

IV Iberian Congress of Biological Systematics

Palma de Mallorca (Spain)
15th-17th January 2018

2018

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Dear Friends and Colleagues:

On behalf of the Local Organizing Committee, we are proud to welcome you to the *IV Iberian Congress of Biological Systematics* | CISA2018 in Palma from 15th to 17th January 2018. The meeting is hosted by members of the Departament of Animal and Microbiological Biodiversity of the Institut Mediditerrani d'Estudis Avançats (IMEDEA, CSIC-UIB) and the Department of Biology of the Universitat de les Illes Balears (UIB).

As in the previous highly successful editions in Madrid, Barcelona and Vitoria, the main objective of CISA2018 is presenting leading research in biological systematics to the scientific community and the general public, encouraging the participation of young researchers and promoting inspiring discussions in the field in a friendly atmosphere. We also have organized an attractive social activity program to facilitate scientific and non-scientific conversations and to get a glimpse to the beautiful city of Palma.

We are convinced that you will find in CISA2018 an appealing program with excellent plenary speakers and interesting talks and poster communications on DNA barcoding, taxonomy & systematics, phylogeography, phylogenetics and evolutionary biology sessions.

We particularly thank Direcció General d'Innovació i Recerca de la Comunitat Autònoma de les Illes Balears including European funds from FEDER program for the financial support to carry out CISA 2018 congress.

Joan Pons and the Organizing Committee





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Lumping and splitting at once: genera and species of long bodied sphaerodorids (Sphaerodoridae, Annelida) in the North Eastern Atlantic

Presenter: Maria Capa

Authors: Maria Capa, Joan Pons, Torkild Bakken, Arne Nygren

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Abstract:

Ephesiella, *Ephesiopsis* and *Sphaerodorum* are three closely related and morphologically homogenous genera of cosmopolitan, benthic, marine bristle worms (Sphaerodoridae, Annelida). They share the overall appearance and features unique among sphaerodorids (two longitudinal rows of dorsal microtubercles and macrotubercles with terminal papillae, and an eversible pharynx). Differences between genera rely on the chaetae morphology. Members of *Ephesiella* are characterised by having compound chaetae, *Sphaerodorum* bear only simple chaetae, and *Ephesiopsis* have both compound and simple chaetae in all parapodia. Revision of museum collections (including type material) of several species revealed that intermediate forms (pseudocompound chaetae) are found in some members of the three genera, questioning the legitimacy of this feature to discriminate between the genera. In fact, phylogenetic analyses of mitochondrial and nuclear DNA sequences recovered paraphyletic compound and simple chaetae clades suggesting the need the synonymization of these genera of long-bodied sphaerodorids. Two species of long bodied sphaerodorids are reported from the North East Atlantic (NEA): *Ephesiella abyssorum* and *Sphaerodorum flavum*, both with a wide geographic and bathymetric distribution range. Species delimitation analyses including specimens collected in several localities and depths of the NEA allowed assessing the species boundaries of this group of annelids and revealed the presence of at least eight species in this area.



Molecular studies revealed cryptic speciation in cosmopolitan cossurid species *Cossura pygodactylata* Jones, 1956

Presenter: Anna Zhadan, Tatiana Neretina

Authors: Anna Zhadan, Tatiana Neretina, Nicolas Lavesque

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Abstract:

Cossura pygodactylata Jones, 1956 (Annelida, Cossuridae) is the single cossurid species known to bear intercirral anal processes. It has a wide geographical distribution. It is reported from Arctic to boreal and tropics zones and from Atlantic to East and West Pacific (depth range from 1 to 2700 meters). These facts allow to suggest presence of cryptic species. We studied specimens of *C. pygodactylata* from Arcachon bay (France) and from the Kara and White Seas (Russia) using traditional taxonomic methods and molecular methods (18S rRNA sequences). Specimens were uniform morphologically but 18S rRNA sequences revealed significant differences. The distance between Kara Sea and White Sea specimens were 0.4%, 1% between Arcachon and White Sea specimens, 3% between *C. pygodactylata* and *C. candida* and 4.6% between Cossuridae and Paraonidae used as outgroups. These distances could mean species-level differences between Arcachon and White Sea specimens as 18S rRNA is a quite conservative gene. The species status of Kara sea specimens remains questionable. Future studies are needed to reveal all cryptic species in *Cossura pygodactylata* complex: investigations of other nuclear and mitochondrial genes (16S, COI), comparison of our molecular and morphological data with specimens from the type locality (California) and other regions.



Phylogeographic and morphometric analysis of *Forficula auricularia*, with emphasis in Iberian populations

Presenter: Rubén González Miguéns

Authors: Rubén González Miguéns, Eva Nozal, Paloma Mas-Peinado, Yolanda Jiménez-Ruiz & Mario García-París

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Abstract:

Forficula auricularia Linnaeus, 1758 (Dermaptera) presents a wide geographic distribution in the Palearctic Region with introduced populations in north America and Australasia. Previous studies on reproductive biology and mitochondrial DNA have demonstrated that *F. auricularia* is a complex of two cryptic species that already developed reproductive incompatibility. The distribution of these two species overlap on the only areas of Western Europe, where they have been studied. Each of these two species has colonized North America independently, one was established along the Pacific Coast and the other along the Atlantic Coast. Each species is represented by a particular mitochondrial lineage. The distribution of these two lineages is not known, with only a few European populations studied (in France, Belgium and one in Italy). The objectives of this work are to: 1) perform a phylogeographic study with partial sequences of the mitochondrial gene *cox1* using a large number of European, Asian and African populations, and 2) execute a morphometric analysis of different Iberian populations of each of the cryptic lineages to check if discrimination is possible, by using five quantitative measurements. The results of this study show the existence of five reciprocally monophyletic mitochondrial lineages within the area of the species, three more than previously suspected. The morphometric discriminant analyses allow us to identify morphologically one of the Iberian lineages. In conclusion *F. auricularia* is a complex of at least five species, one of them morphologically diagnosable.



Recognizing *Conus* (Gastropoda: Conidae) with Artificial Intelligence tools

Presenter: Lara Lloret

Authors: Ignacio Heredia, Lara Lloret, Jesús Marco, Rafael Zardoya, Manuel Jiménez

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Abstract:

Deep Learning provides an extremely useful tool for identifying and classifying animal exemplars based on pictures. With this in mind we have launched an application for Android that automatically identifies cone snails at species level based on shell colors and banding patterns. This tool provides an easy plug-and-play framework enabling experts and amateurs to classify, easily and on the fly, images of specimens taken with their own mobile phone. The application categorizes the species according to their scientific names by mean of a Convolutional

Neural Network. The application provides as well a direct link to Wikipedia allowing the user to check the common name together with the main characteristics of the species under study. The application has been trained using researchers images and has proved an excellent performance even when dealing with not very high resolution pictures. In summary, this application represents an extremely useful piece for a citizen science toolbox achieving a very good identification accuracy and providing Android users with a robust and fast system for cone snails identification based on the current state of the art for Computer Vision.



Molecular phylogeny of the land snail genus *Xerocrassa* (Geomitridae) in the Iberian Peninsula

Presenter: Luis J. Chueca

Authors: Luis J. Chueca, Amaia Caro, Alberto Martínez-Ortí, José R. Arrébola & Benjamín J. Gómez-Moliner

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Abstract:

Xerocrassa Monterosato, 1892, is one of the most diverse genera of land snails in southern Europe, with at least 50 recognized species. The genus shows a disjunct distribution within the Mediterranean Basin with two centres of radiation, that is, the eastern complex (Greece and Middle East) and the western complex (Iberian Peninsula and Balearic Islands). In this study, we focused on the endemic *Xerocrassa* species from the Iberian Peninsula where this genus of land snails has undergone extensive genetic diversification, with the presence of several cryptic species. A comprehensive study, including 120 specimens belonging to all nominal species present in the Iberian Peninsula was carried out to assess the actual diversity of this genus within this region.

Combination of morphological and genetic (mitochondrial COI and 16S rRNA and the nuclear gene cluster 5.8S-ITS2-28S rRNA) data reveals the presence of over 25 species in the western complex, without considering the Balearic species. By applying a Bayesian molecular clock, the evolutionary history of the genus was examined and compared with the current biogeographical patterns within the Iberian Peninsula. Our results revealed the occurrence of several hitherto and unrecognized cryptic species, and indicated that taxonomy of several Iberian species should be revised.



Polycladida (Platyhelminthes) from the Macaronesia. Taxonomy and phylogenetic reassessment

Presenter: Daniel Cuadrado

Authors: Daniel Cuadrado, Jorge Rodriguez, Leopoldo Moro, Carolina Noreña

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Abstract:

In the present work the Polycladida species of the archipelagos belonging to Macaronesia complex have been studied for the first time. The Macaronesia is composed by the archipelagos of Azores, Canary Islands, Cape Verde, and Madeira and Savage Islands, and a small region of Moroccan coast. This ecoregion is characterised for sharing the same geological (volcanic origin), climatic and faunistic conditions as well as high degrees of endemism and speciation processes. The material obtained in the different islands and archipelagos has been studied from the morphological and molecular point of view. Both methodologies allow us to characterize and delimit concisely the species with morphological and molecular data. This whole specific information allows us to establish kinship relationships and phylogenetic points between the different species and genera.

A total of 39 species have been identified and located for the Macaronesia's archipelagos. Eleven of them are new records, *Prostheceraeus moseleyi* and *Imogine* sp. for Azores, *Discocelis tigrina* and *Gnesioceros* sp. for Canary Islands, *Anonymus ruber*, *Pericelis cata*, *Pseudoceros velutinus* and *Pseudoceros mororum* for Cape Verde, *Planocera pellucida* for Madeira and finally *Imogine stellae* and *Stylochus neapolitanus* for Morocco. In other hand 4 new species to science have been described, belong to the genera *Pseudoceros*, *Pericelis* and *Eurylepta*.



Exploring species delimitation and mito-phylogenomics in the *Hyaella* (Amphipoda: Crustacea) species-flock in the Titicaca

Presenter: José Antonio Jurado-Rivera

Authors: José Antonio Jurado-Rivera, Joan Pons, Geoff Boxshall, Edmundo Moreno, Damià Jaume, Carlos Juan

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Abstract:

The ancient Lake Titicaca biota, at an altitude of 3089 m s.n.m. in the Central Andes, encompass several species-groups that have experienced a remarkable morphological diversification. One of these assemblages is constituted by the genus *Hyaella* –the only continental water epigean amphipod genus of the American Continent– that in the Titicaca Basin displays at least 18 *Hyaella* species, of which 17 are endemic. However, material collected in past scientific expeditions point out to a higher number of undescribed taxa, suggesting that a lake species radiation and perhaps intra-lacustrine morphological diversification has been taking place. This is reinforced by the high disparity of *Hyaella* morphologies in the Titicaca, with species displaying integuments richly ornamented with spines and flanges, with no clear explanation available for the origin of these forms. Here we present an exploratory phylogenetic survey of Titicaca *Hyaella*, including representatives from the major lake but also from adjacent waterbodies in this huge Basin in the High Andes. We use mitochondrial cytochrome oxidase subunit 1 (cox1) and Histone H3 sequence datasets to explore species diversity using species delimitation methods. Secondly, based on the species delimitation hypothesis obtained, we select key representative taxa of the main species lineages to build a Titicacan *Hyaella* robust phylogeny based on mitogenomic data obtained by NGS methods. The emerging picture from a still uncomplete sampling suggests the presence of at least twenty species and three major relatively ancient monophyletic species groups in the Titicaca Basin, with remarkable disparities between morphological and molecular results. Further work will consist in a detailed study of the phenotypic disparity of the extant species and exploring the causes of the molecular and morphological data discrepancies.



Genus *Lucilia* (Diptera, Calliphoridae) in northern Spain: a molecular and morphogeometrical approach in species with forensic interest

Presenter: Alberto Fuentes-López

Authors: Matteo Carelli, Alberto Fuentes-López, Elena Romera, Teresa Bonacci, José Galián

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Abstract:

The correct identification of species is an essential step in studies of forensic entomology, since incorrect identification can lead to errors in the calculation of Post Mortem Interval (PMI). This task is more complicated when it comes to closely related species, with morphological differences difficult to observe in damaged or poorly conserved specimens. That is the case of the species *Lucilia ampullacea*, *Lucilia caesar* and *Lucila illustris* (Diptera, Calliphoridae). When specimens of these species are not well preserved, it is difficult to differentiate them with morphological techniques, so that other tools are needed.

The objective of this study is the phylogenetic and morpho geometric analysis of these *Lucilia* species collected between 2012 and 2014 in northern Spain. We have amplified and sequenced the mitochondrial fragment cytochrome oxidase I (COI) and the nuclear fragment internal transcribed spacers II (ITS2). They have been analysed phylogenetically by distance methods with Neighbor-Joining and phylogeographically through haplotype networks. We have defined 18 reference points on the fly wings and compared the differences using principal component analysis (PCA) and canonical variable analysis (CVA).

The phylogenetic and phylogeographic analyses have shown a clear difference between *L. ampulacea* and the other two species, but there was no clear distance between *L. caesar* and *L. illustris*. Intra and interspecific distance has shown the lack of genetic differences between these two species. The morpho geometric analysis of the wings corroborated the separation of *L. ampullacea*. The separation of *L. caesar* and *L. illustris* by PCA analysis was not evident. However, the CVA analysis showed two well-differentiated groups with a small gap zone. Therefore, these tools could be the key to differentiate these species of forensic interest.



Molecular Phylogeny of the Land Snail Subfamily Leptaxinae (Gastropoda: Helicoidea: Hygromiidae)

Presenter: Amaia Caro

Authors: Amaia Caro, Marco T. Neiber, María José Madeira, Benjamín J. Gómez-Moliner¹

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Abstract:

The Leptaxinae Boettger, 1909 is enclosed within the highly diverse land snail family Hygromiidae Tryon, 1866. Without a neat diagnostic morphological differences, the subfamily status is currently based solely on molecular information and it includes three disjunctly distributed tribes, Leptaxini, Cryptosaccini and Metafruticicollini. However, the phylogenetic relationships between the tribes are not fully resolved and, besides, the clustering of some of the genus to the tribes is not statistically supported. To solve the relationships within Leptaxinae and their position within Hygromiidae, we reconstructed their phylogeny using two mitochondrial genes and eight nuclear genes. The phylogeny was further calibrated to infer the biogeographic history of the group. We restricted Leptaxinae to Cryptosaccini and Leptaxini. Metafruticicollini, conformed by the genera *Hiltrudia*, *Cyrnotheba* and *Metafruticicola*, was elevated to subfamily level (Metafruticicolinae) sister to the rest of Hygromiidae. The Lusitanian genus *Portugala* was transferred to Leptaxini tribe, previously containing uniquely the Macaronesian genus *Leptaxis*. All the genus grouped in Cryptosaccini are endemic to the Iberian Peninsula. Moreover, a new genus strictly confined to Sierra de la Cabrera must be considered within this tribe. According to our phylogenetic reconstruction, Leptaxinae was originated in the Iberian Peninsula from where the Macaronesian Islands were colonized. Madeira archipelago was colonized first and, then, the Azorean *Leptaxis* arose from a single Madeiran group. Oral presentation - DNA barcoding and metabarcoding



Majorcan mosquitoes and the species concept. What is the problem? and why should we care?

Presenter: Claudia Paredes Esquivel

Authors: Paredes-Esquivel, Claudia; Delgado, Sofía; Viader, Miriam; Miquel, Marga and Miranda Miguel Ángel

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Abstract:

Mosquitoes are responsible for the death of millions of people each year. Not all mosquitoes are capable of transmitting diseases; therefore, their correct identification is a crucial step to establish effective control measures as different species vary in their ecology, behaviour and vector competence. Although there is compelling evidence that morphology is not enough to distinguish many mosquito species; in Spain the identification of these vectors relies almost entirely on morphology. DNA barcoding is a promising tool that has proven to be efficient to identify mosquitoes; furthermore it has been used as a first step in the identification of cryptic species, which are particularly common within the genus *Anopheles*. We have carried out a phylogenetic analysis using the Cytochrome Oxidase I gene region to test the accuracy of the morphological identifications of Majorcan mosquitoes. We have found that different species concepts lead to different conclusions on determining the mosquito fauna in this island. We discuss the importance of including molecular-based techniques to uncover cryptic speciation and phenotypic plasticity in Spanish mosquitoes.



First-feeding assessment of flying squid paralarvae by Laser-Capture-Microdissection and DNA metabarcoding

Presenter: Fernando Ángel Fernández-Álvarez

Authors: Fernando Ángel Fernández-Álvarez, Annie Machordom, Ricardo García-Jiménez, César A. Salinas-Zavala, Roger Villanueva

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Abstract:

Cephalopods are primarily active predators throughout life, with a few exceptions. Flying squids (family Ommastrephidae) represents the most abundant, widely distributed and ecologically important family of cephalopods. While the diets of adult flying squids have been extensively studied, the first-feeding diet of early paralarvae remains a mystery. The morphology of this ontogenetic stage notably differs from other cephalopod paralarvae, suggesting a different feeding strategy. Here, a combination of Laser Capture Microdissection (LCM) and DNA metabarcoding of wild-collected paralarvae gut contents for eukaryotic 18S v9 and prokaryotic 16S rRNA was applied, covering almost every life domain. The gut contents of early paralarvae were mainly composed by fungus, plants, algae and animals of marine and terrestrial origin, as well as eukaryotic and prokaryotic microorganisms commonly found in fecal pellets and particulate organic matter. This assemblage of gut contents is consistent with a diet based on detritus. The detritus-based diet of early ommastrephid paralarvae is an unexpected finding, since posterior ontogenetic stages are voracious predators. A first-feeding diet based on detritus is a unique life strategy among predatory cephalopods and is potentially one of the reasons for the ecological success of the Family Ommastrephidae in the oceanic realm. This ontogenetic shift in the diet allows ommastrephid squids to take advantage of an almost ubiquitous and accessible food resource during their early stages, such that they do not directly compete with conspecifics of later ontogenetic stages for the same prey or with other cephalopod paralarvae. Since detritus is almost ubiquitous, competition for trophic resources between early ommastrephid paralarvae should also be minimal. LCM was successfully applied for the first time to tiny, wild-collected marine organisms, proving its utility in combination with DNA metabarcoding for dietary studies.



A Rapid Biodiversity Inventory of Spanish National Parks: DNA barcoding of spider communities in white-oak forests

Presenter: Marc Domènech Andreu

Authors: Marc Domènech, Luís Carlos Crespo, Alba Enguïdanos, Jagoba Malumbres-Olarte & Miquel Àngel Arnedo

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Abstract:

The current global biodiversity loss calls for the development of rapid approaches to inventory species and obtain information for conservation strategies. The conservation status of arthropods is particularly difficult to assess since these organisms are megadiverse and abundant yet poorly understood taxonomically and ecologically. To overcome these limitations, two solutions have been proposed: Rapid Biodiversity Assessments (RBA) and DNA barcoding. RBA are protocols that generate inventories with the minimum necessary amount of time and resources. DNA barcoding is a technique that uses a standard 650bp fragment of the mitochondrial gen Cytochrome c oxidase (COI) to identify animal species, thus automatizing and improving species identification, particularly of juvenile stages.

Spiders play a key role in terrestrial ecosystems as one of the most abundant, diverse and ubiquitous predators. Our aim here is to reveal the large-scale biogeographic patterns of the spider communities of the Iberian Peninsula and to understand the drivers of their diversification. With this purpose, we have implemented a RBA protocol in six Spanish National Parks, specifically chosen to represent a strong environmental gradient across Iberia.

We identified 377 morphological species, 10 of which are putative new species and 8 are new records for Iberia or Spain. Identification by DNA barcoding largely matched morphological identifications, but also revealed some discrepancies. In this presentation, we will discuss some of the detected incongruences, which mostly corresponded to either unexpected morphological polymorphisms (e.g. *Metopobactrus* dwarf spiders) or to putative cases of hybridisation (e.g. *Theridion* cobweb spiders). We will further discuss ongoing efforts to identify the juveniles collected using metabarcoding techniques and to infer phylogenetic diversity by building and analysing multi-gene super-matrices.

Despite the challenges in data analyses and interpretation, the complementation of morphological identification with barcoding is a powerful approach to unravel community patterns and evolutionary relationships, and ultimately, to provide biodiversity data for conservation management.



Non-invasive identification of endangered tiger beetle species (Coleoptera: Cicindelidae) from soil samples

Presenter: José Herrera-Russert

Authors: José Herrera-Russert, Alejandro López-López, José Serrano, José Galián

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Abstract:

When studying endangered species, alternative methodologies that do not imply the direct manipulation or killing the animal should be preferably used, in order to avoid risking the survival of the wild populations. The advent of new techniques of barcoding has made possible to sequence DNA directly from the environment, avoiding the manipulation of the alive animals. This allows to check the presence of endangered taxa and to identify the different species without collecting specimens.

This work was carried out in Rambla Salada, a locality shared by two *Cephalota* species: *C. litorea* and the endangered endemism *C. deserticoloides*. We used specific protocols to extract DNA from the soil adjacent to the opening of the larval burrows, and from cotton buds that were introduced into the burrow. Two mitochondrial fragments (cox1 and 16S) were sequenced and used to assign each sample to a species using reference sequences previously published.

The extraction and DNA amplification were successful in most of the cases, and these samples could be assigned to species without manipulating or killing the animal. The obtained information allows us to positively identify these species and analyse their ecological and microhabitat preferences. The DNA yield was better from the soil than from the cotton bud. Additionally, a RFLP protocol was designed from the information provided by the DNA sequences, to ease and cheapen the discrimination of these species.



Hidden biodiversity of Arctic invertebrate fauna

Presenter: T.V. Neretina

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Abstract:

Until now the study of biodiversity in the Arctic Ocean using molecular-genetic methods is limited by molecular barcoding, i.e., sequencing of short regions of mitochondrial or (in plants) plastid genome (Hardy et al. 2011, Carr et al 2012, Saarela et al., 2013). Among others WSBS is the very active in this field, we already have annotated more than 1500 sequences of invertebrate species from White Sea to IBOL database.

Nuclear genes are studied much less; it is done just in the context of investigation of phylogenetic relationships in the few individual taxa. Molecular intra-population diversity of nuclear genes in the Arctic populations of invertebrates are still unknown.

Meanwhile, the level of intra-population diversity (described, for example, by virtual heterozygosity π) is an important population genetic parameter, characterizing long-term effective abundance of the population. Marine multicellular species are often characterized by the very large size of populations and correspondingly high level of genetic variability. For example, the record for the value π of multicellular animals belongs to the marine ascidian *Ciona savignyi* ($\pi=0,08$; Small et al. 2007). Despite of it, our preliminary data shows an extremely low level of intra-and inter-population polymorphism of many arctic species.



Barcoding Achantocephala. A neglected phylum of parasitic helminths

Presenter: Sofía Delgado-Serra

Authors: García-Salguero, Alex; Delgado-Serra, Sofía, Juan-Amengual, Mateu; Miranda, Miguel Ángel; Sola-Sánchez, Jessica and Paredes-Esquivel, Claudia

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Abstract:

Acanthocephalans infect the small intestine of vertebrates. These parasites can cause serious damage in their hosts which may lead to death. We conducted a survey of the parasites of the hedgehog *Atelerix algirus* in Majorca and found acanthocephalans in two locations, adult specimens in the small intestine, which morphology corresponded to *Moniliformis moniliformis* and larvae outside the peritoneal cavity which could not be identified using morphological tools. We used the barcoding region of the Cytochrome Oxidase I gene to determine the identify both parasitic forms. The adult specimens were in fact those from genus *Moniliformis saudi* and the larvae was identified as *Plagiorhynchus cylindraceus* a species that infect birds and which had not been reported in *Atelerix algirus* before. These results show the importance of using DNA-barcoding techniques to identify parasites at larvae stages when morphology cannot solve species identity. A correct identification of pathogens results in more effective treatments and have direct implications in animal conservation programs.



Polychromatism in the speckled skate, *Raja polystigma* (Chondrichthyes: Rajidae) along the western Mediterranean

Presenter: Sergio Ramírez-Amaro

Authors: Sergio Ramírez-Amaro, Francesc Ordines, Cori Ramon, Bàrbara Terrasa, and Enric Massutí

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Abstract:

Skates (Order Rajiformes) are the most diverse group of chondrichthyan fishes, being characterized by a highly conserved morphology. In particular, dorsal color patterns are widely used as an important diagnostic feature in the identification of species belonging to the genus *Raja*. However, the intraspecific dorsal color variability (polychromatism) that occurs within this genus may results in misidentifications with the close relative species. Speckled skate (*Raja polystigma*) is an endemic species of the Mediterranean. This small-sized skate (up to 60 cm total length) inhabits soft bottoms on the continental shelf and upper slope between 50 and 400 m depth. This species shows a dorsal coloration very similar to *Raja montagui*, which can confuse their identification. Therefore, a complementary approach based on molecular markers must be applied to overcome these morphological ambiguities. Here, we use DNA mitochondrial barcoding gene (cytochrome c oxidase subunit I, COI) to examine the polychromatism in this species in the western Mediterranean. A total of 18 specimens of *R. polystigma* were collected during the MEDITS bottom trawl surveys carried out between 2013 and 2016 along the Iberian Peninsula and the Balearic Islands. In order to have adequate identification, these specimens were genetically compared to other specimens of *R. polystigma* available in GenBank. Phylogenetic analyses showed that our specimens and GenBank samples were genetically similar and shared haplotypes, corroborating the identification of all samples as *R. polystigma*. Our study specimens showed a remarkable variation in color patterns of the dorsal surface, as has been recorded for other skate species in the Mediterranean. Polychromatism could be related to local adaptation in response to varying environmental condition such as type of benthic habitats.



Unraveling the evolutionary history of the spider genus *Dysdera* (Araneae: Dysderidae) in the archipelago of Madeira based on multiple loci

Presenter: Luís Crespo

Authors: Luís Crespo, Isamberto Silva, Alba Enguídanos, Pedro Cardoso & Miquel Arnedo

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Abstract:

The spider genus *Dysdera* colonized the macaronesian archipelagos, where it underwent extensive diversification. Approximately, 50 endemic species are known from the Canaries, and 11 from Madeiran. While Canarian species have been the subject of taxonomic revisions, Madeiran endemics remain mostly undescribed. Because of the existence of many ecologically and functionally specialized species, this genus may provide insights on the mechanisms of diversification in remote islands. We analysed a multi-locus matrix combining mitochondrial and nuclear loci under several analytical frameworks. Results point to a large clade comprising all Madeiran species but one, found on an islet of Porto Santo Island. Within the group, the species from the oldest island, Porto Santo (14 M.y.), represent a monophyletic group, suggesting that local diversification post-dated colonization of the younger islands in the archipelago. Madeira and Desertas Islands (5 M.y.), on the other hand, share events of back and forth colonization. Morphological analyses corroborate these results and further support the discovery of 8 new species to science.

Ongoing analyses are aimed at understanding the back and forth colonization between Madeira and Desertas, while detailed morphological analyses can shed light into the evolutionary relevance of the population structure observed in some widespread species.

Preliminary data hints at an Iberian ancestry for the Madeiran taxa, over a Canarian or North African ancestry. This would be similar to the patterns observed in other speciose non-flying taxon in the region, and may be related to the common volcanic history that links Madeira with the southwestern most part of the Iberian Peninsula.



Genomic analysis with ddRAD data of a strict contact zone of lineages of the Pyrenean desman in the Iberian Range

Presenter: Lídia Escoda

Authors: Lídia Escoda, Jorge González-Esteban, Asunción Gómez, Jose Castresana

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Abstract:

The Pyrenean desman (*Galemys pyrenaicus*) is a semiaquatic and endangered mammal endemic to the Iberian Peninsula. Previous studies revealed a strong phylogeographic structure, with the presence of four mitochondrial lineages and strict secondary contact zones formed after postglacial recolonization. Phylogeographic breaks based on mitochondrial data may have been generated by particular female dispersal patterns and therefore more studies based on genomic data should be performed to better understand the evolutionary history of the species. Here we studied this species in four rivers of the Iberian Range, where the mitochondrial lineages A and B meet in a narrow contact zone with almost no spatial mixing between them. Using the ddRAD technique, we obtained 912 SNPs from each specimen and analyzed their genomic structure. Both the genomic tree and the PCA analysis revealed the presence of four groups comprising individuals from the same river independently of their mitochondrial clade. We also found admixture between individuals belonging to different mitochondrial lineages in this zone, suggesting differential dispersal patterns in males and females. Relatedness analysis, which can inform about contemporary dispersal, confirmed that desmans frequently disperse within rivers and much less between rivers. These results show that genomic information can be crucial to better understand the dispersal patterns of endangered species and thus help in developing adequate conservation plans.



New insights into the evolution of biodiversity in the Brazilian Atlantic Forest using land planarian data

Presenter: Marta Álvarez-Presas

Authors: Marta Álvarez-Presas, Ricard S. Gascón-de-Gotor, José F. Sánchez-Herrero, Julio Rozas and Marta Riutort

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Abstract:

The Brazilian Atlantic Forest (BAF) is one of the most diverse and endangered biomes in our planet. The knowledge of biodiversity evolution is critical when planning conservation policies. Low dispersal animals, such as land planarians (Platyhelminthes), have been proposed as accurate indicators of the history and conservation state of the region. In a previous study that analysed a broad region of BAF using one land planarian species, some clues about the evolution in the region were found, but the few genetic markers available resulted in a low resolution, pointing to the need for new molecular data. Consequently, here we test the validity of three newly developed nuclear markers obtained from next generation sequencing data (DOM4, DOM5 and DOM6), in combination with the mitochondrial COI gene, for the comparative phylogeographic study of two species, *Cephaloflexa bergi* and *Imbira marcusii*. We have also reduced the study area to a region near the city of São Paulo, to focus on some interesting questions raised in the previous broader study. Our results show the validity of these new markers giving consistency to the results obtained in previous works. The preliminary phylogeographical analyses suggest an ancient origin for the diversity in the forest, and that it may have been shaped by events older than the last glaciations. Our results also point to the existence of putative glacial microrefugia in the areas of lower altitude of the sampling region and to several possible secondary contacts that occur in the central regions of the studied area.



Patterns and processes of diversification in the nocturnal geckos of the *Ptyodactylus hasselquistii* species complex

Presenter: Héctor Tejero Cicuéndez

Authors: Karin Tamar, Héctor Tejero-Cicuéndez and Salvador Carranza

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Abstract:

An accurate comprehension of species diversity is critical for a wide range of biological studies from an evolutionary perspective. The development of molecular-based species delimitation methods has been greatly enhanced with the incorporation of coalescence theory, the conceptual advancements regarding the species concept and the abundance of DNA sequence data. Coalescence-based methodologies provide a rigorous framework for exploring boundaries between phylogenetic lineages and they have been used in a growing amount of studies in the last years, perhaps with a special interest when applied on morphologically conserved and/or allopatric species. That is the case of the *Ptyodactylus hasselquistii* species complex - a group of relatively large nocturnal geckos from northeastern Africa and large parts of Arabia in which recent studies have shown high levels of genetic variability that contrast with a conserved morphology. In this study, we assembled a geographically comprehensive set of samples covering the entire range of this complex, comprising broad molecular and morphological datasets, including six markers and more than 400 specimens measured. We analyze these datasets with coalescence-based methods and multivariate analyses in order to unravel their relationships and degree of phenotypic diversification. Our results suggest that, despite several taxonomic revisions, there is still a high level of undiscovered diversity within *Ptyodactylus*, especially in the mountainous regions of southwestern Arabia. We hypothesize that, unlike other Arabian geckos, the high level of specialization and adaptation to exploit the same rocky environments is a key factor to understand how diversity has been generated and maintained in this group of geckos.



Genetic characterization and demography of an introduced population of *Mauremys leprosa* in Mallorca (Reptilia, Geoemydidae)

Presenter: Enrique Pantoja

Authors: Enrique Pantoja, Samuel Pinya, Marta Bassitta & José A. Jurado-Rivera

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Abstract:

The chelonian species *Mauremys leprosa* is distributed across South-East Europe and North-West Africa, where two different subspecies have been phylogenetically distinguished: *M. leprosa leprosa* and *M. leprosa saharica*. The introduction of this species has been recorded at least in five countries, of which Spain has been the only one where the species has established successfully. An interesting case in this country is the establishment of a reproductive population in Mallorca (Balearic Islands), whose phylogeographical origin and population demography parameters are still unknown. The aim of this study is to shed light on these questions, as such information could be essential for its population management. A total of 23 individuals of *M. leprosa* were caught up using funnel turtle traps. Sex and biometric parameters as well as venous blood samples were collected before releasing the specimens back to their habitat. DNA was extracted from blood tissue and used to sequence a fragment of the mitochondrial cytochrome b gene (cytb). All analyzed samples shared the same cytb sequence. A TCS haplotype network was generated using the obtained sequence together with available *M. leprosa* cytb sequences in GenBank. Our inferences showed that the studied population belongs to a widely-distributed haplotype of the subspecies *M. leprosa leprosa* across the Iberian Peninsula and sporadically in North Africa. Regarding population parameters, the samples showed a homogeneous demographic structure of approximately 40 estimated individuals in well body condition. Future studies will focus on the analysis of additional mitochondrial and nuclear DNA markers to determine more accurately the population structure and the geographical origin of both sex lineages.



Phylogeography and species delimitation of the genus *Phoxinus* Rafinesque, 1820 (Actynopterygii: Cyprinidae) in the Iberian Peninsula

Presenter: Andrea Corral

Authors: Andrea Corral, Irene Cobos and Ignacio Doadrio

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Abstract:

Currently, 21 species from the genus *Phoxinus* Rafinesque, 1820 are considered as valid inhabiting Eurasia and North America (Kottelat & Freyhof, 2007; Bianco, 2015). In Europe, the genus is distributed in almost every stream and river, except in the southern of the Iberian Peninsula, northern Scandinavia, Apennine and Balkan peninsulas (Kottelat, 2007). The taxonomy of this group has been traditional considered confused due to its complex morphology, which is highly influenced by the habitat (Collin & Fumagalli, 2011; Ramler et al., 2016). This phenotypic plasticity, even at intra-population level, has derived in an over-description of numerous species. Most of these species have been posteriorly considered as junior synonyms of other. The application of a variety of tools based on molecular data are gaining importance in the taxonomy of the genus *Phoxinus* helping to detect the presence of cryptic species and phenotypic plasticity. Previous studies assumed that *P. phoxinus* (Linnaeus, 1758) was the unique species of this genus distributed in the Iberian Peninsula (Doadrio & Grazon, 1986). Nevertheless, a recent work found differences between *P. phoxinus* and the species distributed in the Iberian Peninsula, which was renamed as *P. bigerri* Kottelat 2007. This study suggested that it was likely that several species of this genus *Phoxinus* could be coexisting in the Iberian Peninsula (Kottelat, 2007). The aim of this study was to improve the comprehension of the taxonomy of the genus *Phoxinus* in the Iberian Peninsula. For that purpose, the sampling design was intended to cover the maximum distribution of the genus *Phoxinus* within the Iberian Peninsula including 372 individuals of 40 localities. Based on mitochondrial and nuclear marker, Cytb and RAG1 respectively, we analyzed the genetic structure of populations determining its spatial configuration. Our preliminary results have drawn a different scenario in which at least two species of the genus *Phoxinus* are present in the Iberian Peninsula as well as presence of genetic introgression in some localities.



Assessment of the role of *Wolbachia* on mtDNA paraphyly and the evolution of unisexuality in *Calligrapha* (Coleoptera: Chrysomelidae)

Presenter: Jesús Gómez-Zurita

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Abstract:

All unisexual species of *Calligrapha*, originated independently through hybridization, are monophyletic for mtDNA, clustering with some individuals of their bisexual parental species, in turn deeply polyphyletic for mtDNA. This pattern, suggestive of a selective sweep, together with taxonomic incongruence for mtDNA and the evolution of unisexuality, raised the hypothesis that *Wolbachia* might be responsible for these observations. I tested this hypothesis investigating correlates between *cox1* diversity and phylogeography in a sample of +500 specimens of four species of *Calligrapha*, two of them unisexual, against their *Wolbachia* diversity based on standard multilocus sequence typing. *Wolbachia* was highly prevalent (83.4%) and fifteen new MLST strains were characterized, belonging to three main groups. One occupied the whole range of the species, the others were narrowly parapatric, and most beetles (71.6%) bore double infections of the former with one of the others. The main mtDNA lineages of *Calligrapha* were associated to specific types of infection, but these shifted according to expectations based on cytoplasmic incompatibility among types. Data supports that *Wolbachia* is not responsible for selective sweeps and does not manipulate reproduction in *Calligrapha*, but also that unisexuality predates the origin of unisexual species, with some bisexual species consisting of cryptic species differing in their reproductive mode, isolated due to bacterial incompatibility dynamics.



Evolution of the life cycle in subterranean beetles

Presenter: A. Faille

Authors: A. Faille, A. Cieslak, I. Ribera

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Abstract:

Beetles represent more than 30% of the species in the animal kingdom and are sharing with the other holometabolous insects a peculiar life cycle including a larva radically differing from the adult in terms of ecology and morphology and a complete metamorphosis. Presence of larval stages is arguably considered as an evolutionary key innovation fuelling lineages diversification. However, in few cases, alternative strategies emerged; this is the case of some lineages of Coleoptera that colonize the subterranean environment. There are some species where larval life is so strongly abbreviated that the hatched, non-feeding larva pupates immediately without moulting. Such strategy is known in the two groups of beetles that successfully diversified in Subterranean Environment, Leiodidae Leptodirini and Carabidae Trechini, in which it is associated with a reduction in the number of ovarioles. The comprehensive phylogenies available for these two groups in the Pyrenean area (France, Spain) allow to understand the origin of these remarkable convergent strategies.



Genomic data reveal deep genetic structure but no support for current taxonomic designation in a grasshopper species complex

Presenter: Vanina Tonzo

Authors: Vanina Tonzo¹, Anna Papadopoulou², Joaquín Ortego¹

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Abstract:

Recent species radiations provide an attractive model system for studying the processes that ultimately lead to new species formation. Montane grasshoppers of the subgenus *Dreuxius* (genus *Omocestus*) comprise nine species exclusively distributed in the Iberian Peninsula (6 species) and Northwestern Africa (3 species). Most taxa are distributed in allopatry, often isolated on mountain tops. Preliminary mtDNA data indicated a very recent time of divergence among taxa, which makes this complex an excellent study system to investigate the process of speciation. Here we focus on *Omocestus antigai* and *O. navasi*, two sister taxa of the complex that inhabit the Pyrenees, pre-Pyrenees, and Catalan Pre-Coastal Range. These two taxa were originally described based on subtle phenotypic differences and distinct habitat associations (alpine vs. Mediterranean-montane habitats). However, mitochondrial markers have failed to recover reciprocal monophyly of the two-putative species. To test species boundaries and understand the factors that contributed to lineage divergence, we integrated phenotypic information (linear and geometric morphometric analyses) and genomic data (genome-wide SNPs from ddRADSeq) for 95 specimens representing 16 populations of both species across their entire known distribution. Our phylogenomic and Bayesian clustering analyses rejected the hypothesis of two taxa and suggest instead that all sampled populations constitute a single species with a deep hierarchical genetic structure along a west to east gradient. Our analyses point to geographic isolation, not environment, as the main factor determining contemporary patterns of genetic variation within this complex of montane/alpine grasshoppers.



Tempo and mode of diversification in the diurnal geckos of the genus *Pristurus*

Presenter: Marc Simó Riudalbas

Authors: Marc Simó-Riudalbas, Héctor Tejero-Cicuéndez & Salvador Carranza

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Abstract:

The life history and population biology of mainland and insular taxa of a specific radiation are fundamentally distinct. In mainland, communities are often assumed to be complex and composed by many species that share a long history of coevolution. In such scenario, most of the ecological niches will be filled, high levels of inter-specific competition are expected and, in turn, these factors will tend to limit niche expansion and, consequently, morphological diversification. This contrasts with insular groups, which, in many cases, can move across new adaptive landscapes provided by islands (ecological opportunity) and, as a result of that, may experience higher rates of phenotypic diversification and often higher levels of disparity compared to mainland taxa. Yet, empirical evidence suggests that exceptions to the so called “island effect” do exist. In this study, we test this hypothesis using a completely sampled mainland-island system, the diurnal geckos of the genus *Pristurus*, distributed mainly across Arabia, the Horn of Africa, and the Socotra Archipelago. To such purpose, we generated a calibrated molecular phylogeny of *Pristurus* using a multilocus coalescent-based approach, on which we mapped several ecologically relevant phenotypic traits. We then explored whether island and mainland taxa shared the same morphospace and if they differed in their tempo and mode of evolution. Furthermore, in order to see if habitat use was correlated with morphological change, we reconstructed the ancestral habitat across the phylogeny and tested the level of phenotypic disparity and the differences in morphological trait evolution between the different habitats.

Our integrative approach combining both molecular and morphological data provides substantial insight into the evolution of *Pristurus*. Contrary to diversifications without apparent morphological change observed in other geckos inhabiting such extreme environments, the members of the genus *Pristurus* exploit different niches and exhibit a wide variety of morphological and behavioral adaptations to them. The main results revealed a complex scenario in which: 1) continental species present higher levels of phenotypic diversification compared to insular groups, highlighting the importance of taxon-dependent factors at determining patterns of morphological diversification (involving differences in trait evolvability among taxa); and 2) different characters may experience similar evolutionary patterns depending on the microhabitat, providing an insight into the evolution of associated traits within adaptive radiations (ecological specialization) as well as the structuring of ecological communities.



Relation between wing development and diversification in the Macaronesian *Rhopalomesites* beetles (Coleoptera: Curculionidae)

Presenter: Hernández-Teixidor David

Authors: David Hernández-Teixidor, Heriberto López, Víctor García y Pedro Oromí

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Abstract:

The phytophagous weevils of the genus *Rhopalomesites* constitute a lineage endemic to Macaronesia, occurring in the Canary, Madeira and Azores archipelagos. Recently, we have studied the importance of geographical versus ecological barriers in the diversification of this genus, and evidence was found for two *Rhopalomesites* monophyletic lineages. A lineage associated with *Euphorbia* host plants has vicariant species in the Madeira and Canary archipelagos. In this lineage, an ancestral association with *Euphorbia mellifera* in the two island groups was deduced, which has subsequently undergone shifts to related host plants in marginal areas. A second, ecologically generalist lineage exploiting decaying wood from Lauraceae and other forest trees, is also present on such islands along with the Azores and part of Atlantic Europe. These results point to a quasi-parallel colonization of Macaronesia by the two lineages dating to the early Pliocene, followed by allopatric isolation in more recent times according to the presence of suitable habitats on particular islands.

The flight ability of different species is a determining factor for dispersion; could the wing development degree have played a decisive role in the diversification of this genus?

Here we present the preliminary results of a study to establish relationships among the genetic structure of the different species of these two *Rhopalomesites* lineages and the characteristics of their wings. For this, we performed a geometric morphometric analyses with specimens of each species, using landmarks on the wing venation.

The preliminary results shown that both species lineages are separated by the characteristics of their wings, one of them including the species with fully development wings (functional), and the other one the species with different wings reduction grade (not functional).



E Unibus Pluram: Testing adaptive radiation and speciation mechanisms in *Dysdera* spiders from the Canary Islands

Presenter: Miquel Arnedo

Authors: Miquel Arnedo, Nuria Macías-Hernández, Alba Enguídanos

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Abstract:

Islands are well-reputed for providing text book examples of adaptive radiation processes, some of which contributed to the development of the Darwinian thinking. Contrary to conventional wisdom, the adaptive radiation process, i.e. the rapid proliferation of eco-phenotypic divergence, may not require the involvement of natural selection during speciation, and hence the mechanisms of speciation and the drivers of diversification may be uncoupled.

The ground-dweller *Dysdera* spiders are a model system for the study of speciation and adaptation, as they exhibit high rates of speciation, along with ecological and morphological diversification. Here, we will focus on the species radiation undergone by the genus in the Canary Islands to get insights on the adaptive nature of the radiation process and the relationship between speciation mechanisms and diversification drivers.

We will discuss the emerging patterns gathered from ongoing research on the Canarian endemics and how they reconcile with our working hypothesis. Our available data points towards the involvement of non-adaptive processes in the formation of new species, and suggest that ecological diversification is largely the result of post-speciation, interspecific competitive processes.



More than a Happy Face: Did interspecific competition drive diversification of *Theridion* spiders in the Hawaiian Islands?

Presenter: Adrià Bellvert

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Abstract:

The endemic *Theridion* spiders of the Hawaiian archipelago, among which the iconic Happy face spider (*Theridion grallator* Simon 1900), were first described by the French arachnologist Eugene Simon at the turn of the 20th century. For over 100 years, no further taxonomic study has been conducted on the group. Following examination of the larger specimen collection of Hawaiian *Theridion* specimens put together to date, we have been able to discover seven new species, provide new diagnosis for the former species and illustrate for the first time some of the males and females never described before. Most species are easily diagnosed based on the male and female genitalia, but we also reveal the existence of additional somatic characters that differ among the species, including cheliceral teeth, leg length and body size. Phylogenetic analyses of mitochondrial and nuclear markers revealed low levels of genetic divergence among endemics but supported the delimitation of all morphological diagnosable species. Time divergence analysis further supported the recent origin of the species, which traces back to the emergence of the present day oldest large island, Kauai. Finally, we constructed a complete distribution map of the different species based on 50 years of field collections. Many species overlap distribution ranges and some co-occur in the same localities. The somatic differences detected among coexisting species point towards the existence of ecological segregation among them and suggest the group may be a case of adaptive radiation.



Understanding the genomic basis of evolutionary innovation across the Metazoa Tree of Life: an all-phyla approach

Presenter: Rosa Fernández

Authors: Rosa Fernández & Toni Gabaldón

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Abstract:

Animals (Metazoa) are fascinating creatures that represent one of the main groups of eukaryotes and that have dwelled on Earth over 600 million years. Modern animals can be grouped by the arrangement of their body plans (based on similarities in development, form and function) into 35 phyla, each one exhibiting different morphology, anatomy and physiology. While some phyla are charismatic and well-known (such as arthropods, tardigrades or craniates, including vertebrates), many of them have been traditionally neglected and are rarely included in comparative studies, partly due to the difficulties in their finding and identification. As a result, we lack sufficient understanding of the genetic bases of the evolution of body plans across all phyla. To fill this gap and shed new light on the evolutionary innovations across the Animal Tree of Life, we undertook a comparative genomics approach. We compared more than 200 transcriptomes including representatives of all animal phyla. Moreover, we interrogated 14 genomes representing all major animal lineages through the lens of comparative genomics, namely Ctenophora, Porifera, Placozoa, Cnidaria, Deuterostomia, Lophotrochozoa, Ecdysozoa, Xenacoelomorpha and Chaetognatha (the later two represented by transcriptomes in this analysis). Our results, based on more than 3.7 million transcripts and 260,000 gene trees, showed that lineage-specific gene expansions (in synergy with transposable elements in some cases) have been putatively a key generator in shaping the evolutionary novelties specific to each lineage, such as the neural system in Ctenophora or the ecdysis machinery in Ecdysozoa. In this talk, we will discuss our results from a systematic and evolutionary perspective.



Mitochondrial genomes and biogeographic patterns in anchialine cave shrimps

Presenter: José A. Jurado-Rivera

Authors: José A. Jurado-Rivera, Joan Pons, Fernando Álvarez, Alejandro Botello, William F. Humphreys, Timothy J. Page, Thomas M. Iliffe, Endre Willassen, Kenneth Meland, Carlos Juan, Damià Jaume

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Abstract:

Atyidae cave shrimps from three genera (*Typhlatya*, *Stygiocaris* and *Typhlopatsa*) show a highly disconnected distribution (Eastern Pacific, Caribbean, Atlantic, Mediterranean, Madagascar, Australia). The combination of a wide distribution and a limited dispersal potential suggests a large-scale process has generated this geographic pattern. Vicariance through tectonic plates fragmenting ancestral ranges has been assumed to cause this process. Thus, the ancestors of these cave shrimps are believed to have inhabited the ancient Tethys Sea, with three particular geological events hypothesised to have led to their isolation and divergence; (1) the opening of the Atlantic Ocean, (2) the breakup of Gondwana, and (3) the closure of the Tethys Seaway. We have tested the relative contribution of vicariance and dispersal in the evolutionary history of this group using mitochondrial genomes to reconstruct phylogenetic and biogeographic scenarios with fossil-based calibrations. Given that the Australia/Madagascar shrimp divergence postdates the Gondwanan breakup, our results suggest both vicariance (the Atlantic opening) and dispersal, although the Tethys closure appears not to have been influential.



Mitochondrial metagenomics and the phylogeny of Ochthebiini: A new batch mitogenomes example

Presenter: Adrián Villastrigo

Authors: Adrián Villastrigo, Carmelo Andújar, Paula Arribas and Ignacio Ribera

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Abstract:

Phylogenetic trees are not always recovered with enough support to test particular hypothesis. An increase in the number of gene fragments usually improves support, but traditional PRCs and Sanger sequencing is time consuming, the selection of markers is always problematic, and the costs increase linearly with the number of sequences. An easy, fast, cheap and trustworthy way to increase the amount of sequence, recognised by researchers who started using mitochondrial metagenomics (MMG), is the recovery of batch mitogenomes from a single Next-Generation Sequencing run. We present here a pipeline to perform MMG from a pool of DNA extractions using the Illumina MiSeq Sequencing platform. We recovered ca. 40 multiple complete or partial mitogenomes from a single Illumina run, and combined them with a dataset of Sanger sequences of two mitochondrial and two nuclear markers for 245 species to try to improve the support of a phylogeny of the water beetle tribe Ochthebiini (Coleoptera: Hydraenidae).



From species to lineages

Presenter: Morten Stokkan

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Abstract:

The stygobiontic amphipods from the genus (*Pseudoniphargus* Chevereux – Pseudoniphargidae) have a great potential for convergent morphology and thus cryptic speciation driven by the subterranean habitat where it is found. Investigating these using molecular delimitation methods together with thorough morphological analysis revealed a potential 18 new species and morphotypes. A broad sampling covering the entire distribution of the genus laid the groundwork to further investigate the lineages within the entire genus. By amplifying a total of 33 mitochondrial genomes across the entire distribution of the genus a fully resolved phylogeny of the genus was recovered. Finally by placing this phylogeny in a special temporal framework using different calibration points an unprecedented level of dispersal for subterranean amphipods was revealed.



West Africa cone snails (Gastropoda: Conidae) diversity and evolution inferred through mitogenomics

Presenter: Samuel Abalde

Authors: Samuel Abalde, Manuel J. Tenorio, Carlos M.L. Afonso, Juan E. Uribe, Rafael Zardoya

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Abstract:

Cone snails (Gastropoda: Conidae) are a key ecological component of the intertidal and subtidal ecosystems in all tropical and subtropical seas around the world. With an astonishing diversity of more than 800 accepted species, cones form one of the largest groups of marine animals. Despite most of this diversity is located in the IndoPacific region, there is a peak of diversity in West Africa, mainly concentrated in Angola, Senegal and the Cabo Verde archipelago (accounting for 10% of the world diversity). Thus far, the description of these species has relied on shell characters such as shape, color and banding patterns, which are prone to homoplasy. Here, we sequenced the complete or nearly complete mitochondrial (mt) genomes of more than 100 species covering most of cone snail diversity of Senegal and Cabo Verde. We use the reconstructed molecular phylogeny to infer the evolutionary history of the group and to test current species delimitation. Our results supported the double origin of cones endemic to Cabo Verde, which can be ascribed to two different genera, *Africonus* and *Kalloconus*, of Mediterranean and African origins, respectively. Cone snails endemic to Senegal (including *Lautoconus guanche* from the Canary Islands) need to be ascribed to a new genus, as *Lautoconus* was found to be paraphyletic. Within *Africonus*, up to four main lineages were identified. *Africonus* species have larvae without pelagic stage, and thus limited dispersal capacity. Diversification in the archipelago followed allopatric speciation triggered by climate oscillations and eustatic sea level changes during the Miocene and Pliocene. Based on the reconstructed phylogeny and sequence divergence comparisons, we propose to reduce the number of species in the Cabo Verde archipelago to half, highlighting the unreliability for species delimitation of shell characters, which led in many instances to misidentification or overestimation of species.



Phylogenetic analyses of *Pimelia* suggest multiple colonizations and ancient lineage diversification in the Iberian Peninsula

Presenter: Paloma Mas Peinado

Authors: Paloma Mas-Peinado, David Buckley, José Luis Ruiz & Mario García-París

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Abstract:

The genus *Pimelia* Fabricius, 1775 consists of approximately 320 species distributed mainly in xeric environments of the western Palaearctic region and northern deserts of the Afrotropical region. It is represented by a very heterogeneous group of tenebrionid in spite of its conserved morphology. We carried out a phylogenetic and biogeographic study based on two mitochondrial (cox1 and 16S) and five nuclear markers (ITS1, ITS2, 18S, Wg and H3) to provide a comprehensive phylogenetic hypothesis for species within *Pimelia*, re-evaluate the taxonomic status of subgenera within the genus, establish a temporal framework and a historical scenario for the evolution and diversification of *Pimelia*. Based on our results, we propose a new taxonomic structure for the genus *Pimelia* including fourteen subgenera. Some of the morphological characters used in previous taxonomic studies are homoplastic. Our divergence time estimates indicate an Early Oligocene (Rupelian) origin for the genus *Pimelia*, while the reconstruction of ancestral areas indicate Northern Africa as the most likely area of origin. Representatives of five subgenera inhabit the Iberian Peninsula as a result of multiple lineages crossways and diversifications events. Multiple species of ancient subgenera cohabit together as the result of recurrent processes of vicariance (across the Iberian, Betic-Rif and Kabylia regions and the Alboran Basin), and dispersal (fostered by the Iberian-African connections) through time.



A glimpse on the evolutionary history of the cave-dwelling spiders in the Dinaric karst

Presenter: Martina Pavlek

Authors: Martina Pavlek^{1, 2}, Silvia Adrian¹, Fulvio Gasparo³, Miquel A. Arnedo¹;
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Abstract:

In Dinaric caves, dysderid spiders are among the most conspicuous animals. Their relatively large size, orange colour and active foraging lifestyle makes them hard to miss in the seemingly empty cave environment. In the subfamily Rhodine, 13 species from 5 genera are currently recognized in the Dinarides: genus *Rhode* with mostly epigean representatives in the central and western Mediterranean basin but with 4 cave adapted species in the study area, and 8 species from Dinaric endemic and strictly cave-dwelling genera *Stalita*, *Parastalita*, *Mesostalita* and *Stalitella*. The debate remains on the placing each of these 8 related species in its own genus or combine them all under *Stalita*. Rhodinae are distributed mostly through the northern Dinarides, with a few remarkable exceptions reaching far south areas. All but one species have restricted distribution ranges as expected under the assumption of habitat fragmentation and isolation of the different karst areas. As top predators, these species play a key role in the fragile cave ecosystems. Here we present the preliminary results of the first mutli-locus phylogenetic analysis of the subfamily Rhodinae. A sound phylogenetic hypothesis will represent a major step forward to our current understanding on the origins and evolution of these beautiful creatures and of the whole Dinaric karst system - the World's hot spot for cave biodiversity.



Molecular Phylogeny of the species *Achondrostoma arcasii* (Steindachner, 1866): evidence from mitochondrial and nuclear markers

Presenter: Silvia Perea

Authors: Silvia Perea, Lourdes Alcaraz, Joana Robalo, Carla Sousa-Santos, Ignacio Doadrio

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Abstract:

The genus *Achondrostoma* Robalo, Almada, Levy and Doadrio, 2006 is an endemic cyprinid freshwater fish from the north and central Iberian Peninsula, inhabiting rivers in both Atlantic and Mediterranean slopes. The genus comprises five species and is characterized by the absence of the horny layer that is present in other *Chondrostoma* s.l. species. Within the genus, the species *Achondrostoma arcasii* has the wider distribution range in the Iberian Peninsula. Previous genetic studies based on the mitochondrial gene cytochrome b have demonstrated a high genetic structure within the species, with genetic distances among groups ranging from 2.5 and 7.3%. Nevertheless, the absence of a molecular analysis of this species based on nuclear markers as well as morphology hinders the systematics of the group. In this study, we evaluate the monophyly of these different mitochondrial groups providing a phylogenetic hypothesis of *Achondrostoma arcasii* based on mitochondrial and nuclear markers. Our results confirm the existence of very different mitochondrial groups, though nuclear relationships differ from mitochondrial topology. We also propose a molecular clock hypothesis in order to test the species diversification according to the main biogeographic episodes occurred in the Iberian Peninsula since the Cenozoic period.



Investigating the evolution of regeneration and reproduction in Syllidae (Annelida)

Presenter: Rannyele P. Ribeiro

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Abstract:

Syllidae is one of the largest groups within Annelida in terms of biodiversity, with a wide variety of reproductive modes and different regenerative processes. Syllids have striking abilities to regenerate anterior and posterior body, including as a normal developmental program of both sexual (schizogamy) and asexual (fission) reproduction. Sexual reproduction occurs by two types namely schizogamy and epigamy. Although regeneration is not a natural stage of the epigamic reproductive mode, epigamous species are also able to regenerate. Another feature that involves regenerative response in syllids is autotomy, a loss of parts of the body as self-defence mechanism. All those features endorse the presence of regeneration in these animals. In this study, we aim to assess the phylogenetic distribution of the whole-body regeneration, taking into account anterior and posterior regeneration abilities and reproductive modes across Syllidae. We used phylogenetic methods to trace the evolution of regeneration, using mitochondrial and nuclear markers (16S, COI) and nuclear marker (18S). Additionally, we reviewed the available data on regeneration in syllids, covering descriptions of regenerative mechanisms in different species, as well as regeneration in relation with reproductive modes. Our results suggest that posterior regeneration is widely distributed in syllids, whereas anterior regeneration is limited in most of the species, excepting those reproducing by fission. Anterior regeneration is extensive in syllids reproducing by fission and disappeared at least twice in two different clades of epigamous species. This reproductive mode is well known for Autolytinae and a few species of Eusyllinae and Syllinae that, interestingly, show a pattern of fission areas along the body. Our survey reveals that aberrant forms such as bifurcated animals and bodies with multiple heads have been observed in several species. Some of these aberrations indicate a change in the antero-posterior polarity of segments, which can also be observed in the branching body pattern of some species of syllids.



Species delimitation in *Amblyosyllis* (Annelida, Syllidae)

Presenter: M.T. Aguado

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Abstract:

Amblyosyllis is a genus of benthic marine worms (Annelida, Syllidae). They are remarkable creatures, well known among the marine worm specialists mostly because of their notable beauty. They usually exhibit bright colourful patterns and have outstanding long and coiled appendixes. *Amblyosyllis* is a homogeneous group; however the species boundaries are, in most cases, not well defined. Nominal species have been described based in unique combinations of the few features that show variation among members of this group without considering, in most cases, intraspecific variation. Intermediate forms reported in literature are, either assigned to new species, or contrary, have been assumed part of the range of variation within particular species causing lumping and synonymisation of species names. This later solution results in some of the nominal species showing broad geographic distribution. Herein, we aim to assess the species boundaries of members of *Amblyosyllis* with molecular data (nuclear and mitochondrial DNA sequences). Members of *Amblyosyllis* collected from a broad range of geographic areas were considered in the analyses. Species boundaries are determined using a broad range of analytical methods. Results corroborate the validity of several morphospecies, suggest new ones, as well as intraspecific diversity.



Molecular clocks on Chelicerata suggest an early colonization of land by arachnids and support the monophyly of mites

Presenter: Jesus Lozano-Fernandez

Authors: Jesus Lozano-Fernandez; Alastair R. Tanner; Jakob Vinther, Gregory D. Edgecombe & Davide Pisani

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Abstract:

Animal life has marine origins, with only few phyla completing their entire life cycle outside water. The process through which organisms adapt to life on land is known as terrestrialisation, and it is one of the most extreme cases of adaptation to a new habitat that happened in animal history. The chelicerates (pycnogonids, horseshoe crabs, spiders, scorpions) are an ancient group of arthropods, with an astonishing fossil record dating back to Cambrian, and includes the second largest clade of fully terrestrial organisms, the arachnids. Morphological phylogenies support a single land colonization event by placing marine horseshoe crabs as sister group of arachnids, but phylogenomic studies nest this aquatic lineage within Arachnida (implying multiple terrestrialisation events). To identify how many times and when arachnids adapted to life on land we need to assess chelicerate phylogeny, and its evolutionary timescale.

Here, we present a timescale for Chelicerata designed to test how many times and when arachnids adapted to life on land. We used an expanded multigene dataset covering most chelicerate diversity and the largest set of fossil calibrations to date. Our results recover monophyly of Chelicerata, Euchelicerata and Arachnida, suggesting a single terrestrialization event. Furthermore, we found Acari as monophyletic (Parasitiformes+Acariformes) and recover Tetrapulmonata (Araneae+Pedipalpi) in alliance to Scorpiones (Arachnopulmonata) or allied to a clade composed by Scorpiones+Pseudoscorpiones. Our results reconcile previous results based on morphology and molecular evidence, and suggest a Cambrian-Ordovician colonization of land by arachnids, substantially predating trace or body fossil evidence.



Phylogenetic relationships of Platyhelminthes based on the currently available complete mt genomes

Presenter: M.T. Aguado

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Abstract:

The complete mitochondrial genomes of all the available Platyhelminthes have been analysed. The mt genomes contain 36-37 genes including 12 of the 13 protein-coding genes characteristic for metazoan mitochondrial genomes, two ribosomal RNA genes, and 22 transfer RNA genes. We explored the phylogenetic relationships of this group through maximum likelihood and bayesian inference analyses. Catenulida is the sister group of the rest of platyhelminthes, and Polycladida, Tricladida and Neodermata are monophyletic and strongly supported. Within Neodermata, Monogenea is, in all the performed analyses, paraphyletic. The gene order in the different groups has been compared and possible evolutionary scenarios are proposed. In comparison with the parasitic Neodermata, our analysis reveals a great diversity of gene orders within free living Platyhelminthes. Our results agree, in general, with previous phylogenetic hypotheses about the Platyhelminthes based on different molecular data (nuclear markers and transcriptomes). The usefulness of mitochondrial sequences for deep phylogenies is herein confirmed. In contrast to the well investigated Neodermata, the available mitochondrial data for the free living taxa is considerably scarce. These kind of data are still missing for interesting groups such as Rhabdocoela, Proseriata, and Lecithoepitheliata, whose inclusion in future studies will undoubtedly help us to understand the evolution of these interesting animals.



Size shift without genetic divergence in the Eurasian water shrew *Neomys fodiens*

Presenter: Alfonso Balmori-de la Puente

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Abstract:

Neomys fodiens is a species of water shrew with a Eurasian distribution for which different subspecies have been proposed. One of them, *N. f. niethammeri*, which is distributed across the north-central part of the Iberian Peninsula (from the Cantabrian Mountains to Navarre), is much bigger than the nominal subspecies and has even been suggested to represent a valid species in general references of mammalian taxonomy. In this work, we used skull samples from both subspecies present in the Iberian Peninsula (*N. f. fodiens* and *N. f. niethammeri*) in order to perform multilocus genetic analysis and clarify their taxonomic status. For this purpose, we developed six novel intron markers of short length and high variability within the genus. Results from haplotype genealogies, concatenated nuclear phylogenies and mitochondrial trees do not support *N. f. niethammeri* to be genetically differentiated from *N. f. fodiens*. In addition, coalescent-based multilocus analysis shows that *N. f. fodiens* and *N. f. niethammeri* are not independent evolutionary lineages. Thus, we conclude that *N. fodiens* experienced in the north-central part of the Iberian Peninsula an increase in size that was not accompanied by an observed genetic differentiation. The increase in size could have been a response to novel ecological conditions found by *N. fodiens* during the postglacial colonization of this area while the lack of genetic differentiation between the two morphotypes could be due to recent diversification (in which subtle genetic differences would not be reflected by the genetic markers used), high gene flow between them or a combination of both.





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