



Societat Catalana
de **BIOLOGIA**

XV Jornada de Biologia Evolutiva

Organitzada per la Secció de Biologia Evolutiva de la SCB

INSTITUT D'ESTUDIS CATALANS

Carrer del Carme 47

Barcelona

23 de juny de 2015

XV Jornada de Biologia Evolutiva

PROGRAMA

Organitzadors:

Fyodor Kondrashov (CRG)

Josefa González (IBE)

Secretaria de la SCB:

scb@iec.cat

- 9 -9:20 Registration
- 9:20- 9:30 Welcome
- 9:30- 10:20 Invited speaker talk. Title TBD. **Erich Bornberg**
- 10:20-10:35 Evolutionary genomics and transcriptomics of the adaptive radiation of *Dysdera* (Araneae) in the Canary Islands. **Joel Vizueta**
- 10:35-10:50 Uncovering the phylogeography of the habitat-specialist land snail *Xerocrassa montserratensis*. **Cristina Català**. Universitat de Barcelona.
- 10:50-11:05 Contrasting genome diversity in two closely related postharvest pathogens: *Penicillium digitatum* and *Penicillium expansum*. **Irene Julca**. CRG-UPF.
- 11:05-11:30 Coffee break
- 11:30-11:45 The Role of *FBti0019985* Transposable Element in *Drosophila melanogaster* Adaptation: molecular mechanism and functional consequences. **Miriam Merenciano**. Institut de Biologia Evolutiva (CSIC-UPF).
- 11:45-12:00 5S rDNA high dynamism in plants: transposable elements and evolution. **Sònia Garcia**. Universitat de Barcelona.
- 12:00-12:15 Mapping selection onto embryo development in *Drosophila*. **Marta Coronado**. Universitat Autònoma de Barcelona.
- 12:15-12:30 Caracterització del locus *Hsp70* a nivell de seqüència i organització genòmica a *Drosophila subobscura*. **Marta Puig**. Universitat Autònoma de Barcelona.
- 12:30-13:20 Invited speaker talk. Evolutionary Genomics of Adaptation to the Environment. **Angela Hancock**
- 13:20-14:45 Lunch break
- 14:45-15:00 The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. **Begoña Dobon**. Institut de Biologia Evolutiva (CSIC-UPF)

- 15:00-15:15 The genomic analysis of the Andaman islanders gives a new insight on the spread of modern humans in Asia. **Mayukh Mondal**. Institut de Biologia Evolutiva (CSIC-UPF).
- 15:15-15:30 Chimpanzee origins and geospatial genetic diversity. **Marc de Manuel**. Institut de Biologia Evolutiva (CSIC-UPF).
- 15:30-15:45 What can we learn from comparative genomics? New insights into reproductive isolation genes in the house mouse. **Laia Capilla**. Universitat Autònoma de Barcelona.
- 15:45-16:10 Break
- 16:10-16:35 Metabarcoding analysis reveals new metazoan diversity and ecological roles in European coastal samples. **David López-Escardó**. Institut de Biologia Evolutiva (CSIC-UPF).
- 16:35-16:50 Uncovering ecological diversification processes in islands: the case study of endemic reptiles in Socotra. **Xavier Santos**. CIBIO/InBIO Universidade de Porto.
- 16:50-17:05 Especiació i hibridació en el gènere *Rhaponticum* Vaill. (Asteraceae) als Alps. **Gemma Mas de Xaxars**.
- 17:05-17:20 Flux gènic asimètric entre poblacions del cranc marí *Liocarcinus depurator*. **Victor Ojeda**. Universitat de Barcelona.
- 17:20- 17:45 Break/Prevosti Prize Committee Meeting
- 17:45 Announcement of the Prevosti Prize winner. End of the meeting

Note to participants:

Please make your slides and talk in English so that both invited speakers and the co-organizer can understand your talk and ask questions. Thanks.

VIII Premi Antoni Prevosti de Biologia Evolutiva, any 2015

Amb l'objectiu de fomentar la participació i la discussió de la recerca dels joves investigadors, pre i postdoctoral, en tots els camps de la Biologia Evolutiva, l'any 2007 fou instaurat per primera vegada el premi Antoni Prevosti de Biologia Evolutiva per premiar la millor comunicació presentada per un jove investigador a la jornada.

El premi consisteix aquest any en 250 € que es lliuraran al finalitzar la darrera sessió de la Jornada. El receptor del premi haurà de ser present a la sala per rebre'l. Si no és així, el premi passarà a la comunicació que hagi quedat en segon lloc, si n'hi hagués, o podria ser declarat desert.

La comissió que decidirà el premi de l'edició de l'any 2015 estarà formada per.

President: Antonio Barbadilla (UAB)
Secretaria: Marta Pascual (UB)
Vocal 1: Elena Bosch (IBE-UPF)
Vocal 2: Aurora Ruiz-Herrera (UAB)
Vocal 3: Manuel Irimia (CRG)

Les regles per atorgar el premi són:

- Cada membre de la comissió s'abstindrà de votar a les persones del seu grup.
- El receptor del premi haurà de ser present a la sala per a rebre'l. Si no és així, el premi passarà a la ponència que hagi quedat en segon lloc.

Modular domain rearrangements epitomise the principles of protein evolution, drive adaptation and developmental novelties and pave the way for next-generation protein analysis algorithms

Erich Bornberg

Over two decades ago it was established that proteins evolve, to a large extent, by modular rearrangements of domains, their evolutionary, functional and structural building blocks. Very little, however, has this knowledge been used for analysing genome evolution and adaptive processes beyond the classical methods of sequence based substitutions.

Based on analyses of several phylogenetic groups, such as insects, fungi, vertebrates, floral plants and diatoms, we showed that the major mechanisms which drive the creation of new domain arrangements are gene duplications, fusions and terminal losses of domains. Period we determine rates of these processes and demonstrate that domain loss is amazingly frequent but follows a fairly stochastic process while the emergence of new domains is very rare but associated to strong adaptive processes such as environmental adaptation and development.

We show how this knowledge can be used for fast and memory efficient algorithms for homology detection (even when complicated rearrangements such as circular permutations are involved), orthology clustering, genome rearrangements and phylogeny reconstruction.

Related publications:

Bitard-Feildel T et al., BMC Bioinformatics 16:154, 2015.
Kemena C et al., BMC Bioinformatics 16:19, 2015.
Terrapon N et al., Bioinformatics 30:274, 2014.
Terrapon N et al., Nature Communications 5:3636, 2014.
Kersting A et al., New Phytologist, doi: 10.1111/nph.13211, 2014.
Kersting A et al., Genome Biol. Evol., 4:316, 2012.
Bornberg-Bauer E and MM Alba, Curr Opin Struct Biol 23: 459, 2013.
Moore AD et al., Bioinformatics, 30:282, 2014.
Moore AD et al. Biochim Biophys Acta - Proteins 1834:898, 2013.
Moore AD and E Bornberg-Bauer; Mol Biol Evol, 29:787, 2012.
Moore AD et al., Trends Biochem. Sci., 33:444; 2008.
Werren J et al.; Science, 327:343; 2010.
Weiner J 3rd et al., FEBS J, 273:2037; 2006.
Weiner J 3rd et al., Mol Biol Evol., 23:734, 2006.

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Evolutionary genomics and transcriptomics of the adaptive radiation of *Dysdera* (Araneae) in the Canary Islands

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Oceanic island biotas have been long recognized as simplified natural experiments of evolution, providing tractable case studies for assessing the genomic mechanisms underlying the generation of biodiversity. Using the terrestrial radiation of *Dysdera* (Araneae) in the Canary Islands as a model system, we investigate the genomic features associated with global pattern of diversification, as well as with specific ecological (dietary specialization) shift processes undergone by the genus.

We use comparative genomics and transcriptomics to identify the genomic determinants of the above mentioned processes, including nucleotide changes in coding and non-coding sequences or differences in gene copy number and gene expression patterns. For the study, we compare tissue-specific transcriptomes (RNA-seq) from endemic *Dysdera* species, distributed in two pairs of generalist/specialist (regarding the type of diet) closely related lineages, and one generalist outgroup species (*D. silvatica*), with information of two newly sequenced complete genomes as references. All sequences were obtained using next generation sequencing technologies (either illumina paired-end or paired-end/mate-pair libraries).

Furthermore, the particular design of our study (i.e. organ specific transcriptomes) will shed light about the specific members of gene families involved in spider smell and taste, which will provide key data to understand the origin and evolution of the chemosensory system in chelicerates and hence in arthropods.

Uncovering the phylogeography of the habitat-specialist land snail *Xerocrassa montserratensis*

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4 Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto

Species with high habitat specialization and potential low dispersal abilities are expected to have high genetic structure. *Xerocrassa montserratensis* is an endangered land snail endemic of Catalonia (Spain). Its distribution is highly fragmented and restricted to xerophilous stony slopes of conglomerate ground with little vegetation. In this study, a total of 152 individuals from eight populations, covering the whole range of the species, were sampled. We sequenced the mitochondrial gene Cytochrome Oxidase I (COI) to uncover the genetic relationship among *X. montserratensis* populations. The haplotype tree identified four genetic groups partially coincident with its geographical distribution. The central group contains shared haplotypes among different populations and seems to be the ancestral one, whereas the remaining three groups are each one restricted to a single locality (Els Munts, Montcau and Sant Jeroni). Els Munts is the most geographically and genetically isolated locality and its genetic differentiation may correspond to a long range expansion and posterior isolation. However, the geographic distance not always explains the genetic differentiation: Montcau is not geographically isolated from the central group although it is highly genetically differentiated probably due to a historical fragmentation and posterior secondary contact; and Marina, despite being separated from the central localities, shares haplotypes with them, suggesting passive large dispersal through the streams. Our study uncovers a complex phylogeographic scenario that can be explained by geomorphological dynamics and unexpected dispersal ability. These results can be useful for the application of conservation programs of endangered species as *X. montserratensis*.

Contrasting genome diversity in two closely related postharvest pathogens: *Penicillium digitatum* and *Penicillium expansum*

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Penicillium digitatum and *Penicillium expansum* are two closely-related fungal plant pathogens causing green and blue mold in harvested fruit, respectively. The two species differ in their host specificity, being *P. Digitatum* restricted to citric fruits and *P. expansum* able to infect a wide range of fruits. Although host-specific *Penicillium* species have been found to have a smaller gene content, it is so far unclear whether these different host specificities impact genome variation at the intra-species level. Here we assessed genome variation across four and seven isolates from geographically distant regions in *P. digitatum* and *P. expansum*, respectively. Our results show very high similarity (average 0.06 SNPs per Kb) between globally distributed isolates of *P. Digitatum* pointing to a recent expansion of a single lineage. This low level of genetic variation contrasts with that of similarly distributed *P. expansum* isolates (2.44 SNPs per Kb). Interestingly, polymorphisms in *P. expansum* were not uniformly distributed along the genome and we show here that this is, at least in part, the result of genòmic recombination among genetically different strains. We suggest that these contrasting patterns reflect underlying differences in population structures that may be related with host specificities and agricultural practices in the respective host species.

The Role of *FBti0019985* Transposable Element in *Drosophila melanogaster* Adaptation: molecular mechanism and functional consequences

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A way to study environmental adaptation is by elucidating the relationship between mutations and their phenotypic effect. Transposable elements are mobile DNA sequences that can induce genetic variations and have been previously shown to be a considerable source of adaptive mutations in *Drosophila melanogaster*. *FBti0019985* is a putatively adaptive transposable element insertion present at higher frequency in out-of-Africa populations compare to Africa populations, where *D. melanogaster* was originated. According to the annotated reference genome, *FBti0019985* has 54 nucleotides inside the 5'UTR region of *CG18446* gene, which function is still unknown. We have confirmed by 5'RACE that flies with the element have the transcription start site of *CG18446* inside the transposable element. Moreover these flies are more resistant to cold stress conditions than flies without the insertion. In addition, they also show higher expression levels of *CG18446* gene. Recently, we have found that *FBti0019985* has, at least, five different insertion sites at lower frequency around *CG18446* among natural populations. We have demonstrated that *FBti0019985* play an important role in *D. melanogaster* cold stress adaptation only when is located in the same position as it reported in the reference genome, but not when it is located in alternative sites. In other *FBti0019985* alternative positions, the transposable element is inverted or too far from *CG18446*, preventing it from causing any phenotypic effect. We have also seen different cold stress phenotypes in different fly strains that have the insertion located in the same alternative position. Overall, these results suggest that the phenotypic effect of *FBti0019985* depends on its position and also on the genetic background of each fly strain. These findings provide another example of a transposable element insertion involved in environmental adaptation.

5S rDNA high dynamism in plants: transposable elements and evolution

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5S ribosomal DNA (rDNA) is a crucial molecule for the synthesis of ribosomes, thus for life on Earth. As a ubiquitous component both of prokaryotes and eukaryotes, its origin probably dates back to the beginning of life. Yet, many features of this sequence remain enigmatic, particularly regarding its expression, genomic arrangements and mobilisation mechanisms.

Some data suggest that the mobility and evolution of 5S rDNA is triggered by the activity of transposable elements (TE). Our research performs a comparative study of this gene across different plant species, searching TEs or their remnants in 5S sequences and *vice versa*. We have constructed DNA matrices with representative plant 5S rDNA and flanking sequences. We have compared/screened sequences from these matrices with databases/software, respectively, such as RepeatMasker (Institute for Systems Biology), CENSOR (GIRI and EMBL) and P-MITE (a plant MITE database). These applications either query sequences against a reference collection of repeats, including TEs or related sequences, or screen DNA for certain motives.

To the previously known Cassandra TRIM (Class I - DNA transposons) and EnSpm from superfamily CACTA (Class II - retrotransposons), other TEs including 5S rDNA sequences were found, such as PIF/Harbinger, Mutator and hAT (Class II). In all cases, the Internal Control Region of the gene is highly conserved. Besides, we found traces of various TEs flanking 5S rDNA. An approximate 25% of our sequences contained TE related motives. From Class I, regions with high homology with Gypsy, Copia and LINE retrotransposons were found. From Class II, EnSpm, MUDR, DADA, Sola, Helitron and hAT have also been detected.

Additionally, while screening for 5S rDNA from whole sequenced genomes in species from *Medicago*, *Solanum* and *Vitis*, we found that: 1) flanking sequences of 5S rDNA tend to be enriched in TEs or their remnants, 2) the presumed regular tandemly arranged 5S rDNA structure is difficult to recover and usually 5S pseudogenes and TEs intermingle with regular genes and spacers.

The results from this survey contribute information on the role of TEs in the evolution of 5S rDNA while questioning, to some extent, the concerted evolution model proposed for repetitive DNA families.

Mapping selection onto embryo development in *Drosophila*

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Developmental genes that differ in their spatiotemporal expression patterns have not been systematically compared regarding their intraspecific genetic variation. Embryonic development can now be described at the microevolutionary level by integrating omics developmental data and population genomic data. In this work, we combine available expression data from *Drosophila melanogaster* to define 40 spatiotemporal subregions of gene expression across embryogenesis. Applying the DFE- α estimator to *D. melanogaster* polymorphism data and divergence out to *D. yakuba*, the regimes of natural selection on these different parts of the embryo has been inferred. Thus, we test whether there are some areas or tissues of the embryo which are enriched in genes under either adaptive (positive) or purifying (negative) selection. The “phylogenetic age” of each gene expressed in each subregion has also been measured. We have found several regions whose genes show evidences of positive or negative selection. The embryonic stages «completed germ-band extension» and «end of embryogenesis» are the most and less evolutionary dynamics stages of the *D. melanogaster* embryo, respectively. Specifically, those subregions exhibiting higher adaptation levels correspond to the primordium of the germ band, the nervous system and the somatic muscle. On the other hand, constrained regions are associated with the embryonic epidermis, the embryonic hindgut and the lateral neuron cord. Interestingly, we have found that those regions with the highest adaptation express genes which are phylogenetically younger compared to the regions under purifying selection. This novel approach mapping population genetics parameters onto spatiotemporal development phenotype is a promising one to know how natural selection acts on all the different parts of the body.

Caracterització del locus *Hsp70* a nivell de seqüència i organització genòmica a *Drosophila subobscura*

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El drosofíl·lid *D.subobscura* pertany al grup obscura i és originari de la regió Paleàrtica (Europa, sud-oest asiàtic i nord d'Àfrica). Fa més de tres dècades va ser descrit per primer cop al continent americà, per on s'ha estès de 10 a 15° de latitud a tots dos subcontinents¹. *D.subobscura* presenta un patró ric d'ordenaments cromosòmics a tots cinc cromosomes acrocèntrics (A, E, O, J i U). En estudiar la freqüència de nombrosos ordenaments descrits en diverses poblacions d'aquesta espècie, s'ha trobat que alguns d'ells segueixen clines latitudinals, que poden veure's alterades pel canvi d'estació i l'augment global de la temperatura². Dos ordenaments del cromosoma O particularment ben descrits són O₃₊₄ i Ost. O₃₊₄ és típic de climes càlids, mentre que Ost augmenta de freqüència a mesura que ens acostem als pols, no només a la regió Paleàrtica, sinó també a les Amèriques.

Un dels loci que podrien explicar l'aparició i manteniment d'aquests clines seria el gen induïble *Hsp70*, pertanyent a la família de proteïnes de xoc tèrmic (HSP). Aquest locus el trobem a *D.subobscura* al segment I del cromosoma O, dins la regió invertida O₃₊₄. Un estudi va detectar diferències significatives dels nivells de proteïna d'*Hsp70* en condicions basals de temperatura entre dues soques homocariotípiques per als ordenaments Ost i O₃₊₄³. Per tal d'esbrinar els mecanismes responsables d'aquestes diferències, hem partit d'una doble aproximació amb l'objectiu, d'una banda, d'observar la localització i nombre de còpies d'*Hsp70* i de l'altra, d'obtenir la(es) seqüència(es) d'aquest gen en dues soques isocromosòmiques per als ordenaments Ost i O₃₊₄₊₇.

Els resultats obtinguts fins a dia d'avui mostren que la(es) còpia(es) d'*Hsp70* es troben localitzades en un únic punt dins del segment I del cromosoma O, que canvia de posició dins del segment d'acord amb l'ordenament de la soca. D'altra banda, hem estat capaços de recuperar un clon positiu per a *Hsp70* de l'ordenament Ost, que ens ha permès descriure a nivell molecular les característiques d'aquest gen i les seves regions flanquejants. Els resultats obtinguts indicarien que *Hsp70* podria diferir en nombre de còpies respecte d'altres espècies del grup obscura, com ara *D.pseudoobscura*.

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The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape

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East Africa is a strategic region to study human genetic diversity due to the presence of ethnically, linguistically, and geographically diverse populations. Here, we provide new insight into the genetic history of populations living in the Sudanese region of East Africa by analysing nine ethnic groups belonging to three African linguistic families: Niger-Kordofanian, Nilo-Saharan and Afro-Asiatic.

A total of 500 individuals were genotyped for 200,000 single-nucleotide polymorphisms. Principal component analysis, clustering analysis using ADMIXTURE, FST statistics, and the three-population test were used to investigate the underlying genetic structure and ancestry of the different ethnolinguistic groups. Our analyses revealed a genetic component for Sudanese Nilo-Saharan speaking groups (Darfurians and part of Nuba populations) related to Nilotes of South Sudan, but not to other Sudanese populations or other sub-Saharan populations. Populations inhabiting the North of the region showed close genetic affinities with North Africa, with a component that could be remnant of North Africans before the migrations of Arabs from Arabia. In addition, we found very low genetic distances between populations in genes important for anti-malarial and anti-bacterial host defence, suggesting similar selective pressures on these genes and stressing the importance of considering functional pathways to understand the evolutionary history of populations.

The genomic analysis of the Andaman islanders gives a new insight on the spread of modern humans in Asia

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Andamanese is a native-population living in Andaman Island, India. Andamanese and other “Negrito” populations in South-East Asia are phenotypically different from other Indian populations and resemble to African pygmies. Andamanese have been isolated from other populations with limited admixture with other populations. Thus they are a key population to study the dispersal of humans into South-East Asia.

Using whole-genome-sequence data of Andamanese we tested (i) whether these populations share an origin with other Asian populations, (ii) quantify the presence of other ancient hominids in Andamanese, and (iii) how natural selection has shaped the genome of these populations.

We generated whole-genome-sequence data of 10 individuals from Andaman islands, and 60 individuals from Mainland India. Using D-stat our analysis suggest: (i) Andamanese share a common ancestry with other Asian populations, originated in a single out of Africa expansion. (ii) They have similar amount of Neanderthal ancestry to other Out-of-Africa populations, though they lack Denisova ancestry. We also find, in the Andaman genomes, traces of ancient genomes that are neither Neanderthal nor Denisovan. (iii) Selection have acted strongly on height related genes in Andamanese populations.

Our findings suggest that Andamanese populations don't have a different origin than other Asian populations, contrary to the hypothesis of a first Out-of-Africa that would populate the Andaman Islands, where they would remain, having been substituted in mainland Asia. Their phenotypical differences are mainly due to strong selection on specific type of genes (i.e. height) which might be the result of convergent-evolution producing the Negrito phenotype.

Chimpanzee origins and geospatial genetic diversity

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The goal of this project is to resolve the fine-scale phylogeography and demographic history of chimpanzees with possible application towards conservation genetics, by determining the geographic origin of unknown confiscated animals. By using full genome sequencing in a panel of 60 chimpanzees, we have found remarkable genetic structure within subspecies, showing that geography is the first predictor of diversity and highlighting the recent population history of chimpanzees. Although the origin of modern humans has been extensively explored, the origin of chimpanzees, our closest living relatives, remains largely unknown. Here, we analyzed geographic patterns of linkage disequilibrium (LD), genetic diversity and population differentiation of chimpanzees. The observed patterns are consistent with an origin of chimpanzees in central Africa.

What can we learn from comparative genomics? New insights into reproductive isolation genes in the house mouse

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By investigating how chromosomal rearrangements play a role in evolution, together with the identification of genes that are involved in reproductive isolation much can be learned about the mechanisms involved in speciation. In this context, it is known that chromosomal rearrangements act as an impermeable barrier to gene flow through suppression of recombination, facilitating the accumulation of genetic incompatibilities. In this work, we use comparative genomics to determine evolutionary breakpoint regions in rodents and the factors that could promote them by the study of reproductive isolation genes in rodents. We identify novel lineage and clade-specific evolutionary regions within Rodentia and analyze their gene content. We detect an accumulation of protein-coding genes, and more specifically, genes implicated in reproduction isolation. They include the Krüppel gene family, a group of transcription factors with zinc finger (ZnF) domains, among which the *Prdm9* gene is the most representative. Given the role of this gene in mouse hybrid sterility, we study the evolutionary constraints that may affect the *Prdm9* gene across a natural population of house mice with chromosomal fusions in polymorphic state. Our results reveal an extreme allelic diversity in both ZnF copy number and sequence with the characterization of 12 different alleles. The analysis of meiotic recombination in a subset of these mice reveals that mean recombination rates were positively correlated with a decrease in the number of ZnF domains. Overall, the presence of genes related to species-specific phenotypes (such as reproductive isolation) and low recombination rates reinforces the adaptive value of genome reshuffling.

Metabarcoding analysis reveals new metazoan diversity and ecological roles in European coastal samples

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Marine environments are key to the life on Earth. Thus, understanding the diversity of marine environments is important to human well-being. In this regard, animals are an important component of marine biodiversity, and most of the metazoan phyla have marine representatives. However, we still do not fully understand the diversity of marine micrometazoans and its implications in marine ecology and in animal evolution. To address this, we applied a high-throughput DNA and RNA sequencing (454 pyrosequencing of 18S rRNA gene) approach to characterize the biodiversity of metazoans across different European coastal locations, size fractions and depths. The data show that metazoan reads represent a large percentage of the total eukaryotic reads. Reads from copepods and tunicates are the most abundant ones in the water column, while polychaetes, crustaceans, and platyhelminths appear as the most abundant groups in sediments. Interestingly, our dataset contain a high percentage of novel 18S rRNA metazoan sequences, including a potentially novel environmental metazoan group likely close to tunicates. Moreover, our data suggest that the metazoan sperm might play a relevant role as a source of organic carbon at the pico and nano fraction of the plankton. Overall, our study provides an important dataset, in which to analyze not only abundance and richness patterns of metazoans in marine coastal habitats, but also the possibility to investigate potential novel metazoan lineages that can provide new interesting phylogenetic information.

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Uncovering ecological diversification processes in islands: the case study of endemic reptiles in Socotra

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Islands are biodiversity hotspots, and prominent models for observing and interpreting ecological and evolutionary patterns. Ecological diversification on islands typically results in divergence of ecological niches. The Socotra Archipelago (Yemen) is a fragment of the Gondwana Supercontinent that was isolated from the Indian Ocean around 20 Myr ago when the Arabian and African plates separated. The reptile community living on this Archipelago is composed by 31 species, 29 of them endemic. In this study, trophic niche diversification (diet from faecal samples and stable isotopes from tail tips) of six gecko species of genera *Haemodracon* (two species) and *Hemidactylus* (four species) was examined. Each group conforms a monophyletic lineage with further intra-island speciation. Faecal samples and stable isotopes gave similar interspecific divergence between the six species examined. Models detected trophic-niche differences between sister species and also similarities between species of distant lineages. Microhabitat selection was a major factor that explained stable-isotope variation. Our results suggest that interspecific diet variation could be promoted by the occupation of different available microhabitats during ecological diversification. In a phylogenetic context, our study highlights some mechanisms that are driving reptile diversification and speciation in Socotra.

Especiació i hibridació en el gènere *Rhaponticum* Vaill. (*Asteraceae*) als Alps

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El paper de la hibridació en els processos d'especiació és un tema que és i ha estat molt discutit pels evolucionistes. El seu estudi és especialment interessant en plantes on, si bé tothom afirma que la hibridació s'hi dona de forma generalitzada, els estudis filogenètics es continuen presentant majoritàriament amb arbres els quals no poden reflectir les relacions reals entre les espècies en aquests escenaris d'hibridació generalitzada. Per altra banda, les zones híbrides (enteses com les zones de contacte entre dues espècies on poden produir-se híbrids de diferents generacions) es consideren un bon laboratori natural per comprovar els possibles resultats de la hibridació. En aquest treball presentem dues espècies del gènere *Rhaponticum* dels Alps, *R. heleniifolium* Gren. & Godr. i *R. scariosum* Lam., les quals malgrat viure molt properes i ser morfològicament similars no van aparèixer com a espècies germanes en el primer estudi filogenètic del gènere. No obstant, en estudis posteriors alguns individus mostraren indicis d'hibridació. Per tal d'aclarir si la hibridació és un procés que s'està donant actualment i quantificar-ne la freqüència o bé s'ha donat antigament es va realitzar un mostreig poblacional a la zona dels Alps francesos, més intens a l'única localitat on cohabitaven, i es dissenyà un experiment de germinació. Els resultats obtinguts mostren, però, que les dues espècies híbriden en baixa freqüència (1-2%) i no germinà cap aqueni de l'únic espècimen híbrid adult que es trobà durant el mostreig. Per altra banda s'han trobat també indicis d'hibridació antiga entre aquests dos tàxons i s'ha datat de principis del plistocè. Les implicacions de la hibridació actual i l'antiga i els possibles esdeveniments d'introgressió i reforçament de les barreres reproductives es discuteixen en aquesta comunicació.

Flux gènic asimètric entre poblacions del cranc marí *Liocarcinus depurator*

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En les espècies marines, les discontinuïtats oceanogràfiques poden ser permanents i asimètriques, permetent un cert flux gènic principalment unidireccional. No obstant, aquest fronts poden fluctuar i provocar canvis en las direccions migratòries. Hem analitzat la diferenciació genètica espacial del cranc *Liocarcinus depurator* prenent mostres a l'oest de la Mediterrània on es troben les tres principals discontinuïtats oceanogràfiques d'aquesta zona: l'Estret de Gibraltar, el Front Almeria-Oran i el Canal d'Eivissa. S'ha seqüenciat un fragment del gen *citocrom oxidasa I* en més de 400 individus capturats en 5 localitats i en 4 períodes diferents. D'aquesta manera aquests canvis genètics es poden estimar en l'espai i el temps. Les diferències interanuals han anat variant en les poblacions de mostreig, probablement degut a canvis locals dels patrons de circulació del flux asimètric. Aquest estudi posa de manifest la importància de les anàlisis temporals per tal d'entendre millor l'estructura genètica de les espècies.

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