
# Important links

**Live symposium at:**

**CONECTA CSIC**: https://conectaha.csic.es/b/pau-8ob-ywx-zbk

(Please, use an updated version of your browser, preferably google chrome in order to avoid problems)

**Workspace (Q&A, posters, round-table, chats, voting):**

**SLACK**: https://tinyurl.com/IBEPhDSymp2021Slack

(It will be open from 2nd to 28th February)

If you have connection problems please use this link

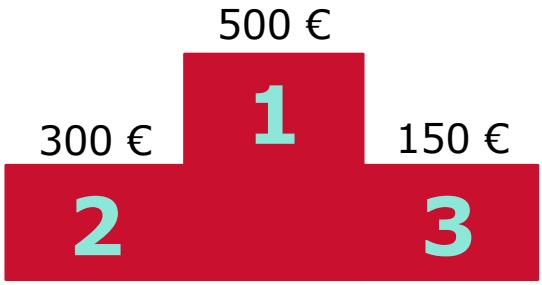
#troubleshooting: (https://ibephdsymp2021.slack.com/archives/C01KZA2EYMB)

or contact the organizing team

# Prizes

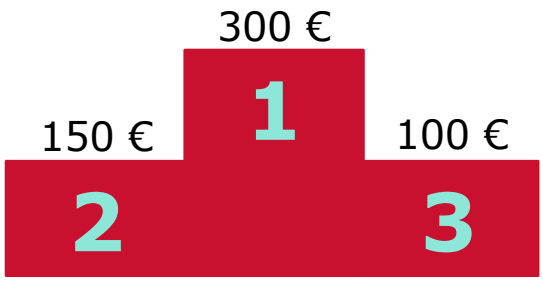
## Talks

This prize will be selected taking into account: 1) a jury with representatives from each program (50%) and 2) the audience's criteria (50%). Moreover, the feedback will be collected and handed over to the participants, as this should be useful for their own skills development.




## Posters

This prize will be chosen based on a quick voting system.




# Voting system

At the end of each session

**Session 1**: https://forms.gle/ZVSyjZmNL3AbPo5J6

**Session 2**: https://forms.gle/EQMonWFEjMsYynYM7

**Session 3**: https://forms.gle/62FVTN64ZF9y1Rhp7

**Session 4**: https://forms.gle/GrwUsimWb2CTczVD8

Form to vote your favorite **poster**:

https://forms.gle/r5LHXyaipVAQ5hBD9

# Program

## Thursday, 4th February

| | |
|---|---|
| **9:00 – 9:20** | **Opening** |
| **9:20 – 9:40** | Voting system and presentation of students group |
| **9:40 – 10:40** | **Talk session I** |
| *9:40* | **Konstantina Mitsi** (Multicell Genome Lab) |
| *9:55* | **Aleksandra Kożyczkowska** (Evolution of Eukaryote Genome Lab/Multicell Genome Lab) |
| *10:10* | **Neus Font Porterias** (Human Genome Diversity Lab) |
| *10:25* | **Rocío Caro Consuegra** (Evolutionary Population Genetics Lab) |
| **10:40 – 11:00** | **Break** |
| **11:00 – 12:30** | Round table - **Scientific careers** |
| **12:30 – 13:30** | **Talk session II** |
| *12:30* | **Pau Balart García** (Metazoa Phylogenomics Lab) |
| *12:45* | **Pablo Carrión Quilis** (Paleogenomics Lab) |
| *13:00* | **Santiago Radío** (Evolutionary and Functional Genomics Lab) |
| *13:15* | **Joan Carles Hinojosa** (Butterfly Diversity and Evolution Lab) |

## Friday, 5th February

| | |
|---|---|
| **9:00 – 10:00** | **Talk session III** |
| *9:00* | **Paula Esteller** (Comparative Genomics Lab) |
| *9:15* | **Héctor Tejero Cicuéndez** (Systematics, Biogeography and Evolution of Reptiles and Amphibians) |
| *9:30* | **Marina Álvarez Estape** (Comparative Genomics Lab) |
| *9:45* | **Leonardo Platania** (Herbivore Beetle Evolution Lab) |
| **10:00 – 10:50** | **Poster session**<br>*Available in Slack platform from 2nd February 2021* |
| **10:50 – 11:35** | **Talk session IV** |
| *10:50* | **Alba Ventós Alfonso** (Evolution of Insect Metamorphosis) |
| *11:05* | **Mireia Rumbo Roig** (Insect Reproduction Lab) |
| *11:20* | **Blai Vidiella Rocamora** (Complex Systems Lab) |
| **11:35 – 12:00** | **Break** |
| **12:00 – 13:00** | Invited speaker: **Dr. Aida Andrés** (UCL Genetics Institute) |
| **13:00 – 13:30** | **Closure and prizes** |

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# Detailed program (I)

## Thursday, 4th February

**9:00 - 9:20** **Opening**
**9:20 - 9:40** **Voting system and presentation of students group**
**9:40 - 10:40** **Talk session (I)**

**9:40** **Konstantina Mitsi** (Multicell Genome Lab)
Seeing the world through molecular eyes

**9:55** **Aleksandra Kożyczkowska** (Evolution of Eukaryote Genome Lab/Multicell Genome Lab)
Emerging of unconventional model organism - *Corallochytrium limacisporum* - to study origin of animal multicellularity

**10:10** **Neus Font Porterias** (Human Genome Diversity Lab)
Genomic insights into an admixed and underrepresented population: the Romani

**10:25** **Rocío Caro Consuegra** (Evolutionary Population Genetics Lab)
Deciphering signals of positive selection in Peruvian populations from three ecoregions

**10:40 - 11:00** **Break**
**11:00 - 12:30** **Round table - Scientific careers**

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# Detailed program (II)

## Thursday, 4th February

**12:30 - 13:30** **Talk session (II)**

**12:30** **Pau Balart** (Metazoa Phylogenomics Lab)
Smelling in the dark: phylogenomic insights into the chemosensory system of a subterranean beetle

**12:45** **Pablo Carrión Quilis** (Paleogenomics Lab)
Ancient Genomes at the Roman Empire Balkan Frontier

**13:00** **Santiago Radío** (Evolutionary and Functional Genomics Lab)
The role of structural genomic variants in environmental adaptation in *Drosophila melanogaster* and Humans

**13:15** **Joan Carles Hinojosa** (Butterfly Diversity and Evolution Lab)
How do butterflies speciate? Hybrid speciation in *Spialia* butterflies

# Detailed program (III)

## Friday, 5th February

**9:00 - 10:00** **Talk session (III)**

**9:00** **Paula Esteller Cucala** (Comparative Genomics Lab)
Insights into the evolution of gene regulation in primates through the study of LCLs as a model system

**9:15** **Héctor Tejero Cicuéndez** (Systematics, Biogeography and Evolution of Reptiles and Amphibians)
Squamate biogeographic patterns in Afro-Arabia: the impact of Earth's history on the evolution of biodiversity

**9:30** **Marina Álvarez Estape** (Comparative Genomics Lab)
Genomic study of a reintroduction of Cuvier's Gazelles

**9:45** **Leonardo Platania** (Herbivore Beetle Evolution Lab)
Microendemicity in a hotspot of biodiversity: speciation modes and microendemic patterns in New caledonian leaf beetles

**10:00 - 10:50** **Poster session**
*Available in Slack platform from 2nd February 2021*

# Detailed program (IV)

**Friday, 5th February**

**10:50 - 11:35** **Talk session (IV)**

**10:50** **Alba Ventós Alfonso** (Evolution of Insect Metamorphosis)
DNMT1 Promotes Genome Methylation and Early Embryo Development in Cockroaches

**11:05** **Mireia Rumbo Roig** (Insect Reproduction Lab)
Ecdysone downregulation effects in oogenesis in the cockroach *Blattella germanica*

**11:20** **Blai Vidiella Rocamora** (Complex Systems Lab)
Terraforming our planet: an overview

**11:35 - 12:00** **Break**
**12:00 - 13:00** **Invited speaker Dr. Aida Andrés** (UCL Genetics Institute)
**13:00 - 13:30** **Closure and prizes**

# Round Table Participants (I)

PhD at *Multicellgenome Lab* led by Dr. Iñaki Ruiz-Trillo analyzing metabarcoding data from marine samples to identify new unicellular linages. Currently working as a communication and outreach manager in the Institute of Environmental Assessment and Water Research (IDAEA).

Dr. Alicia Arroyo

Dr. Amparo Hidalgo

PhD at IBE under the supervision of Dr. Ignacio Ribera and Dr. Ali Cieslak. Currently working as a scientific illustrator.

From evolution of Insect Metamorphosis to Analytical Method Development in a CDMO company of biologics products.

Dr. Ferran Borràs

# Round Table Participants (II)

I did my PhD in Gonzalez Lab (IBE). After that, I studied a postgrade program on Innovation and Project Management and started working as innovation project manager at I3PT (Parc Taulí Universitary Hospital). The main purpose is to bring new solutions from research to the market, thus, solving uncovered needs and generating economic return.

Dr. Anna Ullastres

Dr. Elena Gómez-Díaz

Senior postdoc in Carranza Lab (IBE). Currently leading a research group studying epigenomics in malaria in the Institute of Parasitology and Biomedicine "López-Neyra". Also, coordinator of the equality comission of the IPBLN. Founder of the community "Mujeres en Malaria".

During my PhD at IBE, I studied the morphogenesis and evolution of the tracheal system in insects. Currently working as a senior researcher in "My Personal Therapeutics" in London developing personalized therapies for cancer patients.

Dr. Cristina de Miguel

# Talks

- **REMINDER!** Talks will be 15 minutes in total. You have 8-10 minutes for your presentation and the rest for questions. **We will let you know when you have reached 8 minutes.**

- In your turn, we will give you permissions to share your screen. Just in case there are technical issues, you can send us your slides before the session (optional).

# Posters

- Although there is a specific slot scheduled for the poster session, questions and answers will take place in Slack **from Tuesday to Friday**.
- If you want, you can record yourself going through your poster and paste the link in your associated channel in Slack. This is completely optional.

# Posters (available in Slack channels)

**#poster_01** **Laura Batlle Masó** (Comparative Genomics Lab)
Genetic characterization of non-familial hemophagocytic lymphohistiocytosis

**#poster_02** **Joan Carles Hinojosa** (Butterfly Diversity and Evolution Lab)
The specialization/speciation continuum: diversification linked to larval host in the butterfly *Eumedonia eumedon*

**#poster_03** **Johanna Krüger** (Comparative Genomics Lab)
Enriching a metagenome from ancient sediments

**#poster_04** **Marcel Lucas Sánchez** (Human Genome Diversity Lab)
The effects of isolation in functional variation in a Tunisian Imazighen population

**#poster_05** **Ana Mendizabal** (Evolutionary Systems Biology Lab)
BaYaka pygmies: population structure and positive selection

**#poster_06** **Laia Pérez Sorribes** (Systematics, Biogeography and Evolution of Reptiles and Amphibians)
An integrative approach to the systematics, biogeography and evolution of the *Ptylodactylus hasselquistii* species complex

# Posters (available in Slack channels)

**#poster_07** **Patricia Suárez Ara** (Multicell Genome Lab)
Developing CRISPR in unicellular relatives of animals

**#poster_08** **Héctor Tejero Cicuéndez** (Systematics, Biogeography and Evolution of Reptiles and Amphibians)
Lizard diversity in earth's deserts

**#poster_09** **Blai Vidiella Rocamora** (Complex Systems Lab)
Terraforming our planet: the semiarid ecosystems case

**#poster_10** **Pablo Villegas Mirón** (Evolutionary Systems Biology Lab)
Intronic enhancers regulate the expression of genes involved in tissue-specific functions and homeostasis

**#poster_11** **Ylenia Cañadas** (Nutritional Signals in Insects Lab)
Role of BgILP8 in the conglobate gland of *Blattella germanica*

**#poster_12** **Konstantina Mitsi** (Multicell Genome Lab)
Diversity, structure and phylogenetic novelty of the microbial eukaryotic community in Sanabria Lake as revealed by metabarcoding

# Organizing team

**Pau Balart -** pau.balart@ibe.upf-csic.es
**Laura Batlle Masó -** laura.batlle@upf.edu
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2nd IBE PhD Symposium
4-5 FEBRUARY 2021
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2nd IBE PhD Symposium
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ABSTRACT
BOOK

# Session I

## Seeing the world through molecular eyes

**Konstantina Mitsi**

**Abstract:** The transition to animal multicellularity is an evolutionary event of great biological interest that gave rise to an unprecedented diversity of lifeforms. The circumstances that permitted this leap are a long-standing open evolutionary question. Animals together with their closest unicellular relatives form the eukaryotic group Holozoa. Unicellular holozoans hold a key phylogenetic position to elucidate the mechanisms behind animal multicellularity. To expand the extant holozoan genomic dataset, here we report the nuclear and mitochondrial genomes of *Txikispora philomaios*, a unicellular holozoan parasite that infects at least two amphipod genera. The genome was acquired following a metagenomic pipeline, an approach that is commonly used to describe complex prokaryotic communities but is still in limited use for studies of eukaryotes. The mitochondrial genome is compact and typical of an aerobe. Phylogenomic reconstruction based on 85 single-copy protein domains revealed that this novel unicellular holozoan species belongs to Filasterea. Comparative analysis revealed that the *T. philomaios* genome encodes for a complete flagellar toolkit, the integrin adhesome and many transcription factors involved in animal development. In addition, *T. philomaios* possesses a two- component signal transduction system, present in all Holozoa and absent from animals. As a parasite, *T. philomaios* has reduced metabolism in comparison to the other members of the Filasterea clade and lacks the ability for *de novo* pyrimidine biosynthesis. Overall, our results add to our understanding of the genomic repertoire of the last unicellular common ancestor of animals, reinforce the current holozoan phylogeny by expanding the available dataset and provide insights into the mechanisms that facilitate a parasitic lifestyle in a filasterean.

## Emerging of unconventional model organism - *Corallochytrium limacisporum* - to study origin of animal multicellularity

**Aleksandra Kożyczkowska**[a], Sebastián R. Najle[a], Eduard Ocaña-Pallarès[a], Cristina Aresté, Iñaki Ruiz-Trillo[a,b,c], Elena Casacuberta[a]

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*c ICREA, Passeig Lluís Companys 23, 08010 Barcelona, Catalonia, Spain.*

**Abstract:** The Holozoa clade emerges as an important group for comparative cell biology analyses among eukaryotes. In addition to a well-studied Metazoa group, it includes four different unicellular lineages (Choanoflagellata, Filasterea, Ichthyosporea and Corallochytrea). Interestingly, these unicellular lineages are highly heterogeneous in their ecological distribution and have diverse developmental modes, cell morphologies, and life stages. Importantly, some species in each of the unicellular holozoan clades can transiently form multicellular structures resembling those in animals. The best way to understand in depth their biology, in particular their complex life cycles is by performing functional analysis. To do so we need to have genetic tools available in each of the four lineages.

So far, genetic tools have been recently established in all of those holozoan lineages, except for Corallochytrea, a clade that occupy a key phylogenetic position as sister-group to Ichthyosporea. To have the complete approach for comparative cell biology among this relevant eukaryotic group, we need to develop genetic tools, ideally stable transfection, in the remaining lineage of Corallochytrea.

Corallochytrea includes two taxa described so far, *Corallochytrium limacisporum* and *Syssomonas multiformis*. *C. limacisporum* is an understudied marine free-living walled saprotroph, that in addition to its key phylogenetic position, has features that make it relevant to be developed as a model organism: a peculiar and still uncharacterized life cycle. *C. limacisporum* has also a well-annotated genome which contains several conserved homolog genes with animals. It grows fast and it can be cultured in axenic conditions, in both, liquid and solid medium facilitating the isolation of clonal lines.

We here report a set of genetic tools that allow stable transfection in *C. limacisporum*. We have also developed a battery of cassettes tagging key cellular components, such as nucleus, plasma membrane, cytoplasm and actin filaments, that can serve for a better understanding of life cycle of *C. limacisporum*. Using nuclear labelling we have already gained some insights into particularities of *C. limacisporum* cell biology. We discovered that *C. limacisporum* is bi-nucleate for the majority of its life cycle. Interestingly, unlike most studied eukaryotes, the nuclear division is decoupled from the cellular division. We could also identify that *C. limacisporum* can go through multinucleate stage, hence the life cycle is non-linear. Progress and the potential implications of our research will be presented and further discussed.

## Genomic insights into an admixed and underrepresented population: the Romani

**Neus Font-Porterias**

**Abstract:** The Roma population (misnamed as “Gypsies”) is the largest transnational minority ethnic group in Europe. They have an Indian origin and their demographic history includes multiple founder effects and gene flow from non-Roma groups. Yet their South Asian and West Eurasian ancestry components have not been deeply characterized, and the influence of different demographic forces in the genomes is not fully resolved. Through the analyses of whole-exome sequences and genome-wide array data from European Roma, we have been able to describe the sources and timing of the gene flow events, which involve both common and group-specific genetic ancestries. In addition, we show that founder effects have reduced their genetic diversity and proportion of rare variants, while gene flow has counteracted the increase in mutational load. Understanding how demography shapes the genome of an admixed population provides an opportunity to elucidate how variation is modelled in human groups.

# Deciphering signals of positive selection in Peruvian populations from three ecoregions

**Rocio Caro-Consuegra**[1], Maria A. Nieves-Colón[2,3], Erin Rawls[3], Alexandra Obregón-Tito[4], Raul Tito[4], Cecil Lewis[4], Karla Sandoval-Mendoza[2], Carlos D. Bustamante[5,6], Genevieve L. Wojcik[7], Chris Gignoux[8], Julie Baker[6], Laura Fejerman[9], Tatiana Vidaurre[10], Beatriz Lizárraga[11], Verónica Rubin de Celis[12], Anne C. Stone[3], Andrés Moreno-Estrada[2], Elena Bosch[1].

*1 Institute of Evolutionary Biology (UPF-CSIC), Department of Experimental and Health Sciences, Pompeu Fabra University, Barcelona, Catalonia, Spain. 2 Laboratorio Nacional de Genómica para la Biodiversidad, Unidad de Genómica Avanzada (LANGEBIO-CINESTAV), Irapuato, Guanajuato, MX. 3 School of Human Evolution and Social Change, Arizona State University, Tempe, Arizona. 4 Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, Norman, OK. 5 Department of Biomedical Data Science, Stanford University, Stanford, CA. 6 Department of Genetics, Stanford University, Stanford, CA. 7 Department of Genetic Epidemiology, Johns Hopkins University, Baltimore, MD 8 Colorado Center for Personalized Medicine, University of Colorado, CO. 9 Department of Medicine, University of California San Francisco, San Francisco, CA. 10 Instituto de Enfermedades Neoplásicas, Lima, Perú. 11 Emeritus Professor, Facultad de Ciencias Biológicas, Universidad Nacional Mayor de San Marcos, Lima, Perú. 12 Laboratorio de Genómica Molecular Evolutiva, Instituto de Ciencia y Tecnología, Universidad Ricardo Palma, Lima, Perú.*

**Abstract:** Perú hosts three extremely diverse ecoregions: The Pacific coast desert, the Andean highlands, and the Amazonian rainforest. Multiple analyses have already identified potential candidate genes for human adaptation to hypobaric hypoxia in highlands, but selection in the Peruvian coast and rainforest remains unexplored.

Genome-wide SNP data (Illumina Infinium® MEGA) from 198 individuals distributed across Perú were used to identify signals of recent positive selection in each ecoregion. Specifically, we computed population differentiation (PBS) and haplotype-based selection scans (iHS and XP-EHH). Across the top 50 candidate regions identified per scan, we explored for strong selective sweeps, as well as for signatures of polygenic selection using gene-set and SNP-trait enrichment approaches.

Among the top 10 genomic signatures of recent positive selection found in highlands, we replicate some previously known candidates (*TBX5*, *TGFA*). We also identify novel signals related to cardiac function, glucose metabolism and epidermal growth factors. In the coast, we identify genes related to the immune system and to vitamin D synthesis. In the rainforest, we detect genes linked to respiratory functions, immune system, heart development and gametogenesis. Furthermore, we identify multiple common candidate regions among ecoregions, including genes involved in lipid metabolism (*CPT2* and *LRP8*) and the immune system (*DUOX2*, *DUOXA1* and *DUOX1*). Gene-set and trait-associated SNP overrepresentation analyses also yield common terms linked to xenobiotic metabolism and insulin. In addition, highland and coastal populations are also enriched in cardiac muscle contraction and lipid metabolism categories, whereas several immune function terms are enriched in the coast and in the rainforest.

In summary, we find genes that provide adaptations specific to the local ecological conditions in the three ecoregions. However, we also detect shared adaptations among ecoregions that point to the recent common adaptive history of Peruvian populations.

# Session II

## Smelling in the dark: phylogenomic insights into the chemosensory system of a subterranean beetle

**Pau Balart**

**Abstract:** The chemosensory system has experienced relevant changes in subterranean animals, facilitating the perception of specific chemical signals critical to survive in their particular environment. However, the genomic basis of chemoreception in cave-dwelling fauna is largely unexplored. We generated *de novo* transcriptomes for antennae and body samples of the troglobitic beetle *Speonomus longicornis* (whose characters suggest an extreme adaptation to the deep subterranean) in order to investigate the evolutionary origin and diversification of the chemosensory gene repertoire across coleopterans through a phylogenomic approach. Our results suggested a diminished diversity of odorant and gustatory gene repertoires compared to polyphagous epigean beetles. Moreover, *S. longicornis* showed a large diversity of odorant-binding proteins, suggesting an important role of these proteins in capturing airborne chemical cues. We identified a gene duplication of the ionotropic co-receptor IR25a, a highly conserved single-copy gene in protostomes involved in thermal and humidity sensing. In addition, no homologous genes to sugar receptors were detected. Our findings suggest that the chemosensory gene repertoire of this cave beetle may result from adaptation to the highly specific ecological niche it occupies, and that gene duplication and loss may have played an important role in the evolution of gene families involved in chemoreception. Altogether, our results shed light on the genomic basis of chemoreception in a cave-dwelling invertebrate and pave the road towards understanding the genomic underpinnings of adaptation to the subterranean lifestyle at a deeper level.

## Ancient Genomes at the Roman Empire Balkan Frontier

**Pablo Carrión Quilis**

**Abstract:** During the times of the fall of the Western Roman Empire, Europe saw important demographic changes, which have direct implications in how the continent is built in the present-day. Although Roman history has been thoroughly studied, not much is known about the genetic origins and ancestral composition of their inhabitants, and possible ancestry changes triggered by the Great Migration Period. Furthermore, the vast extension of the empire makes it problematic to generalize results from ancient genome studies from a particular region onto the whole of the Empire. From all the areas which were under Roman control, the Balkans is a particularly interesting region as it was the midpoint connecting the Western and the Eastern Roman Empires; and, several peoples groups moved through the region during the Great Migration Period, such as Goths, Slavs or Huns. In this project, we have extracted and analyzed aDNA from ancient Roman and post-Roman individuals (n=69) from 3, now inhabited, settlements located in present-day Serbia; most importantly the capital of Moesia Superior Roman province (2$^{nd}$ century), Viminacium. Genetic and Radiocarbon dating analyses results suggest that inhabitants in the Roman Balkans had a high degree of heterogeneity in their ancestral origins. Most importantly, we observe two major ancestry clusters: a local ancestral component similar to Balkan Bronze and Iron Age populations, and a Near Eastern ancestral component. Moreover, we detect new ancestral components incorporating into the gene pool during the course of the Imperial period. After the fall of the Western Roman Empire, though, we can observe an ancestral profile dominated by a higher European signal, together with an apparent loss of diversity and near Eastern ancestries.

## The role of structural genomic variants in environmental adaptation in Drosophila melanogaster and Humans

**Santiago Radío**

**Abstract:** Understanding how organisms deal with stressful environmental conditions is a fundamental question in evolutionary biology. Single-nucleotide polymorphism (SNPs) were initially thought to make-up the majority of adaptive variation, however it is now well-established that structural variation (SV) represents a significant source of adaptive variation. SVs remain largely understudied as a consequence of technological limitations in the length of high throughput sequenced reads. Nowadays, with the rapidly increasing sophistication in the long-read sequencing technology we are in an ideal position to study the role of SV in rapid environmental adaptation. Our aim in this work is to shed light in the contribution of SVs to the eukaryotic stress response, in particular in D. melanogaster and Humans. Among structural variants, transposable elements (TEs) play an important role in rapid environmental adaptation. In Humans, we focus our analysis on four stress regulatory networks: hypoxia, immune stress response, oxidative and xenobiotics. In particular, we assess the role of TEs in re-wiring and fine-tuning stress regulatory networks by adding Transcription Factor Binding Sites (TFBSs). For this, we take advantage of publicly available ChIP-Seq and RNA-Seq data sets obtained under, roughly, the same conditions (cell line and treatment) and analyzed it using a specially designed pipeline. We have found that TEs may have a potentially significant role in the regulation of gene expression in the response to stress. Particularly, we found that the genes differentially expressed in response to xenobiotics show the highest correlation with the presence of TFBSs, being present on average in 50% of up-regulated genes and 35% of down-regulated genes. In the opposite case, 27% of the up-regulated genes and 8% of the down-regulated genes in response to oxidative stress contain TFBSs. Beside this, our results allow us to conclude that there are very few TEs harboring TFBSs in common associated with DEGs between different samples. However, our result clearly shows that at the family level there is a strong enrichment of ERVs families principally ERVK, ERVL and ERV1. In the other hand, in D. melanogaster we studied the evolution and the functional implications of SV in natural population of different geographic origins using long-read sequencing. In this work, we design a bioinformatic tool that allow as to show that 20 genomes were sufficient to access vast majority of common TEs in natural D. melanogaster populations, that TE annotations based on long-reads performed better than those based on short-read and that hundreds of de novo annotated TEs are associated with the expression of nearby genes. Finally, and besides that TEs are often the most common type of SV, we will explore the role of copy number variants in environmental adaptation in this natural D. melanogaster populations as they often contain genic sequence and thus could also have phenotypic consequences.

## How do butterflies speciate? Hybrid speciation in Spialia butterflies

**Joan Carles Hinojosa**

**Abstract:**.Butterflies are among the best studied animals but, despite the research efforts carried out during centuries, our knowledge on the dynamics responsible for the emergence of novel diversity are still incomplete. In this context, hybridisation is classically regarded as a linear process during which two entities diverge from a common ancestor through time. Although this may be true for some cases, hybridisation is also a powerful fuel of new diversity. In this talk, I will present a case of hybrid speciation in Spialia butterflies. *Spialia rosae* is a recently described Iberian endemism, cryptic to the western European *S. sertorius*. Despite their morphological similarities, they exhibit distinct ecologies: *S. rosae* uses *Rosa spp.* as larval host plant and is a mountain specialist while S. sertorius feeds on *Sanguisorba spp.* and is a habitat generalist. We found that *S. rosae* is, in fact, genetically extremely close to *S. sertorius.* However, its mitochondrial genome and part of the nuclear genome are closely related with a third species, *S. orbifer*, nowadays ranging between Italy (Sicily) and Central Asia. This pattern highlights S. rosae as species with hybrid origin in which, the transference of genetic material from *S. orbifer*, would have had implications on its particular ecology and on the reproductive isolation from *S. sertorius*.

# Session III

## Insights into the evolution of gene regulation in primates through the study of LCLs as a model system

**Paula Esteller Cucala**

**Abstract:** Gene expression is controlled by non-coding gene regulatory elements such as promoters and enhancers, for which a consistent annotation in the primate lineage is missing. To gain insight into the evolution of gene expression in primates, we extensively profiled a new panel of human, chimpanzee, gorilla, orangutan, and macaque lymphoblastoid cell lines (LCLs), using ChIP-seq for five histone marks, ATAC-seq and RNA-seq, further complemented with WGS and WGBS. We annotated regulatory elements and integrated chromatin contact maps to define gene regulatory architectures, creating the largest catalog of regulatory elements in primates to date. We observed that most regulatory changes occur in weakly active intragenic enhancers. Remarkably, novel human-specific intragenic enhancers with weak activities are enriched in human-specific nucleotide changes. These elements appear in genes with signals of positive selection and human acceleration, tissue-specific expression and particular functional enrichments, suggesting that the regulatory evolution of these genes may have contributed to human adaptation.

# Squamate biogeographic patterns in Afro-Arabia: the impact of Earth's history on the evolution of biodiversity

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**Abstract:** The geographic distribution of biodiversity is central to understanding evolutionary biology. Paleogeographic and paleoclimatic histories often help to explain how biogeographic patterns unfold through time. However, such patterns are also influenced by a variety of other factors, such as lineage diversification, that may affect the probability of certain types of biogeographic events. The complex and well-known geologic and climatic history of Afro-Arabia, together with the extensive research on reptile systematics in the region, makes Afro-Arabian squamate communities an ideal system to investigate biogeographic patterns and their drivers. Here we reconstruct the phylogenetic relationships and the ancestral geographic distributions of several Afro-Arabian reptile clades (totaling 430 species) to estimate the number of dispersal, vicariance and range contraction events. We then compare the observed biogeographic history to a distribution of simulated biogeographic events based on the empirical phylogeny and the best-fit model. This allows us to identify periods in the past where the observed biogeographic history was likely shaped by forces beyond the ones included in the model. We find an increase in vicariance following the Oligocene, most likely caused by the fragmentation of the Afro-Arabian plate. In contrast, we did not find differences between observed and expected dispersal and range contraction levels. This is consistent with diversification enhanced by environmental processes and with the establishment of a dispersal corridor connecting Africa, Arabia and Eurasia since the middle Miocene. Finally, here we show that our novel approach is useful to pinpoint events in the evolutionary history of lineages that might reflect external forces not predicted by the underlying biogeographic model.

## Genomic study of a reintroduction of Cuvier's Gazelles

**Marina Álvarez Estape**

**Abstract:** Captive breeding programmes represent the most intensive type of ex situ population management for threatened species. They typically begin with very few individuals generating a founder effect that can lead to high inbreeding levels and reduced diversity. Hence, assessing the genetic diversity of founders as well as of their descendants is critical for the reintroduction success and might also improve the overall management of captive bred populations. In 1975 a Cuvier's gazelle captive breeding programme started in Estación Experimental de Zonas Áridas with only four individuals as founders. After over four decades of management in captivity, in 2016 a reintroduction project was undertaken in Tunisia to establish a population in an area historically included within its range. We present the first whole genome data of 30 Cuvier's gazelles comprising 13 captive bred animals, 12 individuals representing the first and second cohort of offspring born in Tunisia, and 5 individuals from a genetically unrelated semi-captive Moroccan population. Our analyses revealed that there is no difference in genetic heterozygosity, the number and length of Runs of Homozygosity, or levels of inbreeding between the founder animals and the offspring group and, that the semi-captive Moroccan population has lower genetic diversity compared to all other gazelles analyzed. Furthermore, genomic inbreeding estimates do not correlate with those estimated from pedigree data from StudBook. These results demonstrate that captive breeding programmes can successfully maintain the levels of genetic diversity through multiple generations as well as serve as source (founders) populations for future reintroductions of the Cuvier's gazelle.

## Microendemicity in a hotspot of biodiversity: speciation modes and microendemic patterns in New caledonian leaf beetles

**Leonardo Platania**

**Abstract:** Microendemicity is a condition of endemicity (i.e., distribution of a species in a given area) referred to the relative small extension of a particular species range. Some regions of the world seem to concentrate more examples of species with narrow ranges across different taxa. It is the case of New Caledonia and Madagascar. Both islands represent optimal systems to study the processes involved in the formation of microendemisms.

I will present the preliminary results of our current work, in which we focus on the diversification dynamics and the geography of speciation of two endemic genera of leaf beetles of New Caledonia, Taophila and Tricholapita. Both genera are characterized by several microendemic species distributed along the main island of Grande Terre, and we try to figure out their macroevolutionary dynamics in order to understand the main factors involved in the origin of their microendemicity patterns.

# Session IV

# DNMT1 Promotes Genome Methylation and Early Embryo Development in Cockroaches

**Alba Ventós-Alfonso**[1], Guillem Ylla[1,2], Jose-Carlos Montañes[1] and Xavier Belles [1]

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**Abstract:** The phenotypic effects of DNA methylation are not well understood. Recent studies pointed out that insects may be excellent models for DNA methylation comparative analyses, due to their great diversity of DNA methylation modes. Until now, however, analyses have focused on holometabolan species, like bees, beetles, wasps, and flies. We have studied DNA methylation in the hemimetabolan insect *Blattella germanica*. We found that an enzyme involved in DNA methylation, the DNA methyltransferase 1 (DNMT1), is expressed in early embryogenesis. RNAi experiments on *DNMT1* resulted in reduction of DNA methylation and impaired blastoderm formation. Moreover, reduced representation bisulfite sequencing data and transcriptomic analyses showed that methylated genes are highly expressed and associated with metabolism, whereas unmethylated genes are low expressed and related to signaling pathways. Interestingly, we found that methylated genes show less expression variability than unmethylated genes.

# Ecdysone downregulation effects in oogenesis in the cockroach Blattella germanica

**Mireia Rumbo Roig**

**Abstract:** Ecdysteroid hormones are crucial for several developmental processes in the life cycle of insects, such as molt or metamorphosis. They are also a key component for the female reproductive physiology. The aim of my project is to determine the Ecdysone action on *Blattella germanica* ovary development by depleting the expression of the Ecdysone Receptor and Shade, the gene that encodes for the enzyme that allows the Ecdysone to be in its active form.

## Terraforming our planet: an overview

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**Abstract:** Planet Earth is currently under multiple threats because of human activity. As result of the industrial revolution, ecosystems have been dramatically altered. Released $CO_2$ is changing the global climate by disrupting temperature regulation, oceans are acidified and polluted by plastic, and many species have become extinct because of unregulated habitat destruction (i.e. deforestation). All these external perturbations are pushing ecosystems towards their limits, so-called tipping points. Such tipping points mark critical thresholds, and once they are crossed, whole ecosystems will undergo dramatic changes in their configuration (often towards a more degraded state). A particular case where this is already happening, is semiarid ecosystems. These natural environments constitute 40% of lands and any increasing temperature will cause more aridity. This in turn, will drastically reduce the vegetated landscape, and turning them into deserts. These environmental changes promote social unrest, i.e., major migrations and wars. To improve this global situation, many interventions have being proposed, e.g. , massive replantation's or artificial dunes fixations. Here, we propose to engineer existing microbes to promote (self-)restoration of their habitats. Theoretical results suggest that using synthetic biology to enhance microbe's functionalities could change the ecosystem's resilience, or even revert the ecosystem to a healthier state. By studying the general limits of ecosystem dynamics, we have found that the dynamics at the tipping point depend on the type of perturbation and the existing community structure. For instance, vegetation in semiarid ecosystems could persist at high temperatures, but eventually it will rapidly become extinct, and even without further increases in temperature. This suggests the astonishing hypothesis that Earth ecosystems could be living in the ghost of their past. Ecosystems would have crossed the threshold, already. Can we save them?