, and Mediterranean scrubland), using Thomas process models to quantify clustering level and generalized linear models to determine the effect of habitat. The results revealed that 60% of the sampled plots displayed a clustering spatial pattern with a critical scale of aggregation, while the remaining 40% showed two critical scales of aggregation. Furthermore, the mean cluster level was highest in the Prairie followed by Scrubland, Islands, and Pine Forest, respectively. The density of dwarf palm varied significantly between habitats, localities, and size classes. The reproductive status and sex ratio also varied significantly between habitats and size classes. Furthermore, we demonstrate how to incorporate this information for an accurate simulation of the spatial distribution of individuals of *C. humilis* in the heterogeneous landscape of the protected natural space of Doñana. The study demonstrated the significant effect of habitat on the parameters that describe the spatial pattern of the dwarf palm. The findings contribute to a better understanding of the ecology and distribution of dwarf palms, providing valuable information for future ecological studies that require an understanding of spatial distribution at the habitat level.

Blowing hot and cold: intralocus sexual conflict and temperature in *Drosophila melanogaster*

Soumya Panyam[1], Jesús Ortega Giménez[1], Jennifer Perry[2], Pau Carazo[1]
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Despite the fact that males and females share most of their genome, selection often acts differently on each sex, resulting in genotypes with conflicting fitness effects between the sexes. This phenomenon, known as intra-locus sexual conflict (IASC), results in a “sex-load” that can reduce the fitness of each sex due to the accumulation of alleles with sexually antagonistic effects. Recent evidence shows that this form of sexual conflict decreases when populations are subject to rapid and extreme changes in the environment, likely due to natural selection operating concordantly on both sexes. However, relatively little is known about whether IASC varies in response to environmental fluctuations within the range they normally experience in nature. In this study, we measured variation in IASC in a population of Drosophila melanogaster at different temperatures within its optimal reproductive range in the wild (20ºC to 28ºC). Using isogenic lines derived from wild flies, we set up competitive assays to measure male and female fitness at four different temperature regimes within this range: 20ºC, 24ºC, 28ºC (stable regimes), and a 24 ± 4ºC temporally fluctuating (complex) regime, which mimics natural conditions. We then calculated the intersexual genetic correlation for fitness between males and females (rmf) at each temperature treatment to estimate the extent of IASC in the population. We found weakly negative correlations between male and female fitness at the stable temperature treatments, consistent with previous studies on IASC. However, we found a positive correlation in the complex regime. Together, the results suggest that previous estimates of IASC under stable temperature regimes might be over-estimates, and that IASC may be minimal under natural temperature conditions.

Systematics of the ornithischian dinosaurs from the Upper Jurassic of the eastern Iberian Peninsula

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Keywords: Mesozoic, Ornithopoda, Stegosauria, taxonomy, phylogeny

The European fossil record of Late Jurassic ornithischian dinosaurs is mainly comprised by ornithopods and stegosaurs. The eastern Iberian Peninsula is one of the places with most ornithischian fossils in all of Europe and a key place for understand the diversity and evolution of these dinosaurs. In the present work, we provide new data about the taxonomy and phylogeny of several specimens from the Villar del Arzobispo Formation. It is a detrital-carbonate lithostratigraphic unit with an age of Kimmeridgian-Tithonian (Late Jurassic) with abundant outcrops in the province of Valencia and Teruel. The systematic study of several stegosaur remains from six different localities (Valencia and Teruel) revealed that they correspond to indeterminate stegosaurs or to *Dacentrurus armatus*. On the other hand, several fossils of an ornithopod dinosaur found in Riodeva (Teruel) revealed the presence of a new taxon, *Oblitosaurus bunnueli* gen. et sp. nov. diagnosed on the basis of five appendicular autapomorphies. *Oblitosaurus bunnueli* is nested at the base of Ankylopollexia as sister-taxon of *Draconyx loureiroi* (lower Tithonian, Portugal). These results lead us to propose a new definition for the clade Ankylopollexia. Furthermore, our results have important taxonomic implications for the genus *Camptosaurus*, as the first phylogenetic analysis to support the monophyly of the three species. The estimated size of *Oblitosaurus bunnueli* suggests that it was much larger than *Draconyx loureiroi*, and any other contemporaneous European taxa, and may be the trackmaker of some large ornithopod tracks found in the Upper Jurassic of the Iberian Peninsula.

Chromatic intrasexual signals show positive allometry in lizards

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Keywords: chromatic signal; intrasexual selection; lizard, static allometry

Sexually selected traits include ornaments and armaments used mainly by males to acquire mates. It has been argued that sexually selected traits should show positive static allometries with overall body size (i.e., larger animals within a sample of conspecific adults should have disproportionally larger traits). However, despite longstanding interest, the evidence for this scaling rule is mixed and controversial. Also, previous studies have emphasized morphological traits, while relatively neglecting colour patches, which function as ornaments and armaments in many taxa. Here, we explore allometric scaling in two iconic lizard chromatic signals: the ultraviolet (UV)-blue ventrolateral patches of *Podarcis* and the blue ventral patches of *Sceloporus*. For comparison, we also examine scaling in head length and interlimb length in *Podarcis muralis*. We found that patch size is sexually dimorphic in both species and exhibits positive allometry in males but not females, with coefficients of 2.096 for *Podarcis* and 1.159 for *Sceloporus*. We also found inter-population differences in the scaling of the UV-blue patches in *Podarcis*, possibly related to differences in habitat and/or the intensity of sexual selection. In contrast, head length (under both natural and sexual selection) and interlimb length (under natural selection) in *Podarcis* are isometric or negatively allometric. These patterns agree with recent work that posits that traits used in intrasexual combat should show positive allometry and confirms the colour patches of *Podarcis* and *Sceloporus* as intra-sexually selected traits that convey information about male quality/fighting ability.

RESÚMENES – Bloque III. Biodiversidad, ecología y evolución de ecosistemas acuáticos

Study of oospores to assess the restoration potential for populations of *Chara canescens*, a bisexual-parthenogenetic charophyte species

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Keywords: Charophytes, *Chara canescens*, brackish waters, oospores, restoration potential

Chara canescens is a charophyte algae, which brings a lot of ecosystem services in the brackish water ecosystems that inhabits. This species is unique within its group because it presents two different reproductive strategies: parthenogenesis, which is unusual in Charophyceae algae, and sexual reproduction. Parthenogenetically reproducing populations are widespread in coastal brackish lagoons world-wide, so they are not considered as rare; however, sexually reproducing populations are restricted to inland brackish water sites, with only a few populations recorded in the last decades, most of them in the Mediterranean region. The genetic diversity of the species and its conservation depends on the genetic flow of both populations' types through stepping-stone habitats, because the parthenogenetically reproducing populations lack some of the genetic recombination mechanisms and consequently are more vulnerable to loss of genetic diversity. Aiming to preserve and restore the populations of *C. canescens*, and to develop effective transnational conservation strategies, the project "ProPartS" (Biodiversa+) assesses, among other objectives, the restoration potential from the species' diaspore bank, the sexual propagules named oospores. The oospores can remain viable in the sediments and act as reservoirs, ensuring mid-term resilience of temporary and/or degraded habitats. We have sampled sediment from different historical and current sites for the species, describing and analyzing the oospores present in the sediment in terms of densities and germination rates. This study allows us to assess the possible differences between the sexually and parthenogenetically produced oospores and may help us, ultimately, to develop effective conservation and restoration actions for the species and its habitat.

Decline of epiphytic lichens across the eastern Spain: biomonitoring and genomic techniques applied to biodiversity conservation

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Keywords: Epiphytic lichens, interaction networks, niche hypervolume, symbiosis, taxonomy

Lichens serve as unique and fast indicators of Global Change owing to their remarkable sensitivity to air pollution, variations in temperature and water availability. In the 1990s, a sampling network for biomonitoring forests was established in northern Castellón and Teruel to assess the effects of air pollution on epiphytic lichen communities. Almost 25 years later, the same localities were visited to re-evaluate the diversity and composition of the lichen community based on ecological indices and molecular sequence data from nine epiphytic macrolichens. The mycobiont and its main symbiont microalgae were identified in order to understand the structure of the lichen communities, and revealed a vast hidden microalgal diversity yet to be described within the genus *Trebouxia*. This methodology facilitated the formal description of a new phycobiont species. Additionally, ecological factors and lichen functional traits were considered to evaluate their influence on fungal-algal interaction patterns and revealed the reproductive strategy of lichens to play the main role in shaping these paradigmatic symbiotic associations. Furthermore, as there is no information regarding how environmental changes affect the performance, or survival of the different components of the lichen thalli (holobiome), metabarcoding was employed to examine alterations in the abundance and structure of algae, fungi, and bacteria communities present in visually damaged and non-damaged lichen thalli.

Dynamics and interaction of three humpback whale (*Megaptera novaeangliae*) populations in Mexico

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Keywords: Mysticetes, Population Dynamics, Distribution, Photo-Identification, Conservation

Three Population Units (PUs) of humpback whales congregate in the Mexican Pacific. The proportion of individuals in each PU in different regions of Mexico, their movements and interactions between them, is unknown. In regions such as Baja California Sur (B.C.S.) and Nayarit-Jalisco (NY/JA) where their distributions overlap, it is difficult to determine from which PU an entangled, stranded, or struck individual belongs to, hindering the protection of higher risk populations. The present study aims to determine the proportions, dynamics, and interactions of whales from each PU throughout the season, elucidate the timing of arrival and departure of each, as well as their movements between different regions of the Mexican Pacific. Sampling was conducted in 2023 and 2024 in Mexico and El Salvador. The tools used were: 1) photo-identification; 2) mtDNA haplotype frequency analysis; and 3) satellite telemetry, through the use of RDW tags. During the 2023 breeding season, 375 photographs of unique flukes and 110 biopsies were obtained. Additionally, that January, 16 satellite tags were deployed in NY/JA. Preliminary analyses would indicate that during November and December, the Central American PU passes through B.C.S. on its migration southward, and during March and April, it passes through B.C.S. again on its northward journey to feeding areas. Later, the whales from the Coastal PU would arrive to B.C.S., and finally those from the Oceanic PU. Lastly, 36 recaptures were recorded between breeding locations; at the beginning of the season heading southward and at the end of the season heading northward.

Using environmental DNA analysis as a monitoring tool for cetacean and other marine vertebrates in the Mediterranean Cetacean Corridor.

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Keywords: environmental DNA, cetaceans, Marine Protected Area, metabarcoding, reference database

The Mediterranean Cetacean Corridor, a marine protected area spanning the Levant and Balearic regions, demand continuous survey of biodiversity. Cetacean species play a crucial ecological role as apex predators in marine ecosystems; thus, their monitoring will contribute to tracking the conservation status of other species in the Spanish Mediterranean. Environmental DNA (eDNA) analysis is a technique in which genetic material from an environmental sample is concentrated, and species composition is identified without the need to isolate specific targeted organisms. We analysed 31 water samples taken in the corridor between 2021 and 2022. Approximately 3L of seawater was collected for each sample, from the surface. DNA was concentrated by filtration and extracted using commercial kits. Using a metabarcoding approach, the 16SrRNA gene was amplified using MarVer3 primers and sequenced on an Illumina platform. From our target taxa, 27 marine vertebrate families were assigned: 20 belonging to Osteichthyes, 4 to Chondrichthyes, 1 Chelonian, and 2 cetacean families: Delphinidae (3 species) and Balaenopteridae (1 species), corresponding to 4 of the 8 cetacean species found in the corridor. Additional ASVs remained taxonomically unassigned, suggesting a lack of reference sequences in the nucleotide database used. However, our data suggest that the amplified target region does not adequately capture the genetic variability among closely related species of the Delphininae. Our results provide a preliminary assessment of the cetacean fauna through the analysis of eDNA off the coast of Valencia and highlight the importance of using robust genetic databases for the taxonomic assignment of DNA sequences. Thesis funded by Generalitat Valenciana through project CETABIOENA (CISEJI/2022/5).

Assessing the spatiotemporal variability of cumulative impacts on cetaceans in the Western Mediterranean

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Keywords: cetaceans; Mediterranean; distribution; modelling; impacts;

Although the Mediterranean Sea is a crucial marine biodiversity hotspot, it faces numerous anthropogenic pressures. Cetacean populations in the region are particularly susceptible to human-induced threats including maritime traffic, acoustic pollution, fisheries by-catch, and habitat degradation. The marine environment, along with its fauna and socioeconomic activities, tends to be highly changeable, which complicates the assessment of species-threat interactions. Therefore, addressing this challenge requires Dynamic Ocean Management (DOM) strategies. To support DOM, it is crucial to understand the spatiotemporal distribution patterns of marine species and maritime activities, as well as their interactions. The presented thesis focuses on the Western Mediterranean, aiming to fill current knowledge gaps by evaluating the cumulative effects of anthropogenic activities on the distribution of cetaceans. A multidisciplinary approach combining recent advances in machine learning, robotics, molecular biology, and operational oceanography, will be employed. Initially, Species Distribution Models (SDMs) will be developed by combining observations from visual surveys, Passive Acoustic Monitoring (PAM), and environmental DNA (eDNA) studies, to assess the habitat preferences of 8 cetacean species. Subsequently, marine traffic maps and underwater noise models will be created based on Automatic Identification System (AIS) data. Lastly, the species distribution models and human pressure maps will be combined to assess possible overlap between cetaceans and their anthropogenic threats. Cumulative impacts of these pressures on each species will be quantified, and conflict zones identified. Ultimately, this research aims to inform spatial planning and management decisions by highlighting areas of conservation priority for each cetacean species in the region.

Phyllodistomum umblae **and** ***Crepidostomum*** **spp. (Digenea) differentiation in the recent radiation of European whitefish**

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Keywords: Speciation, Trematoda, ddRAD-seq, population genetics, phylogenetics

European whitefish, *Coregonus lavaretus* complex, is a widely recognized model system for adaptive radiation research, encompassing numerous closely related species in northern Europe. Despite abundant research on the whitefish complex, our understanding of the diversity of its parasite fauna in recently colonized postglacial lakes remains limited. A recent synthesis within the Stockholm Paradigm proposes taxon pulses and ecological fitting as processes driving current distribution of species. We hypothesize that the whitefish post-glacial expansion and rapid diversification facilitated parasite colonization of postglacial lakes and spatial differentiation. Using ddRAD-seq and de-novo genome assemblies, we investigated the population genetic structure of *Phyllodistomum umblae* and *Crepidostomum* spp. infecting whitefish in perialpine and subarctic lakes. Our analyses revealed that geographic isolation between regions is the main driver of parasite differentiation. Within each region, *P. umblae* populations did not show genetic structure among sympatric whitefish species nor among lakes, whereas *Crepidostomum* spp. differentiated between subarctic lakes. Signals of population expansion in some lakes matched the timing since the post-glacial expansion. Our results support the Stockholm paradigm views with parasite opportunity and ecological fitting for the use of whitefish hosts, rather than a strict phylogenetic tracking of hosts as drivers of these parasites current distribution in postglacial lakes.

Monitoring of marine megafauna and its interaction with anthropogenic pressures in the western Mediterranean

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Keywords: 3D mapping, Bio-logging, Fisheries, Marine traffic, Sea-turtle

Marine ecosystems constitute a dynamic and changing environment in space and time for physical-chemical, biological processes, and of course, human presence and impact. It is possible to monitor these changes thanks to the emergence of new technologies, such as Big Data, computational methods, and new sources of information. Among these sources, electronic ocean monitoring systems and the identification of human pressures stand out. Recent technologies such as Automatic Identification Systems (AIS) and new constellations of microsatellites for terrestrial observation allow us to monitor human pressures such as fisheries or maritime traffic with high precision and temporal resolution. Furthermore, technological advances have also been applied to the monitoring and distribution of marine species. By using GPS-Satellite devices and depth sensors, it is possible to obtain information about the location and depth of marine megafauna species with great precision, allowing the identification of their distribution in both 2D and 3D. The integration of these information sources through statistical and machine-learning models allows the identification of high-risk areas for interaction between human pressures and biological processes, including the verticality and intrinsic dynamism of the ecosystem. With all this, the aim is to improve the understanding of management systems and conservation of marine reserves in the transition from static to dynamic models; models based on the displacement in time and space of protection areas according to the dynamism of the factors involved in marine ecosystems.

Chondrichthyans and actynopterigians remains from upper pennsylvanian of Peru

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Keywords: Chondrichthian, pennsylvanian, assemblage

This work describes the first microremains of fish from the Upper Pennsylvanian locality of Puerto Arturo (Puno), Oriental Andes of the South East of Peru. Amongst the abundant macro invertebrate remains, there stands out a diverse assemblage of microichthyoliths, including teeth, dermal denticles and scales; this represents the first record of the carboniferous vertebrates from Perú and the Central Andes of Latin America. The outcrops from Puerto Arturo belongs to the Copacabana formation (Perú and Bolivia) and are correlated to Tapajos Group (Brazil), typical carbonate shallow water sequences which abundant invertebrate. The conodont assemblage suggests a Upper Pennsylvanian age (Moscovian- Gselian) and the fish assemblages of the Pennsylvanian from Puerto Arturo (Puno) involve important chondrichthians diversity: Symmoriforms, Neoselachians, Euselachians and Ctenacanthiforms and this fauna suggest a shallow water fish of feeding invertebrates, providing important implications for future paleogeographic and paleoecological works.