SESBE VII

CONGRESS OF THE SPANISH SOCIETY FOR EVOLUTIONARY BIOLOGY

SEVILLE, 5-7 FEBRUARY 2020

UNIVERSIDAD DE SEVILLA

SESBE
Sociedad
Española de
Biología
Evolutiva

DECISION
MAKING IN
CELL COLLECTIVES
UNIDAD DE EXCELENCIA MARÍA DE MAEZTU (2017-2021)

Centro
Andaluz
de Biología
del Desarrollo

Estación
Biológica
Doñana
CSIC

Abstract book of the SESBE VII congress,
Seville, Spain, 5th-7th February 2020
Sociedad Española de Biología Evolutiva

Layout: Carmen Benítez Benítez and Estefanía Martínez Borda
Seville, Spain.

VII SESBE BIENNIAL CONGRESS OF THE SPANISH SOCIETY FOR EVOLUTIONARY BIOLOGY

On behalf of the **Spanish Society for Evolutionary Biology (SESBE)** we are pleased to invite you to participate in the **VII biennial congress of SESBE**, which will be held in **Seville, 5-7 February 2020**. The programme will include a number of highly relevant plenary and keynote talks, and also a series of sessions, which will cover a wide variety of topics where the participants can contribute, and a large poster session. We encourage to the evolutionary biology community to participate, and especially to pre- and postdoctoral researchers.

The Conference main topics are:

- Evolutionary Ecology
- Evolutionary Genetics
- Paleobiology and Macroevolution
- Evo-Devo
- Microbial Evolution
- Evolution of and by Humans

This congress is co-organized and supported by the Spanish Society for Evolutionary Biology (SESBE), the University of Seville (US), the Centro Andaluz de Biología del Desarrollo (CABD) and the Doñana Biological Station (EBD-CSIC).

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COMMITTEES AND STAFF

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DAILY SCHEDULE

Wednesday 5th February 2020

- 11:00-11:30 OPENING CEREMONY, Conference Hall, School of Mathematics

  Guests

  Rector of the University of Seville, Prof. Miguel Ángel Castro

  Vicerrector for Research of the University of Seville, Prof. Julián Martínez

  Vicerrector for Internationalization, Prof. Carmen Vargas

  Dean of the School of Biology, University of Seville, Prof. José María Romero

  Dean of the School of Mathematics, University of Seville, Prof. Alfonso Carriazo

  President of the Spanish Society for Evolutionary Biology (SESBE), Prof. Toni Gabaldón

  Representative of the local Organizing Committee, University of Seville, Prof. Juan Arroyo

- 11:30-12:30 OPENING LECTURE by **Beverley Glover**, University of Cambridge: **Evolution and development of petal surfaces that attract pollinators**. Sponsor: AllGenetics
- 12:30-12:45 Introducing the sponsors (AllGenetics, Macrogen, STAB VIDA)
- 12:45-13:15 **Peer Community In: A free process for the recommendation of preprints based on peer review** by Th. Guillemaud (Sophia Agrobiotech), D. Bourguet (CBGP, INRA), B. Facon (PVBMT, INRA) , Conference Hall, School of Mathematics
- 13:15-14:30 Lunch time
- 14:30-16:30 **SESSION S1. EVOLUTIONARY ECOLOGY I**, Conference Hall, School of Mathematics

  Conveners: Conchita Alonso, Montse Arista, Paola Laiolo. *Sponsor:* Genes (MDPI)

  - 14:30-15:00 Keynote**: José Ramón Obeso** (UMIB, UO-CSIC-PA): **Life history variation and ecological gradients.** *[S1.O.0]*
  - 15:00-15:15 Rodrigo Medel: **Experimental dissection of the pollinatormediated selection impact of hummingbirds and bees in the Andean monkeyflower *Mimulus luteus* (Phrymaceae)** *[S1.O.1]*
  - 15:15-15:30 Eric Imbert; Asma Hadjou-Belaid; Sandrine Mauric; Hélène Fréville: **Can plants adapt to climatic changes?** *[S1.O.2]* ○ 15:30-15:45 Monica Medrano; Conchita Alonso; Pilar Bazaga; Esmeralda López; Carlos M. Herrera: **Comparative genetic and epigenetic diversity in pairs of sympatric, closely-related plants with contrasting distribution ranges.** *[S1.O.3]*
  - 15:45-16:00 Quentin Corbel; Roberto Garcia-Roa; Pau Carazo: **Does ageing via sensory perception result from adaptive male responses to female cues?** *[S1.O.4]*
  - 16:00-16:10 Verónica Castaño Sanz; Ivan Gomez-Mestre; Francisco Garcia-Gonzalez: **Experimental insights into transgenerational effects of pesticide exposure in a seed beetle.** *[S1.O.5]*
  - 16:10-16:20 Ana Afonso; Mariana Castro; Catarina Siopa; Juan Arroyo; João Loureiro; Sílvia Castro: **Consequences of genome duplications in floral polymorphism and incompatibility system in the diploid-polyploid *Linum suffruticosum* s.l.** *[S1.O.6]* ○ 16:20-16:30 Francisco Garcia-Gonzalez & Eduardo Rodriguez-Exposito: **Population spatial structure and sexual conflict: insights from experimental evolution** *[S1.O.8]*

- 16:30-17:00 Coffee break, at the poster hall, Hall school of biology
- 17:00-19:00 **SESSION S2. EVOLUTIONARY GENETICS I**, Conference Hall, School of Mathematics

  Conveners: Xavier Picó, Ivan Gómez-Mestre, Elena Casacuberta. *Sponsor:*

Macrogen ○ 17:00-17:30 Keynote: **Josefa González Pérez** (IBE, UPF-CSIC):

Transposable element insertions in adaptive evolution *[S2.O.0]* ○ 17:30-17:45 Gonzalo Nieto Feliner; Inés Álvarez; Myriam Heuertz; Irene Villa-Machío: **Expanding the southern range margin at the cost of massive asymmetric introgression: *Armeria pungens* (Plumbaginaceae)**

[S2.O.1] ○ 17:45-18:00 Marta Barluenga; Ana Santacruz; Gerardo Pérez Ponce de León: **The Major Histocompatibility Complex, a magic trait driving sympatric speciation?** *[S2.O.2]*

○ 18:00-18:15 Mª Ángeles Decena; Sergio Gálvez-Rojas; Federico Agostini; Bruno Contrera-Moreira; Pilar Catalán; Pilar Hernández: **The *Brachypodium pangenome* reveals differently evolved drought responsive dehydrin genes within its species.** *[S2.O.3]*

○ 18:15-18:30 Carlos Sarabia; Vicente Uríos; Bridgett vonHoldt, Jennifer A Leonard: **Genomic structure, demographic histories and differential introgression in two distant populations of African golden wolf** *[S2.O.4]*

○ 18:30-18:40 Daniel Kleinman-Ruiz; Maria Lucena-Perez; Beatriz Villanueva; Jesús Fernández; Nicolas Galtier; Alexander Saveljev; Mirosław Ratkiewicz; Krzysztof Schmidt; Aurora Garcia-Dorado; José A. Godoy: **Whole-genome analysis of the genetic load of Iberian and**

Eurasian lynx populations *[S2.O.5]* ○ 18:40-18:50 Sebastián E. Ramos-Onsins; Jordi Leno-Colorado; Sara Guirao-Rico; María Carmen Rodríguez; Luis Silió; Miguel Pérez-Enciso: **The whole genome effect of selection in wild and domestic pigs** *[S2.O.6]*

○ 18:50-19:00 Armando Caballero & Enrique Santiago: **Trajectory of effective population size inferred from genome-wide linkage disequilibrium** *[S2.O.7]*

- 19:00-20:30 Poster Session at Hall school of biology
- 20:45-22:00 Welcome reception (Tapas): Al-Andalus Hotel

Thursday 6th February 2020

- 9:00-11:00 **SESSION S3. PALEOBIOLOGY AND MACROEVOLUTION**, Conference Hall, School of Mathematics

  Conveners: Francisco Balao, Marcial Escudero, Isabel Sanmartín. *Sponsor:* STAB VIDA

  - 9:00-9:30 Keynote**: Daniele Silvestro** (Univ. Gothenburg, Univ. Lausanne): **Inferring macroevolutionary processes from phylogenies and fossils** *[S3.O.0]*
  - 9:30-9:45 Andrea Sanchez Meseguer; Alice Michel; Pierre-Henri Fabre; Oscar A. Pérez-Escobar; Guillaume Chomicki; Ricarda Riina; Alexandre Antonelli; Carlos Jaramillo; Pierre-Olivier Antoine; Frédéric Delsuc; Fabien L. Condamine: **The origin and drivers of Neotropical plant and tetrapod diversification** *[S3.O.1]*
  - 9:45-10:00 E. Karen López Estrada; Isabel Sanmartín; Juan Esteban Uribe; Samuel Abalde; Mario García París: **Host jump triggered replicated adaptive radiations in a single clade of blister beetles (Coleoptera: *Meloinae*)** *[S3.O.2]*
  - 10:00-10:15 Enrique Maguilla; Marcial Escudero; José Ruiz-Martín; Juan Arroyo: **Origin and evolution of the genus *Linum* L. (Linaceae) and the role of heterostyly on the colonization of new areas** *[S3.O.3]*

  - 10:15-10:30 Lisa Pokorny; Zi Qian Shee; David G. Frodin; Rodrigo Cámara-Leret: **Reconstructing the complex evolutionary history of the Papuasian *Schefflera* radiation through herbariomics** *[S3.O.4]*
  - 10:30-10:45 María Fernanda Moreno-Aguilar; Aminael Sánchez; Itziar Arnelas; Juan Viruel; Pilar Catalán: **Museomics unveil the phylogeny and biogeography of the neglected Juan Fernandez archipelago *Megalachne* and *Podophorus* endemic grasses** *[S3.O.5]*
  - 10:45-11:00 Aurora Ruiz-Herrera; C. Vara; Andreu Paytuví-Gallart; Yasmina Cuartero; François Le Dily; L. Álvarez-Rodríguez; L. Marín-Gual; J. Ventura; Marc A. Marti-Renom: **Evolvability of recombination in mammals: the effect of chromatin organization** *[S3.O.6]*

- 11:00-11:30 Coffee break, at the poster hall, Hall school of biology
- 11:30-13:30 SESSION S4. EVO-DEVO, Conference Hall, School of Mathematics.

  Conveners: José Luis Gómez-Skarmeta, Fernando Casares, Ivan Gómez-Mestre. *Sponsor:* Genes (MDPI)

  - 11:30-12:00 Keynote: **Manuel Irimia** (CRG): **Parallel evolution of neural microexons in insects and vertebrates** *[S4.O.0]*
  - 12:00-12:15 Isabel Almudi; Joel Vizueta; Alexandre de Mendoza; Chris Wyatt; Ferdinand Marletaz; Panos Firbas; Roberto Feuda; Giulio Massiero; Patricia Medina; Ana Alcaina; Fernando Cruz; Jessica Gómez; Tyler Alioto; Carlos Vargas; Jordi Paps; Josefa Gónzalez; Julio Rozas; Alejandro Sánchez-Gracia; Manuel Irimia; Ignacio Maeso; Fernando Casares: **The mayfly *Cloeon dipterum*: a new platform to study insect evolution and morphological novelties** *[S4.O.1]*
  - 12:15-12:30 Alfonso Ferrández-Roldán; Marc Fàbrega-Torrus; Gaspar Sánchez-Serna; Enya Duran-Bello; Alba Almazán-Almazán; Marcos Plana-

Carmona; Ricard Albalat; Cristian Cañestro: **The braveheart story of *Oikopleura dioica*: a cardiogenic loser, but not a heartless chordate** *[S4.O.2]* ○ 12:30-12:45 David Madrid Pulgarín; Antonio Micó; Fernando Rodriguez; Cosme Salas; Francisco M Ocaña: **In vivo optical imaging and hodological data reveal an ancient tectopallial visual pathway in teleost fish** *[S4.O.3]*

- 12:45-13:00 Lee Hyeun-Ji; H. Christoph Liedtke; Ivan Gomez-Mestre: **Population divergence of developmental plasticity in the spadefoot toad, *Pelobates cultripes*** *[S4.O.4]*
- 13:00-13:15 Xavier Belles: **Evolution of insect metamorphosis. Insights from the regulatory mechanisms** *[S4.O.5]*
- 13:15-13:30 David Ricote & Ignacio Maeso: **Towards a novel unifying view of the genotype concept** *[S4.O.6]*

- 13:30-15:00 Lunch time
- 15:00-16:00 **SESBE General Assembly**, Conference Hall, School of Mathematics.
- 16:00-16:30 Coffee break, at the poster hall, Hall school of biology
- 16:30-18:30 SESSION S5. MICROBIAL EVOLUTION, Conference Hall, School of Mathematics.

Convener: Fernando González-Candelas, *Sponsor:* Macrogen ○ 16:30-17:00 Keynote: **Fernando González-Candelas** (Univ. Valencia):

Non-vertical inheritance in the evolution of bacteria *[S5.O.0]* ○ 17:00-17:15 José Jordán Soria; Ricardo Amils Pibernat; Felipe Gómez Gómez: Microbial communities change the environment or the environment change microbial communities? Implications for microbial adaptation in Río Tinto rock coatings *[S5.O.1]*

○

17:15-17:30 Mireia Coscollá Devís & Paula Ruiz: **Phylogenomics and antigenic Variation in *Mycobacterium tuberculosis*** *[S5.O.2]*

○ 17:30-17:45 Mario López-Pérez & Francisco Rodriguez-Valera: **Metastable evolutionary dynamics of the dominant marine bacteria SAR11** *[S5.O.3]* ○ 17:45-18:00 Andrés Moya; José L. Oliver; Miguel Verdú; Luis Delaye; Vicente Arnau; Pedro Bernaola-Galván; Rebeca de la Fuente; Wladimiro Díaz; Francisco M. González; Amparo Latorre; Ricardo Lebrón; Ramón Román-Roldán; Sixto Santamaría: **Progressive genome evolution in Cyanobacteria** *[S5.O.4]* ○ 18:00-18:15 Jaime Iranzo; Yuri I. Wolf; Eugene V. Koonin: **Gene gain and loss drive prokaryotic populations beyond the barrier of homologous recombination and accelerate genome sequence divergence** *[S5.O.5]*

○ 18:15-18:30 Álvaro Chiner-Oms; Fernando González-Candelas; Iñaki Comas: **Evolutionary analysis of the *Mycobacterium tuberculosis* complex: genome-wide signals of positive selection** *[S5.O.6]*

- 18:30-20:00 Poster session, Hall school of biology

Friday 7th February

- 9:00-10:45 SESSION S6. EVOLUTIONARY ECOLOGY II, Conference Hall, School of Mathematics.

Conveners: Conchita Alonso, Montse Arista, Paola Laiolo, *Sponsor:* STAB VIDA ○ 9:00-9:30 Keynote: **Patricia Beldade** (Instituto Gulbenkian de Ciência, Portugal): **The genetic and environmental underpinning of phenotypic variation and diversification** *[S6.O.0]*

  - 9:30-9:45 José M. Gómez Reyes; Francisco Perfectti; Cristina Armas; Eduardo Narbona; Adela González-Megías; Luis Navarro; Lucía DeSoto; Rubén Torices: **Within-individual plasticity in floral phenotype mediates a change in pollination niche** *[S6.O.1]*
  - 9:45-10:00 Nuria Cavia-Polo; R Arribas; Ángel Baltanás; Ivan GomezMestre: **Widespread learned predator recognition and amphibian resilience to alien predators** *[S6.O.2]*
  - 10:00-10:15 Mª Teresa Boquete Seoane; Conchita Alonso; Stuart F. McDaniel; Sarah Carey; Christina L. Richards; Carlos M. Herrera: **Population differentiation for Cu tolerance in two bryophyte species phenotypic and transcriptomic analyses** *[S6.O.3]*
  - 10:15-10:25 Mercedes Sánchez Cabrera; Francisco Javier Jiménez López; Pedro L. Ortiz; Eduardo Narbona; Francisco Romero; Montserrat Arista: **De novo transcripte assembly of *Lysimachia arvensis* identifying anthocyanin biosynthesis genes involved in flower colour polymorphism** *[S6.O.4]*
  - 10:25-10:35 Anupoma Niloya Troyee; Conchita Alonso; Monica Medrano: **If plants could remember about their enemies effect of herbivory on seed production and its potential epigenetic association** *[S6.O.5]* ○ 10:35-10:45 Carolina Osuna Mascaró; Rafael Rubio de Casas; Francisco Perfectti: **Hybridization and adaptive introgression in plants: the case of corolla color in *Erysimum*** *[S6.O.6]*

- 10:45-11:15 Coffee break, at the poster hall, Hall school of biology
- 11:15-12:00 SESSION S7. EVOLUTIONARY GENETICS II, Conference Hall, School of Mathematics

Conveners: Xavier Picó, Ivan Gómez-Mestre, Elena Casacuberta, *Sponsor:* Macrogen

  - 11:15-11:30 Borja Milá & Guillermo Friis: **Rapid diversification of darkeyed juncos (Aves: Passerellidae): phylogenomic and transcriptomic insights into the relative roles of natural and sexual selection** *[S7.O.1]*
  - 11:30-11:40 María Bogaerts-Márquez; Sara Guirao-Rico; Mathieu Gautier; Josefa González: **Temperature, solar radiation, and wind variables drive genetic variation in *Drosophila melanogaster* natural populations** *[S7.O.2]*
  - 11:40-11:50 Pau Carazo; Zahida Sultanova; Philip A. Downing: **The genetic sex determination system and relative Y size are associated with sex-specific lifespan in vertebrates** *[S7.O.4]*
  - 11:50-12:00 Héctor Torrado; Carlos Carreras; Núria Raventós; Enrique Macpherson; Marta Pascual: **Environmental and phenotypic drivers influence differential genomic responses in congeneric fish** *[S7.O.3]*
- 12:00-13:15 SESSION S8. EVOLUTION OF AND BY HUMANS, Conference Hall, School of Mathematics.

  Conveners: Antonio Benitez-Burraco, Juan Arroyo, Pedro Jordano, *Sponsor:* STAB VIDA
  - 12:00-12:30 Keynote**: Antonio Benítez-Burraco** (Univ. Sevilla): **The human self-domestication hypothesis as a way of reconciling the biological and cultural narratives of language evolution** *[S8.O.0]*
  - 12:30-12:45 David Juan; Raquel García-Pérez; Paula Esteller-Cucala; Glòria Mas; Irene Lobón; Valerio Di Carlo; Meritxell Riera; Martin Kuhlwilm; Arcadi Navarro; Antoine Blancher; Luciano Di Croce; José Luis Gómez-Skarmeta; Tomàs Marquès-Bonet: **Gene regulatory architectures dissect the evolutionary dynamics of regulatory elements in humans and non-human primates** *[S8.O.1]*

    12:45-13:00 Barbara Sinigaglia; Sandra Acosta; Mayuk Mondal; Elena Bosch: **Deciphering a biological adaptation in the Andamanese people**

○

[S8.O.2] ○ 13:00-13:15 Ana Roca-Umbert; Rocio Caro-Consuegra; Ruben Vicente; Elena Bosch: **Understanding signatures of positive selection in human zinc transporter genes** *[S8.O.3]*

- 13:15-13:30 **Awards**. Sponsors: SESBE, AEET, Peer, Conference Hall, School of Mathematics.
- 13:30-14:30 CLOSING LECTURE By **Janet Kelso** (Max Planck Institute for Evolutionary Anthropology, Leipzig): **Archaic genomics**. Sponsor: CABD
- 14:30: Farewell and Lunch time

SCIENTIFIC PROGRAM

Opening Lecture

“**Evolution and development of petal surfaces that attract pollinators”** by Beverley Glover, University of Cambridge. Sponsor: AllGenetics

Introducing PCI EVOL BIOL (Peer Community in Evolutionary Biology)

“A free process for the recommendation of preprints based on peer review” by Th. Guillemaud (Sophia Agrobiotech), D. Bourguet (CBGP, INRA), B. Facon (PVBMT, INRA)

Closing Lecture

“**Archaic genomics**” by Janet Kelso (Max Planck Institute for Evolutionary Anthropology, Leipzig). Sponsor: CABD

Sessions

1 **Evolutionary Ecology I**

Conveners: Conchita Alonso, Montse Arista, Paola Laiolo. Sponsor: Genes (MDPI)

Keynote: “**Life history variation and ecological gradients**” José Ramón Obeso (UMIB, UO-CSIC-PA)

2 **Evolutionary Genetics I**

Conveners: Xavier Picó, Ivan Gómez-Mestre, Elena Casacuberta. Sponsor: Macrogen

Keynote: **“Transposable element insertions in adaptive evolution”.** Josefa González Institute of Evolutionary Biology (CSIC-UPF)

3 **Paleobiology and Macroevolution**

Conveners: Francisco Balao, Marcial Escudero, Isabel Sanmartín. Sponsor: STAB VIDA

Keynote: **“Inferring macroevolutionary processes from phylogenies and fossils”.** Daniele Silvestro. University of Gothenburg, University of Lausanne.

4 **Evo-Devo**

Conveners: José Luis Gómez-Skarmeta, Fernando Casares, Ivan Gómez-Mestre. Sponsor: Genes (MDPI)

Keynote: **“Parallel evolution of neural microexons in insects and vertebrates”**. Manuel

Irimia· Centre for Genomic Regulation (CRG)

5 **Microbial Evolution**

Convener: Fernando González-Candelas. Sponsor: Macrogen

Keynote: “**Non-vertical inheritance in the evolution of bacteria”.** Fernando González Candelas. Universidad de Valencia

6 **Evolutionary Ecology II**

Conveners: Conchita Alonso, Montse Arista, Paola Laiolo. Sponsor: STAB VIDA Keynote: **“The genetic and environmental underpinning of phenotypic variation and diversification”.** Patrícia Beldade. Instituto Gulbenkian de Ciencia; CE3C: Centro de Ecologia, Evolução e Alterações Ambientais, University of Lisbon.

7 **Evolutionary Genetics II**

Conveners: Xavier Picó, Ivan Gómez-Mestre, Elena Casacuberta. Sponsor: Macrogen

8 **Evolution of and by humans**

Conveners: Antonio Benitez-Burraco, Juan Arroyo, Pedro Jordano. Sponsor: STAB VIDA Keynote: **“The human self-domestication hypothesis as a way of reconciling the biological and cultural narratives of language evolution”.** Antonio Benítez-Burraco·

Universidad de Sevilla.

ABSTRACTS OF CONTRIBUTIONS

Special Invited Lectures

Opening Lecture

Evolution and development of petal surfaces that attract pollinators

Beverley Glover[1]

(1) University of Cambridge

Flowers and the animals that pollinate them interact at a single key point - the petal surface. It is this single layer of tissue that provides the visual surface that advertises nectar rewards. It is on this layer of tissue that pollinators land. And it is often from this layer of tissue that the scents that attract pollinators over longer ranges are released. Our recent research has focused on the optical effects of the petal surface. The majority of petal morphologies will act to support certain plant/pollinator interactions but not others, leading to greater reproductive isolation and speciation within the flowering plants. I will present recent work on the nanoscale properties of the petal surface, taking molecular developmental, evolutionary and pollinator behavioural perspectives.

Sponsor: AllGenetics

Introducing PCI EVOL BIOL (Peer Community in Evolutionary Biology)

A free process for the recommendation of preprints based on peer review

Denis Bourguet 1 & Thomas Guillemaud 2

(1) Centre de Biologie pour la Gestion des Populations (CBGP, INRA); (2) Institut Sophia Agrobiotech INRA-CNRS-Université de Nice

The current system of scientific publication is faced with several serious problems: its cost and lack of transparency and the long time from the obtainment of scientific results to their publication. We have created Peer Community In (PCI) to tackle these problems by organizing the publication of peer-reviews and recommendations of preprints. Publication costs disappear: PCI validates, distributes and allows consultation of the evaluations of articles submitted free of charge. The time lag to information access is eliminated: the scientific articles evaluated are deposited in open archives as soon as they are written. The system becomes transparent: reviews, editorial decisions, authors' responses and recommendations are published on the website of the scientific community concerned (e.g. PCI Evolutionary Biology, PCI Ecology, PCI Paleontology…)

Closing Lecture

Archaic Genomics

Janet Kelso 1

(1) Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany.

Our laboratory works on methods to retrieve DNA from ancient bones and other tissue remains as well as sediments found at archaeological excavations. We take a particular interest in Neandertals, the closest evolutionary relative of present-day humans. We have generated genomes from a number of Neandertals and also retrieved the genome from a previously unknown extinct Asian hominin group related to Neandertals, which we named "Denisovans". We have shown that gene flow occurred among modern human ancestors and different archaic hominins. Consequently, about 2.0% of the genomes of people living outside Africa come from Neandertals while about 4.0% of the genomes of people living in Oceania come from Denisovans. These genetic contributions have numerous consequences today, for example in the immune system, for lipid metabolism, for adaptation to life at high altitudes in the Himalayas, and for susceptibility for diseases such as diabetes. The archaic genomes also allow the identification of novel genomic features that appeared in present-day humans since their divergence from a common ancestor with their closest extinct relatives. A future challenge is to identify the subset of these features that contributed to that modern humans developed complex culture, technology and art.

Sponsor: CABD

Sessions

ORAL SESSION

SESSION S1. EVOLUTIONARY ECOLOGY I

S1.O.0

Life history variation and ecological gradients

José Ramón Obeso 1
(1) Unidad Mixta de Biodiversidad (UO – CSIC – PA), Universidad de Oviedo, E33600 Mieres,
Spain jrobeso@uniovi.es

To examine the evolution of the major life history traits (age and size at maturity, reproductive investment, reproductive span and aging) it is necessary to consider their impact on lifetime fitness. There are important trade-offs among age and size at maturity, reproductive investment, and lifespan. Variation within and among species in these trade-offs leads to life history variation along a continuum between slow developing, long-lived, low fecundity organisms and rapidly developing, short-lived, high fecundity organisms. As a general rule, populations of harsh environments adopt 'slow' life cycles, involving long lifespan, delayed maturity, slow reproductive rates and strong inversions in parental care to enhance the chance of recruitment. Less severe environments use to determine 'fast' life cycles, including short life span, precocious maturation and strong reproductive investment. These patterns can be observed in both within and among species variation, and exceptions in both animals and plants are often rooted in evolutionary legacies. Intrinsic responses leading to life-history variation can be explained by both phenotypic plasticity and local adaptation. Plastic genotypes bear a cost when compared to locally adapted genotypes, and are generally considered poorly efficient for coping with extreme environments. However, in the case of plants, local adaptation is less common than generally assumed and it existence is independent of life cycle duration.

S1.O.1

Experimental dissection of the pollinator-mediated selection impact of hummingbirds and bees in the Andean monkeyflower *Mimulus luteus* (Phrymaceae)

Rodrigo Medel[1]
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In this work I present the results of a three-year study designed to examine the separate selective impact of hummingbirds (H) and bees (B) on the flower phenotype of the Andean monkeyflower, *Mimulus luteus* (Phrymaceae). The study was performed during the summer seasons of 2016-2018 in a high elevation site located at the west of the Andes Mountain Range, ca. 100 km northeast Santiago de Chile. We randomly setup four 100m2 plots in a 2x2 factorial design corresponding to the following treatments: a) (+H+B) control, b) (+H-B) hummingbird effect, c) (-H+B) bee effect, d) (-H-B) selfpollination effect. We tagged 100 plants within plots, tagged at least three 1-day flowers per plant and recorded the tube length, anther-stigma distance, corolla size, and nectar guide size. Capsules were collected after 2 weeks and seed production was recorded in the laboratory. Analyses for nonadditive effects between pollinator groups upon plant fecundity did not reveal significant interaction effects. This result ensures that Lande & Arnold's phenotypic selection equations account for separate, independent selective effects of hummingbirds and bees on flower traits. Results revealed that unlike hummingbirds, bees were an important agent of pollinator-mediated selection, favoring large corolla size in 2016 and 2018. Likewise, bees promoted flowers with longer anthers than stigmas, shorter tubes, and small nectar guide size. Overall, these results suggest that unlike *Mimulus* species from other latitudes, bees but not hummingbirds seem to account for flower evolution in the Andean monkeyflower *Mimulus luteus*.

S1.O.2 Can plants adapt to climatic changes?

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Global changes, and in particular climate change, represent a selective pressure on natural populations, and many empirical studies have reported phenotypic changes through plasticity or genetic evolution. However, few studies have investigated the effect of these responses on population growth rate. Using Integral Projection Models (IPMs) applied on a long-term dataset (22 years), we investigated the effect of climatic conditions on a major life-history trait, size at reproduction, of a monocarpic plant species, *Centaurea corymbosa*. This species is endemic to the Mediterranean region with only six known populations that have been surveyed since June 1994. Based on the 22-year survey period, we developed IPMs by constructing survival-growth and fecundity kernels as combination of continuous functions depending on plant size and age. Flowering strategies were mainly impacted by temperature rather than the number of wet days. The observed size at flowering increased with increasing temperature following the same direction as the optimal size at flowering, with no loss on population fitness. This can be interpreted as phenotypic adaptive response to warm climate conditions. However, *C. corymbosa* populations would be maladapted to the future climate if populations remain at the current flowering strategy.

S1.O.3

Comparative genetic and epigenetic diversity in pairs of sympatric, closely-related plants with contrasting distribution ranges

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Understanding the complex relationship between genetic and epigenetic variation in the wild and their potential role in ecological and evolutionary processes remains a challenge for evolutionary biologists. One overcoming biological paradigm is that genetic diversity defines the evolutionary potential of a species and is consequently of prime importance to allow populations to adapt to changing environments, but we know next to nothing about the role of epigenetic diversity in promoting diversification in wild plants. Congeneric comparisons of sympatric taxa, that have shared the longterm evolutionary landscape but diverge in an important ecological trait, provide a powerful design to exploring these relationships simultaneously controlling for phylogenetic and geographical effects. Here we investigate seven pairs of congeneric species with contrasting distribution ranges and habitat requirements within Cazorla Mountains (SE Spain). We hypothesized that restricted range species should have lower genetic diversity and higher epigenetic diversity than their widespread congeners. Three populations of each species were surveyed and the same samples were analyzed using Amplified Fragment Length Polymorphism and Methyl Sensitive AFLP. We found that all populations studied exhibited moderate to high levels of genetic polymorphism and that epigenetic diversity was greater than genetic diversity. Only in restricted range species the two variables were positively related. Differences between epigenetic and genetic diversity were greater at populations with low genetic polymorphism. Our results provide foundation to examine the joint effect of genetic and epigenetic diversity on phenotypic differentiation and fitness for a better understanding of the adaptive potential of restricted and widespread species.

S1.O.4

Does ageing via sensory perception result from adaptive male responses to female cues?

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The effect of sensory perception on ageing has elicited growing interest in the last few years, identifying hitherto unrecognized phenomena (i.e. sensory ageing). For example, in *Drosophila melanogaster*, extended exposure (21 days) to female cues accelerates ageing in males that fail to mate, with seemingly maladaptive consequences. However, sensory ageing studies to date have focused on understanding ageing mechanisms, while ignoring its potential functional role. Here, we studied the functional significance of reproductive sensory ageing in *Drosophila melanogaster* by simulating male reproductive failure for 1 day, 3 days, 7 days or 15 days while in the presence (i.e. sensory treatment) or absence (i.e. control) of female pheromones. We found a reproductive advantage of males exposed to the sensory treatment for 1 day, followed by gradual appearance of a reproductive disadvantage with increasing exposure time (i.e. 3-7 days) that eventually leads to net fitness costs of sensory perception in the 15 days treatment. Our results strongly suggest that brief perception of female pheromones triggers adaptive phenotypic changes in males. These results hence constitute the first evidence that sensory ageing might actually be a byproduct of male adaptive response to short-term exposure to female cues. Our findings also show that perception of female cues will only lead to sensory ageing in low quality males (i.e. unable to secure matings within 15 days following emergence), supporting the notion that sensory ageing might intensify the opportunity for sexual selection.

S1.O.5

Experimental insights into transgenerational effects of pesticide exposure in a seed beetle

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Pesticides and fertilizers are used all over the world affecting a myriad of organisms. Pesticides drive evolution by imposing a selective pressure and, furthermore, acting as environmental stressors to which individuals can respond plastically and eventually adapt. Here we investigate whether and how transgenerational effects triggered by pesticide exposure modulate evolution of traits involved in rapid adaptation. We present results in which pest seed beetles of the species *Callosobruchus maculatus* were exposed to sublethal concentrations of a commonly used pesticide, and the effects of such exposure on subsequent generations. This test informs on whether parental exposure to sublethal concentrations of pesticide affects offspring and grandoffspring even if those generations were not exposed to the toxicant pesticide themselves. We determined the lifetime reproductive success (LRS), longevity and fecundity of the parental generation, as well as of the F1, and will also determine the life-history trajectories of the F2. Results show that pesticide exposure in the parental generation has an effect on the longevity and fecundity of their offspring (F1). We expect these effects to be attenuated in subsequent generations; our current investigations will shed light into this question and we will discuss these aspects of transgenerational transmission of pesticides. This research improves our understanding of the consequences of pesticides (and of other environmental stressors and toxicants generally), and show that these chemicals can drive transgenerational effects that may underlie population dynamics and the evolution of resistance. These are key aspects for conservation and agricultural management, and for understanding adaptive evolution.

S1.O.6

Consequences of genome duplications in floral polymorphism and incompatibility system in the diploid-polyploid *Linum suffruticosum* s.l.

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Genome duplications have been related with changes in incompatibility relationships, and are regarded as a mechanism of immediate reproductive isolation. Changes in reproductive traits will be particularly relevant in species with complex breeding systems, such as heterostylous plants. Thus, genome duplications have the potential to drive significant changes on the expression of this polymorphism. *Linum suffruticosum* s.l., is a diploid-polyploid complex distributed throughout the Mediterranean Basin, bearing five main cytotypes (diploids, tetraploids, hexaploids, octoploids and decaploids), and comprising heterostylous individuals with a strong self-incompatible reproductive system. The objective of this study was to evaluate differences in the polymorphism among cytotypes and if these differences might promote assortative mating within cytogenetic entities. For that, we sampled 90 populations comprising all cytotypes and 1) measured floral traits (corolla, anthers and pistil lengths), 2) tested the self- and morph-incompatibility, and 3) performed inter-ploidy crosses at the diploidtetraploid contact zone. The polymorphism is maintained in all cytotypes and the size of sexual organs increase in higher ploidy levels; still, their heights overlap among cytotypes, allowing inter-cytotype pollen flow. In all

cytotypes, legitimate crosses showed profuse pollen tube development, in contrast to illegitimate crosses, suggesting that heteromorphic incompatibility is maintained regardless of the cytotype. Interploidy crosses showed pollen tube development in legitimate crosses, suggesting the production of inter-cytotype offspring. Genome duplications impacted the floral polymorphism in *L. suffruticosum* s.l.; still, the polymorphism and heteromorphic incompatibility are maintained, promoting outcrossing and genetic diversity regardless of the cytotype.

S1.O.7

Population spatial structure and sexual conflict: insights from experimental evolution

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Our knowledge of the causes and consequences of sexual conflict has improved enormously over the last two decades thanks to an increasing number of empirical, theoretical and comparative studies. Yet our understanding of the role of ecological or demographic factors on sexual conflict is still limited. For instance, the influence of population spatial structuring on sexual conflict remains largely unknown. This is surprising since populations are frequently subdivided into demes and the ecology and evolution of metapopulations have been the focus of exciting research for some time now. We have used experimental evolution in an insect model system to assess, for the first time, the independent and interacting effects of selection associated to mating system and population spatial structure on the fitness consequences of sexual interactions. The findings suggest that population subdivision may have important implications for sexual conflict. The results underscore that the evolution of conflict between males and females is contingent on ecological context.

SESSION S2. EVOLUTIONARY GENETICS I

S2.O.0

Transposable element insertions in adaptive evolution

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Transposable elements are not only a major component of genomes but also a major contributor to genomic diversity. By combining genomic analysis with mechanistic studies, we are elucidating the role of transposable elements in the genetic basis of several ecologically relevant traits.

S2.O.1

Expanding the southern range margin at the cost of massive asymmetric introgression: *Armeria pungens* (Plumbaginaceae)

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Armeria (Plumbaginaceae) is a primarily Mediterranean angiosperm genus with low pre- and postzygotic reproductive isolation, in which a number of taxa have been proposed to be of hybrid origin. The southernmost population of a coastal sand-dune IberianCorsica-Sardinian species (*A. pungens*) was reported to be introgressed by a sympatric congener (*A. macrophylla*) based on nrDNA ITS and plastid DNA Sanger sequences, morphometric data, genome size variation and ecological niche. A genotyping-bysequencing (GBS) genomic study reveals that such introgression is markedly asymmetric towards *A. pungens* both for the nuclear and plastid genomes. For the latter, a plastid capture has occurred in the study site, which can be considered a hybrid zone. By contrast, genetic clustering analyses hardly reveal any introgression in its congener *A. macrophylla*. The introgression scenario is consistent with Currat et al.'s (2008) model in which a species invading an occupied territory becomes massively introgressed with local genes. This is due to demographic imbalance between the two species, with reduced population densities of the invader at the colonization front. This scenario is facilitated by factors such as low interspecific reproductive isolation and remoteness of the source of the invasion, which are met in the *Armeria* hybrid zone. Although the recent origin of the introgressed population —and the hybrid zone— is so far based on circumstantial evidence, our results may provide clues for understanding how highly reticulated scenarios are shaped in their early stages.

S2.O.2

The Major Histocompatibility Complex, a magic trait driving sympatric speciation?

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A thrilling topic in evolutionary biology is understanding the mechanisms generating biodiversity. Adaptive radiations are particularly good models for the study of speciation, since phenotypic divergence leading to speciation happens rapidly and repeatedly. The Neotropical Midas cichlid adaptive radiations in Nicaragua are driven by natural selection. Adaptation to alternative habitats and diets linked to morphological shifts has shaped species distribution, and has contributed to the development of reproductive barriers. However, whether this mechanism alone is sufficient to cause and maintain divergence in this system remains to be elucidated. Following on the strong evidence that ecological preference (habitat choice) is the main force shaping populations and driving reproductive isolation, we introduce a new environmental factor that causes differentiation in this system: parasite mediated selection. We evaluate the role of host-parasite interactions as a potential driving force for divergence and speciation mediated by the evolution the Major Histocompatibility Complex (MHC) genes. These genes are responsible of generating diversity (when responding and adapting to different parasites/mutualists), and at the same time of promoting assortative mating and barriers to reproduction in the host (mate preference based on olfaction cues) acting as magic traits.

S2.O.3

The *Brachypodium pangenome* reveals differently evolved drought responsive dehydrin genes within its species

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Dehydrins (DHNs) belong to group 2 LEA (Late-Embryogenesis-Abundant) proteins which play an important role in plant responses to abiotic stresses. DHN data was retrieved from Phytozome and Ensembl Plants and used to perform comparative evolutionary analysis of dehydrin genes in four *Brachypodium* species, 54 B. distachyon ecotypes and five cereal crops (*Aegilops tauschii, Hordeum vulgare, Sorghum bicolor, Oryza sativa* and *Zea mays*). DHN domain analysis across the four *Brachypodium* species dehydrins (Bdhn) revealed eight architectures. The most common architecture was YSK2. In addition, some upstream cis-elements related to exogenous and endogenous stresses were detected. B. distachyon (Bdis) drought-tolerant ecotypes contain a slightly lower number of dehydrins (4 vs. 9), and some of them have a distinct sequence composition. Chromosome distribution of Bdhn genes differ among Bdis ecotypes as well as the number of DHNs in each chromosome. Seven out of nine Bdhn genes are located in Bdis chromosomes 3 and 4 and one gene each in chromosomes 1 and 2. Phylogenetic analysis of DHN sequences show a general evolutionary trend of early diverging B. stacei and its derived (sister) B. hybridum–S subgenome Bdhns, followed by those of B. distachyon and sister B. hybridum–D subgenome Bdhns, and those of *B. sylvaticum*. However *B. sylvaticum*, a moist-environment perennial species, contains nine DHNs, four of which diverge from any of the nine DHNs present in the annual dry-environment *Brachypodium* species. Further analysis of orthologous sequences shows that only Bdhn1 and 2 are present in every grass studied.

S2.O.4

Genomic structure, demographic histories and differential introgression in two distant populations of African golden wolf

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The recently recognized African golden wolf (Canis lupaster) is widely distributed across the Sahara and Sahel of Africa. Large distribution and diversity of habitats have been shown to drive population differentiation in other related canids such as the gray wolf (Canis lupus) but not in others like coyotes (Canis latrans). Also, there is potential for introgression among canids which could affect genetic diversity and adaptation in local populations.

Since African golden wolves may act as top predators in several ecosystems in Africa, understanding the demographic history of the species could inform changes across entire ecological networks. We have used several bioinformatic tools to test for divergence, genetic diversity and introgression from other canids in seven whole genome sequences of African golden wolves from the extremes of their distribution. We have detected different demographic histories in two well-defined groups of this species in Northwestern and Eastern Africa that provide evidence of interconnection during Pleistocene and Holocene climatic changes. We have detected a higher co-ancestry of Ethiopian wolves (Canis simensis) in Eastern than in Northwestern African golden wolf populations, and a clear hybrid ancestry with gray wolves and/or dogs (Canis familiaris) in an Egyptian African golden wolf. Finally, we have found different patterns of genomewide heterozygosity across the range of the African golden wolf. Our results aim to aid the conservation of these little known carnivores, which could play a pivotal ecological role across huge areas in Africa.

S2.O.5

Whole-genome analysis of the genetic load of Iberian and Eurasian lynx populations

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Population genetics theory predicts an increase of genetic load in declining populations as the result of the relaxation of purifying selection. This could hamper the recovery and increase the risk of extinction of many endangered species. However, empirical research on this matter has been scarce, especially for endangered species. Here we resequenced whole genomes of 31 individuals from the two remnant populations of the highly endangered Iberian lynx (*Lynx pardinus*), and 29 individuals of its sister species, the widely distributed Eurasian lynx (*Lynx lynx*), which belonged to three populations with contrasting demographic histories and diversity levels. We identified segregating and fixed derived alleles, annotated the functional impact of these mutations, and estimated individual genetic load as the number of potentially deleterious alleles per individual. Contrary to our expectation, Iberian lynx individuals showed on the average less genetic load than Eurasian lynx. Additionally, within each species we didn't detect differences between populations. This result suggests that the differences between the histories of these populations may have been too recent and/or too small to differentially impact the load observed at the genomic level. Alternatively, purging of deleterious variation may have reduced the load of the smaller populations. Beyond adding to the ongoing debate on the relationship between genetic load and population size and to the impact of genetic factors in endangered species viability, this work contributes a whole-genome annotation catalogue of deleterious variants, which will become a valuable asset for the future conservation efforts of these species.

S2.O.6 The whole genome effect of selection in Wild and Domestic Pigs

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Domestication is a process of artificial selection driven by humans, which modifies the features of an ancestral species into new phenotypical traits, such as less aggressiveness and greater productivity. The study of markers linked to this evolutionary process may shed light on its biological basis. Here, we investigated the distribution of selective pressures at the genome level to discern the impact of the domestication in the pig genome. To that end, we selected 20 wild boars and 26 domestic pigs, which are composed by two different breeds: Iberian and Large White. These domestic populations are very different between them, Iberian is an autochthonous breed with no evidence of introgression whereas Large White is a commercial breed that has been artificially improved and has admixture with Asian pigs in its genome. A new approach which considers positions containing missing information was designed to detect the strength of adaptation in these populations. This

approach used four different estimates of the nucleotide variability, based on different parts of the site frequency spectrum. A significant result was the lack of fixed functional substitutions between domesticated and wild populations, suggesting that the domestication effects are weak (per variant) and have polygenic patterns. Demographic patterns are affecting significantly the segregating patterns between functional and neutral positions, which is also compatible with a significant presence of weak selective effects. We discuss several hypotheses that explain the apparent lack of domestication signal and the different alternatives to detect the effect of domestication on the genome.

S2.O.7

Trajectory of effective population size inferred from genome-wide linkage disequilibrium

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The inference of the recent changes in effective population size (Ne) is key to understand the genetic composition of populations in humans and other species. Current methods to estimate the historical Ne from linkage disequilibrium (LD) between pairs of loci are only applicable approximately to scenarios of linear increases or decreases of Ne, and are unable to detect drastic changes such as bottlenecks or severe population drops, which may have a great impact on genetic variation. We have developed a method, based on the LD spectrum observed in a set of contemporary individuals, to estimate recent (up to about 200 generations before sampling) changes in the historical Ne from SNP data. The method can be applied to samples of fewer than 10 individuals using various types of SNP data: diploid with phased or unphased genotypes, haploid and pseudo-haploid (typically obtained from low-coverage sequencing of ancient DNA). Application of the method to data of ancient British populations resulted in Ne estimations of 3,500 to 5,000 in about 5,000 years BCE. The inferred demography of Jewish populations during the last 2,000 years showed different profiles for Ashkenazim, with reduced Ne for nearly 80 generations, Mizhrahim, with a sudden drop in Ne dated between the 13th and 16th centuries, and Sephardim, with a gradual reduction in Ne. Analysis of a variety of human and animal

populations gave results in agreement in general with previous estimations by other methods or concurrent with historical events.

SESSION S3. PALEOBIOLOGY AND MACROEVOLUTION

S3.O.0

Inferring macroevolutionary processes from phylogenies and fossils

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Present biodiversity represents a snapshot of a very long and complex evolutionary history, during which species and entire clades have originated, diversified and –to a large extent– gone extinct. Reliable estimates of the processes that have shaped diversity through time and in space are crucial to understanding present biodiversity patterns. Here, I present a suite of Bayesian models to infer different macroevolutionary processes including the dynamics of speciation, extinction and dispersal and the evolution of quantitative traits. These methods show that both phylogenies of extant taxa and the fossil record provide valuable information about past and present biodiversity, although their integration remains challenging. Future developments should use an interdisciplinary approach interfacing earth sciences, paleontology, and evolutionary biology to further improve our understanding of the processes driving the evolution of taxonomic and phenotypic diversity.

S3.O.1

The origin and drivers of Neotropical plant and tetrapod diversification

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Understanding the origin and diversification of biodiversity in the world's most biodiverse region, the Neotropics, has been the subject of decades of intense debate.

Controversy mostly focuses on the time of origin (Quaternary vs. pre-Quaternary) and drivers of this diversity (extrinsic vs. intrinsic factors). Here, we evaluate these scenarios by testing whether diversification rates correlate with main environmental trends (climate, mountain uplift) in a large sample of Neotropical clades: 150 phylogenies comprising 12,524 species of seed plants and major tetrapod clades (amphibians, mammals, squamates, and birds). We unveil five main results: (1) most Neotropical clades (97%) originated before the Quaternary; (2) half of the clades diversified at constant rates through time; (3) past environmental variations correlate with diversification changes in 37% of Neotropical lineages, but with contrasting responses such that: (4) endotherm tetrapods (birds and mammals) diversified extensively during warm periods and global cooling resulted in synchronized slowdowns of diversification, while plant diversification generally increased during cooling; and (5) the rise of the Andes mostly impacted diversification of ectotherm tetrapods (amphibians and squamates), with some clades diversifying progressively with the uplift, while others diversified only during the early orogenic stages. Our study demonstrates key evidence for the role of ancient environmental perturbations on diversification, suggesting that, environmental instability over macroevolutionary scales may in fact act as a driving force of Neotropical diversification.

S3.O.2

Host jump triggered replicated adaptive radiations in a single clade of blister beetles (Coleoptera: Meloinae)

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Meloidae is one of the few families of beetles that presents hypermetabolic larval development. Two major traits in this highly complex life-cycle have diverged across the evolutionary history of the family: the mode of larval locomotion to reach to the host nest, and the host itself. Most clades included in the subfamily Meloinae feed on the larvae of Apoidea (Hymenoptera), but two lineages, Epicautini and Mylabrini, feed on eggs of Acridoidea (Orthoptera). Larval locomotion includes phoretic and non-phoretic modes, which may be clade-specific or exhibit intra-clade variability. Species richness differs broadly among major clades in the family. Clades feeding on grasshoppers are the most speciose, with c. 600-700 species/each, while the largest tribes that parasite bees, e.g., Meloini or Pyrotini, do not exceed 200 species. Here, we use macroevolutionary models that tie diversification – speciation and extinction – rates to changes in discrete traits to unroll the evolution of host specificity (Hymenoptera vs Orthoptera), and the role of host jump as a diversification trigger in the subfamily. Specifically, we aim to determine if larval locomotion mode (phoresy vs non-phoretic active searching) was the prior evolutionary event that limited host availability, leading to an exceptional case of parallel non-sister adaptive radiation in the subfamily Meloinae.

S3.O.3

Origin and evolution of the genus *Linum* L. (Linaceae) and the role of heterostyly on the colonization of new areas

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The Mediterranean Basin is one of the richest hotspot in the world, and has been refuge for many species during Quaternary glaciations, and source for later colonization of adjacent areas during interglacial periods. Genus *Linum* s.l. has its center of biodiversity in this region, although some species are distributed in many other places. The study of the origin and diversification of the genus could shed light on the role of the Western Palearctic as center of diversity and potentially source for the colonization of other areas, and how heterostyly could shape diversification rates and colonization patterns. A total of 103 samples of 93 different species were included, analyzing nuclear ITS and plastid ndhF, matK and trnL-F DNA regions. Ancestral area reconstruction was performed using R package “BioGeoBEARS”. Finally, diversification analyses were done for the estimation of diversification rates and correlation with heterostyly. Our results placed the origin of *Linum* in the Eocene to mid Oligocene in the Western Palearctic, where most species diversified.

Within area speciation is the main mechanism of diversification, and most dispersal events occurred from the Western Palearctic to other regions. Diversification rates were constant through the phylogeny without changes in specific clades, reproductive system or geographic areas. Western Palearctic acted as source but never as a sink for dispersal, and all species colonizing new areas were homomorphic. Nevertheless, this is not influencing the dispersal event but the success of the establishment in the new area by self-pollination.

S3.O.4

Reconstructing the complex evolutionary history of the Papuasian *Schefflera* radiation through herbariomics

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Papuasia represents an ideal natural experiment in plant biogeography due to its high endemicity, its complex geological past, and its location at the confluence of the highly diverse Malesian and Australian floristic regions. However, scattered knowledge of its flora and limited representation in herbaria have hindered our understanding of the drivers of its diversity. Using the Hyb-Seq high-throughput sequencing approach with an angiosperm-wide bait kit targeting 353 nuclear orthologs, we inferred molecular phylogenies of the speciose genus *Schefflera* in *Papuasia* from historical herbarium collections. To reconstruct the evolutionary history of the genus we: built a gene tree (in MrBayes) integrating these historical collections with ITS sequences found in NCBI; inferred a species tree (pseudo-coalescent approach) from 304 nuclear loci (in ASTRAL); and estimated divergence times and ancestral areas from a partitioned data matrix comprising 26 nuclear loci (in BEAST). We found strong support for subgeneric morphogroup *Brassaia*, main geographical clades (i.e., western *Papuoschefflera* s.s., northeastern *Ischyrocephalae*, and an eastern clade containing morphogroups *Oreopolae*, *Barbatae*, and *Cephaloschefflera*), and most morphospecies; although some infrageneric and interspecific relationships remain unresolved. Upon landing on the Woodlark plate (coming from Sunda) in the late Oligocene, *Schefflera* is inferred to have migrated westwards and diversified during the Miocene, in agreement with previous reconstructions. Additionally, we show the efficacy of the Angiosperms-353 probe kit to resolve both deep and shallow phylogenetic relationships.

S3.O.5

Museomics unveil the phylogeny and biogeography of the neglected Juan Fernandez archipelago *Megalachne* and *Podophorus* endemic grasses

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Oceanic islands constitute extraordinary natural laboratories to study plant speciation and biogeography. Juan Fernandez is a southern Pacific archipelago of three 5-1 Ma old islands that harbor a remarkable endemic flora. Most endemic grass species belong to *Megalachne* and *Podophorus*, two genera of uncertain taxonomic adscription. *Megalachne berteroniana* and *M. masafuerana* are respectively endemic to the Masadentro and Masafuera islands, whereas the single species of monotypic *Podophorus*, *P. bromoides*, only known from its type locality in Masadentro, is currently considered extinct. We have used museomic approaches to uncover the evolutionary history of these endemic grasses and to date the ages and infer the origins of their ancestors. Genome skimming data were produced from herbarium samples of the three endemics, including the type specimen of *P. bromoides*, as well as for a collection of 38 species representing the main *Loliinae* lineages. Assembled rDNA cistrons and plastomes were used to build their phylogeny. Filtered ITS and trnT-F sequences from these genomes were further combined with a large *Loliinae* data set for accurate biogeographic reconstruction. Nuclear and plastome data recovered a strongly supported fine-leaved Fernandezian clade where *Podophorus* was resolved as sister to *Megalachne*. Bayesian phylogenetic dating and DEC range evolution analyses estimated the split of the Fernandezian clade from its ancestral southern American PampasPatagonian *Loliinae* lineage in the Miocene-Pliocene transition, followed by LDD from the continent to the uplifted volcanic islands. Consecutive Pliocene-

Pleistocene splits and among-islands dispersals paved the way for in situ speciations of the *Podophorus* and *Megalachne* taxa.

S3.O.6

Evolvability of recombination in mammals: the effect of chromatin organization

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Recombination allows faithful chromosomal segregation and the production of new heritable allelic variants. An appreciation of how this variation arises and is maintained is of critical importance to our understanding of genetic diversity and evolution. In is known that recombination varies among species, among individuals within species and between sexes, yet the mechanisms governing this pattern remain unclear. Here, we take advantage of chromosome conformation capture following by deep sequencing (HiC) in combination with SNP genotyping and detailed analysis of crossover events to study how genome folding and recombination landscapes are interconnected. To this aim we analyzed a unique wild population of the house mouse characterized by a recent evolutionary origin and the presence of chromosomal fusions in polymorphic state. We describe how the number of crossovers co-varies among different chromosomes in single nucleus. The proximate basis for this effect is global regulation of chromosome axis lengths in each nucleus, which reflects nucleus level determination of chromatin loops. Moreover, we show that genome reshuffling alters the 3D genome topology in the germ line at different hierarchy levels, causing a profound effect on the inter- and intra-chromosomal interactions. We hypothesize that this reorganization can have a profound impact in both recombination and gene expression regulation, since the redistribution of chromatin interactions can alter both cis- and trans-regulatory regions. We anticipate that our results will provide impetus for further exploration of the functional and structural basis of genomes in a broad context, reinforcing the link between developmental genetics and genome evolution.

SESSION S4. EVO-DEVO

S4.O.0

Parallel evolution of neural microexons in insects and vertebrates

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One of the major challenges for the development of complex multicellular organisms is to generate dozens of cell types from a single genomic sequence. Through differential processing of introns and exons, alternative splicing can produce cell type-specific protein isoforms that allow optimization of their specific cellular roles or even the emergence of novel functions. One of the most striking examples of this is provided by microexons in bilaterian neurons. These tiny exons, which can encode as few as one or two aminoacids, are switched on during neuronal differentiation and show the highest evolutionary conservation of all types of alternative splicing. Remarkably, their sharp neuronal expression depends on a single protein domain that originated in Bilaterian ancestors and that has enabled the emergence of microexon programs. Comparison of loss-of-function mouse and fruitfly models for this protein domain uncovered shared developmental defects as well as multiple lineage-specific microexon functions, which impact distinct aspects of neuronal biology in each clade.

S4.O.1

The mayfly *Cloeon dipterum*: a new platform to study insect evolution and morphological novelties

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The great capability of insects to adapt to new environments promoted their extraordinary diversification. The key phylogenetic position of mayflies within *Paleoptera*, as the sister group of the rest of winged insects together with their life history traits make them an essential order to understand insect evolution. To answer these questions, we have successfully established the mayfly *Cloeon dipterum* as a model species with a continuous culture in the lab. We have sequenced and assembled a high quality reference genome and we provide the first analyses of the genomic bases underlying the evolution of the chemical and visual perception systems and the origin of insect wings, paving the way for a better understanding of how insects colonized the sky and explored a huge variety of new ecological niches.

S4.O.2

The braveheart story of *Oikopleura dioica*: a cardiogenic loser, but not a heartless chordate

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Gene loss has been a significant source of genetic variation during animal evolution, and among chordates, appendicularians such as *Oikopleura dioica* are probably the most successful losers. As a case study, we investigate the impact of gene loss on the evolution of the mechanisms of heart development in *O. dioica*. Our work provides the first modern developmental atlas of the heart of *O. dioica*, which appears as a bidimensional chamber-less structure made of only two layers, the pericardium and myocardium, the latter beating against the stomach wall, likely representing the simplest heart of all chordates. Our work also describes the cell lineage fate map of cardiac progenitors up to tailbud stage, and suggests that the cardiac precursors derive from the most anterior muscular cells and migrate from the anterior part of the tail into the trunk, in a similar way as described in ascidians. Despite the cardio-ontogenic similarities between *O. dioica* and ascidians, our exhaustive *in silico* survey for cardiogenic factors conserved in other chordates reveals striking differences in *O. dioica* regarding its early signaling pathways as well as cardiac transcription factors involved in migration and differentiation. Comparison with 6 other appendicularian species reveals that most of these gene losses are shared among them, suggesting that they are an ancestral synapomorphic trait of this clade, which likely influenced the evolution of this family of urochordates. Thus, our functional analyses of main developmental signaling pathways and primary cardiogenic transcription factors reveals that the braveheart story of *O. dioica* has been shaped by a process of deconstruction of the cardiac genetic toolkit including prominent gene losses, loss of cardiac expression domains, and the abolishment of developmental signaling pathways that are fundamental to make a heart in other chordates.

S4.O.3

In vivo optical imaging and hodological data reveal an ancient tectopallial visual pathway in teleost fish

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The lemnothalamic visual pathway is considered the canonical pathway responsible for processing almost every stimulus that amniotes can see. Nevertheless, the existence of an collothalamic visual pathway seems to be an ancient vertebrate trait as it has been described in cartilaginous fishes, amphibians, reptiles, birds, and mammals. Regarding actinopterygian fishes, the situation is far from being clear since systematic anatomofunctional studies are scarce and opposite results have been described concerning the existence of these two well-differentiated visual pathways to the cortex or pallium. In this study we used tract-tracing methods and in vivo voltage-sensitive dye (VSD) imaging to describe the anatomo-functional properties of the visual pathways from the retina to the pallium (cortex) of goldfish. Hodological data suggest that the lemnothalamic pathway appear to be absent since only a few terminals can be observed in the visual diencephalic relay nuclei after massive tracer injections into the optic nerve. By contrast, the connectivity data reveal the existence of a well-developed retinotectal-pallial (collothalamic) visual pathway. VSD imaging results allowed to precisely localize the pallial visual area receiving visual tectal information, which is confined to a well-defined portion of the goldfish dorsal subdivision of the lateral pallium and not only to show the functional connection between optic tectum and the pallial visual area but also the first functional evidence of a collo-amigdaline visual pathway in teleost fishes. Taking together, our results would lead to a better understanding on the evolution of visual pathways in actinopterygians as well as in the entire vertebrate lineage.

S4.O.4

Population divergence of developmental plasticity in the spadefoot toad, *Pelobates cultripes*

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The Western spadefoot toad (*Pelobates cultripes*) is a developmentally plastic organism. Under benign conditions, it can grow large without significant advancements in development, but it can accelerate its development when ponds begin to dry up quickly, reaching an early metamorphosis and hence avoiding desiccation. Phenotypically plastic responses in divergent environments can be subject to divergent selection, and lead to genetic accommodation. To understand how genetic accommodation occurs, we sampled populations originating from ponds with either short or long hydroperiod, within each of two regions (southern and central Spain). We collected egg clutches from the field and conducted common garden experiments in the lab exposing half of the animals from each population to reduced water levels to characterize their reaction norms. We also conducted RNA-Seq analyses to compare patterns of differential gene expression between highly plastic and non-plastic populations. Developmental acceleration is achieved through increased corticosterone and thyroid hormone, but comes at the expense of a high metabolic cost, increased oxidative stress, and metamorphosing at a smaller size. We employed corticosterone assays to assess stress hormone levels across experimental treatments and explore whether individuals originating from ponds with short hydroperiods constitutively expressed higher levels of corticosterone. We found that while tadpoles originating from the South of Spain were highly plastic if exposed to pond desiccation simulations, tadpoles from central Spain were not, and the region had a much more pronounced effect than local pond type, apparently due to divergence in the length of the larval growing period across regions.

S4.O.5

Evolution of insect metamorphosis. Insights from the regulatory mechanisms

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Insect metamorphosis is a process of post-embryonic development by which immature stages become morphologically and functionally adults. It can be classified into two types: hemimetabolan and holometabolan. The hemimetabolans (like locusts and cockroaches) hatch as nymphs morphologically similar to the adults, which grow through successive molts until the last nymphal instar, and to the adult. Holometabolans (like beetles and flies), hatch as larvae that are morphologically different from the adult, which grow through successive molts until the last larval instar, then the pupal stage, and the adult. Both types of metamorphosis are regulated by the same hormones: ecdysone, which triggers the successive molts, and juvenile hormone (JH), which prevents metamorphosis. JH binds to the transcription factor Methoprene-tolerant (Met), which is the JH receptor, then the hormone-receptor complex induces the expression of Krüppel-homolog 1 (Kr-h1), which represses the expression of E93, a transcription factor that triggers metamorphosis. This regulatory axis, called the MEKRE93 pathway, regulates metamorphosis in all insects studied so far. The main difference between hemimetabolan and holometabolan species is the function of Broad complex (BR-C) transcription factors, which promote the growth of wing primordia in the former, and determine the formation of the pupa in the latter. The universality of the MEKRE93 pathway suggests that the hemimetabolan last nymphal stage is homologous to the holometabolan pupa. Moreover, we propose that changes in the regulation and functions of BR-C have been instrumental in the evolution from hemimetaboly to holometaboly.

S4.O.6

Towards a novel unifying view of the genotype concept

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Understanding the Genotype-Phenotype (G-P) interdependence is fundamental for all biological fields. Surprisingly, discussions about the limits of the G-P dualism have been sidestepped by mainstream scientific discussions, despite the fact that both experimental practice (from mendelian genetics to -omics) and theoretical background (from phenomenology to information theory) have changed profoundly since Johannsen first coined the term genotype in 1911. Indeed, multiple unresolved contradictions between the original G-P formulation and its current use are showing that explicit theoretical reevaluations are urgently needed. In particular, the so-called extragenetic inheritance phenomena have not been possible to accommodate to the genotype concept due to the current lack of a neat distinction between genotype and genome, excluding inherited epigenetic configurations as fundamental and integral parts of the genotypical identity of organisms. Here, we provide a novel proposal towards a unifying theory of genotype based on 4 objective and experimentally verifiable criteria (selftemplating, phenotypic expression, plastic identity and inheritance) that are able to account for all potential sources of biological inheritance as genotypic constitutions, from molecular structures to social behaviour. Our proposal follows a different path than previous related frameworks (such as the replicator concept) because it does not rely on information to delineate the boundary between genotype and phenotype, but on the evolvability conferred by a growing number of nested and interrelated genotypical systems. By doing so, we provide new solutions to several long-standing problems, from the periodic resurgences of lamarckian phantoms to controversies on biological levels and units of selection.

SESSION S5. MICROBIAL EVOLUTION

S5.O.0

Non-vertical inheritance in the evolution of bacteria

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Genetic variation is the fuel of evolution. Without variation no evolutionary change can occur. Traditionally, the generation of variation has been equated to mutation and this is indeed the ultimate source of changes in nucleotide sequences. However, most microorganisms acquire variation from other sources. Horizontal/lateral gene transfer (HGT) and recombination have provided and currently provide many bacteria with new genes and variants that can be used to explore the adaptive landscape. The availability of complete genome sequences of bacterial species has allowed a detailed analysis of the role of HGT and recombination in their evolutionary history but also of their involvement in shaping the genetic variability of others, most notably pathogens. This has important consequences from a practical perspective, because one of the most relevant current evolutionary processes in bacteria is the spread of resistance to antimicrobial drugs. Most genetic determinants of AMR are readily transferred between and within species. Recombination also played a relevant role in the initial stages of adaptation to a new host, the human species, resulting in the emergence of new pathogens, such as *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae* or *Treponema pallidum*. My research group applies population genomics and molecular evolution tools to analyze the genomes of these and other bacterial pathogens. I will review some of our major findings and how we used the technological and analytical advances to bridge the gap between basic and applied scientific knowledge.

S5.O.1

Microbial communities change the environment or the environment change microbial communities? Implications for microbial adaptation in Río Tinto rock coatings

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Río Tinto is a natural extreme acidic environment, and is considered a good geochemical Mars Analogue. One of the poorly studied niche in the system is the rock coatings, composed by clay minerals cemented with Fe in variable quantities. Alexander von Humboldt reported the first rock coating and only recently microbiologist have started to pay attention to these peculiar ecosystems. Their highly oxidative character, the biodiversity present and the biogeochemical cycles operating on a small scale have tremendous interest in microbial ecology and microbial evolution in these environments. We studied a litosthatigraphic unit in the Origin area of Río Tinto. Our objectives were to characterize the physicochemistry, mineralogy, microbial diversity and ecological parameters of the unit to identify associations of microorganisms with different mineral species and their changes. Samples were analysed by XRD, ICP-MS and SEM (EDX); the extracted DNA sequenced by Illumina Mi-Seq and processed bioinformatically. Identified taxonomic groups were contrasted applying in situ hybridizations and enrichment cultures. Our results show a change in the microbial community composition and the specific metabolisms associated to a progressive change in the redox conditions of the system. The selection by environmental conditions is an important factor in evolution. The obtained results allow asking and discussing a basic evolutionary question: ¿are the physicochemical conditions of the environment influencing the microbial diversity or are the microbial metabolisms responsible of promoting environmental changes generating selection pressure?

S5.O.2

Phylogenomics and antigenic Variation in Mycobacterium tuberculosis

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Tuberculosis is the deadliest disease due to a single pathogen according to the latest estimates of the World Health Organization. This is largely due to the host immune status, but also the success of the transmission-infection strategy carried out by *Mycobacterium tuberculosis*. *M. tuberculosis* is diverse, genetically and also phenotypically, including virulence related phenotypes. Genomic differences can distinguish at least eleven *M. tuberculosis* lineages that cause disease in different host and different human populations. We don't know if like other pathogens, *M. tuberculosis* exploits antigenic variation to overcome the host immune system, or even to adapt to specific host or populations. Given the importance of understanding the host specificity and immune evasion strategies of *M. tuberculosis*, we aimed to provide a phylogenomic framework of *M. tuberculosis* in different hosts and study the genomic diversity of antigens. We analyzed both human and animal epitopes of T and B cells, in 12.557 genomic sequences of the different *M. tuberculosis* lineages, including animal associated ecotypes. Through bioinformatic analysis, it was determined presence/absence of epitopes and its genetic diversity in the context of the global phylogeny. We demonstrated differences among T and B cell epitopes, and epitope variability not described before. Our results reveal how antigens vary within *M. tuberculosis*, opening new paths in the development of control strategies to fight tuberculosis.

S5.O.3

Metastable Evolutionary dynamics of the dominant marine bacteria SAR11

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Large heterogeneity at the genomic level has been a source of c1ontinuous interpretational challenges for microbiologists in recent times. In asexual microorganisms, one of the possible scenarios proposed to explain such diversity is the presence of several subpopulations or ecotypes with an ecological adaptation to a discrete microniche that generates barriers that decrease the recombination between them. In another alternative, in the absence of geographical barriers, several populations occupy the same niche and diversity is given mainly by high recombination ratios preventing genomic sweeps in a "quasisexual" manner. In spite of being the most abundant and successful marine microorganism in the global ocean, the study of the SAR11 population dynamics has lagged considerably due to difficult to get by classical culture-based approaches or the paradoxical difficulty to obtain metagenomeassembled genomes (MAGs). Furthermore, due to their abundance in metagenomic studies of marine waters we were able to captured microdiversity patterns in natural subpopulations of SAR11, including freshwater and deep ocean bathytype. In this study, we provided the first glimpse about evolutionary and ecological processes using a metagenomics approach that affect SAR11 genomic diversity. The results indicate that populations of the different subclades of SAR11 behave as metastable populations in which widespread recombination among different groups prevent divergence among them and lead to metastable and diverse populations in which different ecotypes generated by the flexible genome coexist for long periods of time.

S5.O.4 Progressive genome evolution in Cyanobacteria

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Progressive evolution, the tendency towards increasing complexity, is a controversial issue in Biology, whose resolution requires the proper measurement of complexity. To address this challenge, we consider that genomes are the best entities to measure complexity because they record the history and information gain of organisms in their ongoing biotic and environmental interactions. By recurring to six metrics that measure genome complexity, which are not primarily associated to functionality, we report the existence of progressive evolution towards higher genome complexity in the evolution of the

Cyanobacteria phylum. We show that these complexity metrics plus three additional genome parameters present statistically significant phylogenetic signal in Cyanobacteria. Moreover, a ridge regression of genome complexity metrics against evolutionary age shows that three out of six present a positively driven evolutionary trend towards higher complexity. These findings support the existence of progressive genome evolution in this ancient and diverse group of organisms.

S5.O.5

Gene gain and loss drive prokaryotic populations beyond the barrier of homologous recombination and accelerate genome sequence divergence

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Evolution of bacterial and archaeal genomes is a highly dynamic process that involves extensive gain and loss of genes. Therefore, phylogenetic trees of prokaryotes can be constructed both by the traditional sequence-based methods (gene trees) and by comparison of gene compositions (genome trees). Comparing the branch lengths in gene and genome trees with identical topologies for 34 clusters of closely related bacterial and archaeal genomes, we found that the terminal branches of gene trees were systematically compressed compared to those of genome trees. Thus, sequence evolution is significantly delayed with respect to genome evolution by gene gain and loss. The extent of this delay widely differs among bacterial and archaeal lineages. We develop and explore mathematical models demonstrating that the delay of sequence divergence can be explained by sequence homogenization that is caused by homologous recombination. The model explains how homologous recombination can maintain the cohesiveness of the core genome of a species while allowing extensive gene gain and loss within the accessory genome, leading to pangenome expansion. Once evolving genomes become isolated by barriers that impede homologous recombination, gene and genome evolution processes settle into parallel trajectories, and genomes diverge, resulting in speciation. This model of

prokaryotic genome evolution provides a mechanistic explanation of our previous finding that archaeal genomes contain a class of genes that turn over rapidly, before significant sequence divergence occurs, and provides a framework for correcting phylogenetic trees, to make them consistent with the dynamics of gene turnover.

S5.O.6

Evolutionary analysis of the *Mycobacterium tuberculosis* complex: genome-wide signals of positive selection.

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Members of the *Mycobacterium tuberculosis* complex (MTBC), a monophyletic group of bacteria, are the causative agents of the tuberculosis disease in humans and animals. Along its evolution, the MTBC has derived in 7 distinct lineages. In comparison with other pathogens, the MTBC shows a limited genetic diversity. Nevertheless, this diversity is related with a high host-specificity and differential pathogenic phenotypes. We have studied the MTBC genetic diversity by generating a dataset of whole-genome sequences with thousands of samples from all over the world. By doing so, we have been able to study the signals that selection have left on the pathogen's genome. Our analyses showed that (i) single point mutations that create new transcriptional start sites have been positively selected; (ii) the sensor part of the PhoPR two-component system is under positive selection from the MTBC ancestor times until nowadays; (iii) dN/dS profiles through time allowed us to identify changing selective pressures on an heterogeneous set of genes, some of them potentially related to host-pathogen interactions and antibiotic treatments. Overall, our results highlight the importance of studying a bacterial pathogen from an evolutionary perspective to understand how they adapt to their host and how they respond to treatments.

SESSION S6. EVOLUTIONARY ECOLOGY II

S6.O.0

The genetic and environmental underpinning of phenotypic variation and diversification

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Body pigmentation in insects provide some of the most visually compelling examples of how reciprocal interactions between evolutionary and developmental processes shape patterns of intra-specific variation and inter-species diversity. I will use this model to discuss recent work in the lab that addresses the genetic basis of phenotypic variation and diversification, with special focus on developmental plasticity and evolutionary novelty.

S6.O.1

Within-individual plasticity in floral phenotype mediates a change in pollination niche

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Phenotypic plasticity, the ability of a genotype of producing alternative phenotypes when exposing to different environments, is a pervasive feature of life, pivotal to understand the ecology and evolution of most organisms. Within-individual phenotypic plasticity (WIP) is rare in non-labile traits because developmental requirements constrain their ability to respond to environmental stimuli. Here we demonstrate observationally and experimentally the occurrence of complex and reversible WIP entailing the change of the overall phenotype of the flower of *Moricandia arvensis* (Brassicaceae), disentangle its genetic and physiological causes and reveal the consequences for the interactions with pollinators. This species blooms during spring and summer in semiarid areas of the Western Mediterranean, facing two contrasting environments. In response to this environmental change, the same individuals produce two completely different flowers, large, cross-shaped, and UV-reflecting lilac in spring, small, rounded, and UV-absorbing white in summer. Most floral traits changed in a coordinated way producing two different types of flowers with similar morphological integration. In addition, WIP is reversible, because the plants produced again springtype flowers when conditions became milder. *Moricandia arvensis* is also plastic for key foliar traits, changing from C2 photosynthesis in spring to values closer to C4 in summer. By bearing two different flowers, the same plant moved between a pollination niches composed mostly of long-tongued large bees in spring towards a niche composed of small bees and beetles in summer. Multivariate WIP allows *M. arvensis* to jump to a different region of the phenotypic space and explore new biotic and abiotic niches.

S6.O.2

Widespread learned predator recognition and amphibian resilience to alien predators

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Alien predators are one of the major causes of decline and extinction of species worldwide, since native organisms are rarely equipped with specific antipredatory strategies to cope with them. However, phenotypic plasticity and learned predator recognition may help prey populations to survive novel predators. Here we examine learning abilities of larval amphibians (*Pelobates cultripes*) to recognize a harmful invasive predatory crayfish (*Procambarus clarkii*) throughout multiple populations in two different regions of the Iberian Peninsula. We compare the learned behavioral responses of larvae in three populations from central Spain and four populations from southern Spain with different histories of exposure to the presence of the invasive crayfish (crayfish absence, low abundance and high abundance). None of the populations showed innate recognition of chemical cues from the invasive crayfish, and yet they all learned to recognize it. Preliminary analyses show no significant differences in learning abilities among southern populations, but suggest that learned responses may actually differ among central populations. In view of ongoing molecular analyses, we hypothesize that similar responses to the invasive crayfish in the southern populations may have arisen from a combination of longer history of exposure to this introduced predator and higher levels of gene flow, as they inhabit a highly interconnected pond network. In contrast, the populations from central Spain tend to show lower connectivity and they seem more divergent in their plastic responses. Consequently, they may be more likely affected by the predation pressure imposed by the introduced crayfish.

S6.O.3

Population differentiation for Cu tolerance in two bryophyte species: phenotypic and transcriptomic analyses

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Heavy metal (HM) toxicity constitutes a strong selective pressure that has frequently led to ecotype differentiation in flowering plants. In bryophytes, there is still contrasting evidence about the relative contribution of population differentiation and phenotypic plasticity to adaptation to HM pollution, and limited information about the molecular pathways involved. We explored the mechanisms underlying intraspecific variation in HM accumulation and tolerance in the Cu moss *Scopelophila cataractae* (Sc), and the cosmopolitan moss *Ceratodon purpureus* (Cp), two species with contrasting affinity to HM. We sampled four populations of Sc from different contamination levels within a former Cu mine, one population of Cp in an urban area, and studied male and female plants of Cp that were already growing in axenic conditions. After culturing all populations under control and Cu treatments, we measured Cu accumulation and plant performance to understand the response to Cu, and used RNA sequencing to detect expression changes associated with HM exposure. Both species showed populationspecific responses for tolerance, but accumulation was similar within each species. Sc isolates from the most polluted locations in the mine were more tolerant, and the fieldcollected population of Cp grew better than the lab-maintained population under Cu. Cu-treated plants of both species showed differential expression patterns as compared to control plants. Furthermore, in Cp, Cu-treated females had more differentially expressed transcripts than Cu-treated males. These results provide evidence of significant population differentiation for HM tolerance at a very small spatial scale in Sc, and of sex-specific molecular responses to Cu in Cp.

S6.O.4

De novo transcriptome assembly of *Lysimachia arvensis*: identifying anthocyanin biosynthesis genes involved in flower colour polymorphism

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Flower colour polymorphism is a trait codified by genes which are driven by divergent selection, affecting the reproductive isolation. Thus, genes involved in the development of flower colour are good candidates for being considered genes implicated in speciation processes. The most common pigments in flowers are the anthocyanins, which are synthesised in the Anthocyanin Biosynthesis Pathway (ABP). Variations in anthocyanin composition produce colour differences, and this is due to mutations in structural or regulatory genes of the ABP. We aim to detect the molecular and biochemical bases of flower colour polymorphism in *Lysimachia arvensis* (Primulaceae), an annual herb that is widely distributed around the world and presents flower colour polymorphism which seems to be a key trait for its diversification. We extracted RNA samples from petals of 15 individuals (8 blues and 7 oranges) grown in the glasshouse and sequenced with Illumina Hiseq technology. Using Trinity software, we assembled the transcriptome and identified the genes related to the ABP. We calculated the differential expression of those genes between the two colour morphs. We found differential gene expression in some genes involved in the pigment synthesis which correlates with the biochemical composition obtained from HPLC-DAD analysis. As the transcriptions factors that regulate the ABP are associated with the physiological and ecological features of the plant, we expect to find differences in those characteristics between the two petal colour morphs.

S6.O.5

If plants could remember about their enemies: effect of herbivory on seed production and its potential epigenetic association

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Understanding the role of epigenetic variation in plant's defense response to herbivore damage could be crucial to predict the adaptive potential of plants for rapid environmental changes such as insect outbreaks and introduced pests. In particular, DNA methylation has been reported as one of the suitable epigenetic mechanisms that participate in programming gene expression in response to stress within plant's life-time (priming) and across generations (adaptation). Here we study the role of DNA methylation in plant responses to herbivory, using an annual plant *Thlaspi arvense* (Brassicaceae), a biofuel crop. Seeds were collected from three distant European populations and grew under controlled conditions with an aim to assess natural variation in DNA methylation within and across geographic regions. Our experimental design included herbivory as one fixed factor and plants were allocated to two different treatments, (i) insect defoliation by encaged larvae *Pieris brassicae*, a specialist lepidopteran species and (ii) control undamaged plants. In first generation, we found significant decrease in seed mass and seed production per fruit for plants that suffered insect herbivory suggesting that our experimental manipulations impose stress. Ongoing analysis will show whether herbivory further determine changes in global DNA methylation levels or divergence in the methylation profiles obtained by Reduced Representation Bisulfite Sequencing (epiGBS). This work can contribute to understand the comprehensive perspective of plant defense against herbivores that can aid in predicting evolutionary responses of plant-herbivore interaction.

S6.O.6

Hybridization and adaptive introgression in plants: the case of corolla color in *Erysimum*.

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Introgression, defined as the transfer of a small amount of the genome from one taxon to another, is driven by hybridization and repeated backcrossing. This process is currently known to be frequent, especially among closely-related species where reproductive barriers could be labile. However, the actual evolutionary implications of introgression remain to be investigated in detail, partly because an overall understanding of how it operates from a mechanistic and ecological point of view is still missing. Here, we investigated the genomic signature of introgression at the individual/population/species level in the plant genus *Erysimum* (Brassicaceae), a system for which preliminary evidence of hybridization exists. Hybridization has been hypothesized to underlie the transition in corolla color from yellow to purple in this genus. Accordingly, we have explored the hypothesis that purple corollas have evolved repeatedly by adaptive introgression in some southeastern Spanish species. To do so, we sequenced full transcriptomes of yellow and purple flowers from seven *Erysimum* spp (a total of 17 populations of four purple and three yellow species). Then, we used different phylogenetic approaches (i.e., species trees, phylogenetic networks, and Dstatistics, among others) that allowed us to separate the signature of incomplete lineage sorting from that of hybridization. Furthermore, we used genomic analyses of natural selection to determine if genes responsible for flower color had undergone positive selection. Our results showed a signature of widespread hybridization, along with incomplete lineage sorting. We also observed that hybridization patterns were not homogeneous and varies among populations. We detected positive selection in some color genes, suggesting a potential role of adaptative introgression in purple corolla flowers. Altogether, our results demonstrate that hybridization has been rampant in this system, but that its impact differs among populations of the same species. Hybridization, at least in some cases, may be responsible for phenotypic transformations that even change ecological interactions.

SESSION S7. EVOLUTIONARY GENETICS II

S7.O.1

Rapid diversification of dark-eyed juncos (Aves: Passerellidae): phylogenomic and transcriptomic insights into the relative roles of natural and sexual selection

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Recent radiations provide the opportunity to explore the relative roles of neutral and selective factors in driving evolutionary divergence and speciation. We use genomewide markers and patterns of phenotypic variation to reconstruct the evolutionary history of the songbird genus Junco, and understand the mechanisms and timing of their diversification across North America. Analysis of mtDNA sequence data reveals that the striking plumage diversity in the dark-eyed junco evolved within the last 10,000 years as the yellow-eyed junco colonized North America from southern Mexico following the Last Glacial Maximum. In contrast, junco taxa on Baja California, Guadalupe Island, and the highlands of Guatemala, represent divergent lineages that have been isolated for hundreds of thousands of years with little plumage divergence. Maximum likelihood phylograms based on 25,000 neutral SNP loci from a genotyping-by-sequencing approach confirmed the existence of divergent lineages in the south and a rapid diversification of dark-eyed forms in North America. Sexual signaling traits like plumage color have diverged at a faster rate than traits under natural selection like morphological characters, suggesting a major role for sexual selection in the radiation. Using an experimental transcriptomics approach to study the genetic basis of plumage differences among morphs, we found differences in the regulation of melanin-pathway genes, but not in their DNA sequences, suggesting that simple differences in gene expression can give rise to marked differences in plumage color very rapidly. Natural selection also played a role in the junco radiation, and genetic-environment association analyses (GEA) revealed patterns of isolation by adaptation in some forms of the Oregon junco of western North America, as well as the important role of genetic drift in driving divergence of small, isolated populations.

S7.O.2

Temperature, solar radiation, and wind variables drive genetic variation in *Drosophila melanogaster* natural populations

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How organisms adapt to their environment is still an open question in Evolutionary Biology. While several studies in a diverse set of species have shed light on the genes underlying adaptation, our knowledge on the selective pressures that explain the observed patterns lacks behind. *Drosophila melanogaster* is an unrivalled organism to study environmental adaptation because this species originated in Southern Africa and has recently expanded worldwide. Although Europe was among the first continents to be colonized by *D. melanogaster* it has been understudied compared with North America and Australia. In this work, we performed a genome-environment association (GEA) analysis using Bayesian hierarchical models with whole-genome sequencing information from 26 *Drosophila melanogaster* populations, collected in Europe and North America, and 78 environmental variables. We found that environmental variables related with temperature, solar radiation, and wind significantly correlate with allele frequency changes both in Europe and North America suggesting that these are the main selective pressures in both continents. In North America, precipitation, evaporation, and hours of light also contribute to explain genetic variation. Furthermore, we also identified precipitation as one of variables that could be related to seasonal fluctuating SNP frequencies. Functional annotation of the genes identified in Europe highlight some interesting patterns such as leg and wing morphogenesis functions enriched in genes that correlated with the environmental variable wind. Overall, our analysis identifies for the first time the selective pressures driving variation in *D. melanogaster* natural populations, which should facilitate the mapping of these variants to their fitness effects.

S7.O.3

The genetic sex determination system and relative Y size are associated with sexspecific lifespan in vertebrates

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Broad taxonomic patterns in sex lifespan gaps (e.g. males live longer than females in birds and vice versa in mammals) remain a puzzle. We use mortality/lifespan data from 139 species of birds, mammals, reptiles and amphibians to test the prevailing idea that this may be explained by differential expression of recessive mutations in the X/W chromosome of the heterogametic sex: the “unguarded-X” hypothesis (UXh). We found higher mortality in the heterogametic than the homogametic sex in vertebrates, and then collected karyotypic data to examine whether differential mortality is associated with relative X/Z size (i.e., UXh) or with Y/W size. Relative X/Z size was not associated with sex-specific lifespan in birds or mammals, while Y size strongly correlated with male survival and the sex lifespan gap in mammals, where Y are particularly degraded and toxic Y effects and are expected to be strong. Our results confirm the role of sex chromosomes in explaining sex differences in lifespan, but strongly suggest that, at least in mammals, this is best explained by toxic Y ageing mechanisms and/or Y degradation.

S7.O.4

Environmental and phenotypic drivers influence differential genomic responses in congeneric fish

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Connectivity and local adaptation are two contrasting evolutionary forces highly influencing population structure. To evaluate the impact of early life traits and environmental conditions on genetic structuring and adaptation we studied two sympatric fish species, *Symphodus tinca* and *S. ocellatus* reproducing in spring and summer respectively, caught along a temperature/productivity gradient in the Western Mediterranean Sea. For both species, we followed an individual-based approach and measured early life history traits from otolith readings, gathered information on environmental variables and obtained genome-wide markers from genotyping-bysequencing (GBS). The two *Symphodus* species presented contrasting population structure across the same geographic gradient. The reproductive period and the larval traits seem to influence population connectivity and how they adapt to environmental conditions. We identified candidate loci for local adaptation combining outlier analysis (OAs) with environmental (EAAs) and phenotypic (PAAs) association analyses. We show that the degree of population differentiation affects the power of some methodologies to detect signals of selection. Nonetheless, we detected genotype-phenotypeenvironment associations in the two *Symphodus* species. We observed broad genomic signals of selection mediated by environmental conditions (i.e. productivity and temperature) and to a lesser extent to phenotypic variables (i.e. hatching date and settlement size). Globally our study highlights that individual-based approach combining genomic, environmental and phenotypic information is key to unveil detailed patterns of genomic responses.

SESSION S8. EVOLUTION OF AND BY HUMANS

S8.O.0

The human self-domestication hypothesis as a way of reconciling the biological and cultural narratives of language evolution

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Our ability to learn and use languages (commonly referred to as our faculty of language) is usually thought to have resulted from biological processes mostly. By contrast, language diversity is thought to depend on factors internal to languages. Increasing evidence suggests instead that both elements are engaged in a complex feedback loop, with our cognition accounting for key aspects of languages, but with languages affecting our cognition, and that core languages' features also depend on external factors, particularly, the physical and the cultural environments in which humans live. In this talk, I will argue that the hypothesis of human self-domestication (that is, the claim that humans exhibit features also found in domesticated animals) can help reconcile these two narratives. Accordingly, self-domestication might have contributed to both the sort of brain/cognitive changes resulting in our language faculty and to the emergence of the cultural niche that enabled languages to gain complexity via a cultural process.

S8.O.1

Gene regulatory architectures dissect the evolutionary dynamics of regulatory elements in humans and non-human primates

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Genes undergoing substantial evolutionary shifts in their expression profiles are often modulated by critical epigenomic changes that are among the primary targets of selection in evolution. Here, we investigate the evolution of epigenetic regulatory activities and their interplay with gene expression in human and non-human primate lineages. We extensively profiled a new panel of human and non-human primate lymphoblastoid cell lines using a variety of NGS techniques and integrated genome-wide chromatin contact maps to define gene regulatory architectures. We observe that epigenetic and sequence conservation are coupled in regulatory elements and reflect the impact of their activity on gene expression. The addition or removal of strong and poised promoters and intragenic enhancers is frequent in gene expression changes during recent primate evolution. In contrast, novel human-specific weak intragenic enhancers, dormant in our cell lines, have emerged in genes showing signals of recent adaptive selection, suggesting that they echo important regulatory innovations in other cell types. Among the genes targeted by these regulatory innovations, we find key candidate drivers of recently evolved human traits, such as FOXP2 or ROBO1 for speech and language acquisition, and PALMD for neocortex expansion, thus highlighting the importance of regulatory changes in human evolution.

S8.O.2

Deciphering a biological adaptation in the Andamanese people

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Recently, we analyzed signatures of positive selection using whole-genome sequences from the Andamanese, a pygmy population indigenous from the Andaman Islands, and several mainland Indian populations. Among the top 20 most differentiated nonsynonymous SNPs detected under a hard selective sweep model in the Andamanese, we identified the R990G substitution (rs1042636) in Calcium-Sensing Receptor (CaSR) gene as a potential adaptive variant to experimentally follow up. Notably, in vitro studies had already shown that the derived allele of the R990G substitution results in a gain-offunction of the receptor. CaSR has a critical role in calcium homeostasis by directly regulating the urinary calcium excretion and the parathyroid hormone (PTH) secretion. The gene is also expressed across a wide range of tissues and has been described to be involved in many other diverse biological functions. Since no direct adaptive phenotype could be linked to the detected signatures of adaptation, we generated a knock-in mouse for the R990G substitution using the CRISPR-Cas9 technology. To assess the phenotypic impact of the substitution, we explored for potential differences related to the CaSR functions between the homozygote carriers of the ancestral and derived alleles that could result adaptive in the Andamanese. Preliminary results point to unequal fat accumulation and differential weight, with R990G homozygotes showing greater weight and more fat accumulation. Such features could facilitate an earlier sexual maturation in agreement with the hypothesis that the pygmy phenotype could result from selection for an early onset of reproduction since they live in a particularly hostile environment.

S8.O.3

Understanding signatures of positive selection in human zinc transporter genes

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Zinc is an essential micronutrient with many biological functions in the human body, whose homeostasis is tightly regulated through 24 zinc transporter genes (ZTG). Notably, zinc body content is highly dependent on soil zinc levels, and the scarcity of this micronutrient in some environments leads to a high prevalence of zinc deficiency in several human populations. Since differences in the zinc homeostasis may be adaptive to local dietary and environmental conditions, we explored the complete set of human ZTGs for signatures of adaptation by using the 1000 Genomes sequencing data (Phase 3), which comprises up to 26 worldwide populations. Signatures of classical hard sweeps were analyzed through the use of specific statistics (i.e. Tajima's D, iHS, XP-EHH and FST). Since zinc homeostasis is accomplished by the joint action of the 24 ZTGs, we also investigated signatures of polygenic selection by aggregating potential signals of adaptation across the complete set of ZTGs and comparing them versus random regions of the genome. We detected strong signatures of positive selection for some particular genes (Znt9, ZIP11, ZIP5) in specific geographical areas, as well as an extreme pattern of population differentiation for the whole set of ZTGs when comparing African to nonAfrican populations. Moreover, we have found significant differences on zinc transport in HEK293 cells transfected with Znt9, detecting a less efficient transport in those cells that express the derived allele of the non-synonymous variant under selection (rs1047626). Thus connecting the functional molecular basis and the genotype of such variant.

POSTER SESSION

16:30-17:00 and 19:00-20:30 Wednesday 5th Feb - 11:00-11:30, 16:00-16:30 and 18:30-20:00 Thursday 6th Feb - 10:45-11:15 Friday 7th Feb; Hall of the School of Biology

Poster sessions every day will provide an opportunity for discussion in a relaxed setting. Posters are displayed during the whole congress and interested people may view the poster even when the authors are not in attendance, although authors are required to stand at their posters during the Coffee Break/Poster Session held closer to his respective session.

SESSION S1.S6 EVOLUTIONARY ECOLOGY I AND II

S1.S6.P.1

Genetic differentiation of a mountain population of *Colluricincla megarhyncha* (Aves:

Pachycephalidae) in the Kumawa Mountains, New Guinea

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Phylogeographic patterns provide insight into the history of intraspecific lineages and the factors that drive their evolutionary divergence. New Guinea has a very pronounced topography and is composed of a central cordillera and smaller peripheral mountain ranges that have been shown to play a role in population differentiation in species retricted to high elevation habitats. Widespread species at low elevations are less likely to show genetic structure than species restricted to mountainous regions. Species with distributions including both lowland and highland habitats provide an opportunity to study the relative roles of local adaptation and gene flow in driving evolutionary divergence. The Kumawa Mountains are an isolated mountain range in the Bomberai Peninisula in the "bird's neck" of New Guinea (Western Papua, Indonesia). In 2014 and 2017 two expeditions were conducted to sample birds in the Kumawa region. *Colluricincla megarhyncha* (Passeriformes: Pachycephalidae) was a common species in the area and was found in both lowland and highland areas. Because of this large distribution range, the study of *C. megarhyncha* phylogeography could show how mountain islands affects the genetic structure of bird populations. We present preliminary results based on mtDNA gene fragments to test whether highland populations in Kumawa at 1200 m are differentiated from lowland populations at the base of the mountains and other parts of New Guinea (available in GenBank from a previous regional study of the species). Genetic structure and diversity of the avifauna of New Guinea has been poorly studied and our study aims to contribute to better understanding phylogeographic patterns in this pristine region of the world.

S1.S6.P.2

Life-history correlates of coexistence and stability in natural competitive communities: a missing eco-evolutionary link?

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Understanding the impact of demographic rates and life history traits on phenotypic evolution and single-species dynamics is the main goal of current evolutionary theory. However, species in nature are embedded in a network of multi-species interactions, and it is known that these interactions simultaneously act as strong selective pressures and stabilizing mechanisms. A largely untested hypothesis predicts that the ecological requisite of community persistence and stability should constrain the diversity of lifehistory traits of interacting species within a range allowing for multi-species coexistence. Here, we test this hypothesis in 81 competitive communities inhabiting all the terrestrial biomes of the planet. Through the analysis of long-term time-series of abundance, we characterize the interaction network and stability properties of each community, and relate these ecological properties to a suite of eco-evolutionary traits, such as the average longevity or metabolic rates of interacting species. Interestingly, species diversity stand out as the main driver of coexistence and stability: diversity alone accounts for most of the global variation in network connectance, dynamic stability and temporal niche segregation, while life-history correlates seem to play a secondary role. This suggests a larger impact of ecological rules relative to evolutionary constrains in the assembly of natural competitive communities.

S1.S6.P.3

No effects of ectoparasites on the foraging behaviour of an Antarctic penguin

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The tick *Ixodes uriae* has a circumpolar distribution and can be found parasitizing seabirds feeding on their blood. Tick effects on the hosts have been reported including delay in chick growth and adult and chick mortality, although some studies have found no effects, for instance in haematocrit, body mass or adult survival. The presence and distribution of ticks in Antarctica have been recently reported being widely present along the Antarctic Peninsula in the three species of pygoscelis penguins. Presence of ticks affects penguins by reducing survival, transmitting blood parasites (i.e. *Babesia* sp.), diseases (i.e. *Borrelia burdogferi* s.l.), increasing the immune response and the oxidative stress. In general, the effects of ticks on the performance capability of the hosts have been little studied and have never been tested in penguins. Considering the differences found in the density of ticks in a chinstrap penguin rookery, we compare whether this ectoparasite has some effect on the performance at sea during their foraging trips. Foraging behaviour data were obtained by means of GPS and TDR (timedepth recorded) devices attached during five days on the penguins. The studied variables were: Mean duration of the foraging trip, mean foraging trip distance, maximum trip distance, mean number of dives, mean total time diving, mean dive duration and maximum depth. Our results showed no significant differences in any of the considered variables between individuals living in places with different tick density and then no effects of ticks on the foraging behaviour of chinstrap penguins can be concluded.

S1.S6.P.4

Evolutionary transitions of stylar polymorphism in *Narcissus* L. (Amaryllidaceae).

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Studies on evolution of stylar polymorphism, including heterostyly and stylar dimorphism, in *Narcissus* have inferred that these traits arose multiple times along the phylogeny following a particular sequence. Apparently, a particular floral morphology played an important role promoting evolution of stylar polymorphism whereas selfincompatibility did not. Reversions to sexual monomorphism are frequent both among species and populations, which provide insight on the ecological and evolutionary drivers for maintenance of style monomorphism through negative frequency dependent selection. In this work, we used a monophyletic Mediterranean clade of Amaryllidaceae to review these statements and to discuss why stylar polymorphisms arose only in the genus *Narcissus* within this clade. We reconstructed a robust phylogeny of the clade using plastid and nuclear sequences. We determined the stylar condition (polymorphism and kind of herkogamy in monomorphic species), the incompatibility system and floral morphology of each species, and then we performed ancestral reconstruction and correlated evolution analyses to study the evolutionary transitions of these traits. Stylar polymorphism probably arose at least four times along the phylogeny of the group, being approach herkogamy the ancestral condition, followed by the stylar dimorphism and finally heterostyly. Long and narrow tubular corollas were associated with the occurrence of stylar polymorphism while self-incompatibility did not. Reversions to stylar monomorphism appeared at least in seven species presenting either approach or non-herkogamous monomorphism, and might be associated with a transition to selfing, the loss of the pollinators that promote disassortative mating, or the loss of the allele that determine the short style during the hybridization process.

S1.S6.P.5

Molecular analysis reveals high connectivity between Atlantic and Mediterranean populations of the spotted skate through the Strait of Gibraltar

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The spatial distribution of genetic diversity in marine environments is mainly influenced by barriers to population dispersal. The Strait of Gibraltar has been identified as a barrier to gene flow for many marine species, although some studies have also shown that it is not such a barrier for others. Assessing connectivity between Mediterranean and Atlantic populations may be useful for species assessment and management as it indicates the degree of self-dependence of populations in one or another area. This may be particularly important in the case of highly vulnerable species such as elasmobranchs. Here, we use molecular analyses to assess the genetic diversity and connectivity of the spotted skate *Raja montagui*, a North-East Atlantic and Mediterranean benthic species mainly distributed at depths between 100-500 m, in two adjacent areas, one located westwards (Gulf of Cádiz, Atlantic Ocean) and the other eastwards (western Mediterranean) of the Strait of Gibraltar. To do so, we analyzed the sequences of two mitochondrial fragments, dehydrogenase subunit 2 and cytochrome b, from samples collected during the ARSA and MEDITS scientific surveys carried out in each area, respectively. Our results showed low genetic diversity in the two mitochondrial fragments both in the Gulf of Cádiz and in the Mediterranean Spanish coasts. On the other hand, population analyses for both mitochondrial fragments indicated absence of population differentiation, and hence, high connectivity between the

Atlantic and Mediterranean. These results suggest that the Strait of Gibraltar does not act as a barrier to gene flow for the spotted skate.

S1.S6.P.6

Tolerance to Zinc in native *Spartina maritima*, invasive *S. densiflora* and their F1 reciprocal hybrids

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Hybridization is a frequent process in plants that leads to relevant evolutionary and ecological consequences. The novel genotypes obtained by hybridization can produce transgressive phenotypes outside the ranges of variability of parental species due to heterosis or hybrid vigor. Moreover, polyploidization may also drive to important changes in the expression of different plants traits. Reciprocal F1 transgressive sterile hybrids with different chromosome numbers (2n = ca. 65 and ca. 95) derived from crosses between the native European *Spartina maritima* (2n = 6x = 60) and the invasive South American *Spartina densiflora* Brongn. (2n = 7x = 70) are colonizing salt marshes on the Gulf of Cadiz (Southwest Iberian Peninsula). These cordgrasses grow on polluted sediments with metals in the Odiel Marshes. On the other hand, they could be used as biotools for phytoremediation of waters and sediments polluted with metals. Our aim was to analyze the tolerance of *S. maritima*, *S. densiflora* and their hybrids to Zinc. With this aim, we designed a glasshouse experiment in which the four *Spartina* taxa were exposed to four Zinc concentrations (0.04 (control), 12, 60 and 130 mM Zinc). Morphological, ecophysiological and biochemical plant traits and plant growth were recorded. We hypothesized that both hybrids would show higher Zinc tolerance than their parental species due to transgressive traits related to hybridization and polyploidization. Our results showed that stress level increased for every taxon at higher Zinc concentrations. Each *Spartina* hybrid behaved similarly to its maternal species.

S1.S6.P.7

The immune challenge of mating effort: steroid hormone 2 profile, dark ventral patch and parasite burden in relation to intrasexual competition in male Iberian red deer

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Testosterone secretion may regulate reproductive effort and the development of sexual traits, but it may also involve costs at the immunological and metabolic levels. However, the evidence for this trade-off in wild populations is scarce. Similarly, cortisol has also an important role in mediating reproductive and immune functions. In this study, we analysed whether endoparasite burden relates to hormonal levels (faecal testosterone and cortisol metabolites) and/or morphological sexual traits (size of the dark ventral patch, a trait that indicates reproductive effort in males) in male Iberian red deer (*Cervus elaphus hispanicus*). For this purpose, we sampled male red deer harvested during hunting actions in two types of populations in southwestern Spain that differed in structure affecting the level of male-male competition for mates. We used coprological analyses to estimate the parasite burden mainly of gastrointestinal and bronchopulmonary nematodes and of protozoa, and assessed testosterone and cortisol metabolite levels from fecal pellets. We found a positive relationship of parasite burden with both testosterone and the size of the dark ventral patch, but these relationships depended on the intensity of male-male competition in the population, being only found under the high-competition level. These results are discussed under the hypothesis of the handicap of the immunocompetence of testosterone, suggesting a cost at the immunological level, and, therefore, higher susceptibility to parasite infection of males who make a greater reproductive effort. However, this effect seems to be modulated by the social environment (male-male competition) that would lead to different optima in testosterone production and sexual trait development.

S1.S6.P.8

Polyploidy mediates divergence in floral scents and a distinct perception by diurnal and nocturnal pollinators

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Polyploidization is arguably the most extensive process in plant evolution. In addition, the interactions of plants with their pollinators are thought to be a driving force in the evolution of angiosperms. However, the connection between pollination and polyploidy has received so little direct attention. The divergence in the pollinator spectrum as a result of variations in floral-volatile emission is well known in some angiosperm groups, but have never related to changes in the ploidy level. The Iberian endemic carnation *Dianthus broteri* Boiss. & Reuter is an ideal plant system to study this issue since comprises the most extensive ploidy series into the genus with diploid (2n=2x), tetraploid (2n=4x), hexaploid (2n=6x) and dodecaploid (2n=12x) monocytotypic populations. In order to investigate the differences in Volatile Organic Compounds (VOCs), we sampled floral scent from all cytotypes of *D. broteri* using the headspace collection method and the samples were analyzed via GC-MS (gas chromatography coupled to mass spectrometry). Once the analysis revealed that it exists qualitative and quantitative differences in the VOCs emission among cytotypes, we carried out GC-EAD (gas chromatography coupled to electroantenographic detection) analyses to test if the different VOCs from the *D. broteri* cytotypes elicit different responses in three widelydistributed generalist pollinators (*Macroglossum stellatarum*, *Autographa gamma* and *Apis mellifera*). Overall, our results support the hypothesis that changes in VOCs release as a result of chromosome doubling could drive the evolutionary process in the D. broteri complex affecting the pollinators dynamics.

S1.S6.P.9

Dietary carotenoid supplementation facilitates egg laying in a wild passerine

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During egg laying, female birds face a trade-off between self-maintenance and investment into current reproduction. Providing eggs with resources is energetically demanding, since in most species females lay one egg per day. However, the costs of egg laying not only relate to energetic requirements, but also depend on the availability of specific resources that are vital for egg production and embryonic development. One of these compounds is carotenoids, pigments with antioxidant properties and immunostimulatory functions, which are crucial during embryonic development. In this study, we explore how carotenoid availability alleviates this trade-off and facilitates egg laying in the blue tit. Blue tit females lay one egg per day and have the largest clutch size of all European passerines. We performed a lutein supplementation experiment, and measured potential consequences for egg laying capacity and egg quality. We found that lutein-supplemented females had less laying interruptions and thus completed their clutch faster than control females. No effects of treatment were found on the onset of egg laying or clutch size. Experimentally enhanced carotenoid availability did not elevate yolk carotenoid levels or egg mass, but negatively affected eggshell thickness. Our results provide hence evidence on the limiting role of carotenoids during egg laying, However, the benefits of laying faster following lutein supplementation were counterbalanced by a lower accumulation of calcium in the eggshell. Thus, even though single components may constrain egg laying, it is the combined availability of a range of different resources which ultimately determines egg quality and thus embryonic development.

S1.S6.P.10

Thermal environment as a key factor modulating sexual selection

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The question why sexual selection varies so much across taxa is a challenge in evolutionary biology. It has long been long known that ecological factors are crucial to this respect, but studies have so far almost completely neglected the role of temperature, a critical abiotic ecological factor impacting individuals and populations at a global taxonomic scale. Here, we test the general prediction that temperature modulates sexual selection by conducting a meta-analysis of available studies experimentally manipulating temperature and reporting effects on the variance of male/female fitness components and/or traits under sexual selection; as a proxy for the opportunity for sexual selection. Our results show that temperature can have a large net impact on sexual selection. In addition, we present empirical data on an overlooked pathway by which temperature can affect the strength of sexual selection: through its effect on chemical communication. We show that, in *Drosophila melanogaster*, chemically-mediated sexual interactions can be affected by temperature, therefore potentially modulating the strength, form and outcome of sexual selection in this species.

S1.S6.P.11

Is hatching asynchrony an effective defence mechanism to ectoparasitism in altricial birds?: A test of the Tasty Chick Hypothesis in blue tits

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Several ectoparasites, such as fleas and blowflies, parasitize nestling birds with detrimental effects on them. To combat ectoparasites and minimize fitness loss, birds have developed several defence mechanisms. The Tasty Chick Hypothesis (TCH) suggests that hatching asynchrony could be a defence against ectoparasites, given that ectoparasites tend to aggregate on the nestling with the poorest body condition, typically the latest hatched chick. In this way, hatching asynchrony would be adaptive by minimizing the impact of ectoparasites on core nestlings. Here, we tested the TCH in a population of blue tits (*Cyanistes caeruleus*). We determined the presence of fleas and blowflies in nests, as well as the relative concentration of leukocytes and the T lymphocyte-mediated response to phytohaemagglutinin in senior and junior nestlings in each brood. Our results support the TCH since the presence of fleas was detrimental for junior blue tit nestlings –by reducing their body mass– while had no effect on senior nestlings. Moreover, the number of leukocytes per 10,000 erythrocytes was higher in junior than in senior nestlings, indicating that the immune system of junior nestlings was more active. Blowfly presence or abundance did not affect junior more than senior nestlings. The response to phytohaemagglutinin did not differ between senior and junior nestlings. Therefore, we conclude that, in the blue tit, junior nestlings are more affected by fleas than senior nestlings, which gives support to the TCH.

S1.S6.P.12

Life on the border: population differentiation of forest birds in the Southern Palearctic

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The understanding of population differentiation in a given geographical environment usually requires integration of varied information about the patterns and processes underlying the internal diversification of species. As a model case of this, we are studying the extent of population differentiation of forest birds along the IberianMaghreb gradient with a manifold approach involving genomic, morphometric, behavioral and ecological niche variation aspects. Both the Iberian Peninsula and the Maghreb occur in the southwestern corner of the Palearctic, an area where organisms linked to this biogeographical realm reduce their populations until disappearing in the Sahara. We are testing the barrier effect of the Strait of Gibraltar considering, in addition, the potential effect of some environmental gradients on population differentiation. The forest birds under scope are all distributed in areas characterized by their low or high seasonality, and where their populations tend to be either sedentary or migratory, respectively. Preliminary results from morphometrics for one of the bird species under study suggest that morphological structure is related to seasonality (migration) and not with the isolation produced by the Strait of Gibraltar. If confirmed by our ongoing additional analyses, this would highlight the importance of environmental gradient and seasonality responses in convergent population differentiation. Beyond shedding light on the processes involved in the diversification of Iberian and Maghreb populations of forest birds, from a conservationist perspective, we seek the identification of phylogenetic distinct lineages of forest birds that struggle in this southern border of the Palearctic.

S1.S6.P.13

The role of species interactions in eco-evolutionary dynamics

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Understanding interacting communities has been a long-standing question in ecology. Recently, incorporating evolution into these studies has developed into the field of ecoevolutionary dynamics. It states that if ecology and evolution occur at the same time scale, they can generate responses that are rapid enough to feedback and alter each other. Here, we aim to disentangle how different types and numbers of species interactions can alter eco-evolutionary dynamics of a community. To do so, I am working with a microbial system composed of three freshwater species that interact differently with each other: the unicellular algae *Chlorella variabilis*, its lytic chlorovirus PBCV-1 and its symbiotic ciliate *Paramecium bursaria*. Microcosm experiments that combined one, two or the three species were run for over 90 generations in the laboratory. Sampling was undertaken to disentangle the effects of community composition on population dynamics, trait evolution, species coevolution and eco-evolutionary dynamics. Based on what it is already known about this system, I am especially keen in finding out if the algae-virus interaction follows the same evolutionary arms race dynamics of resistance and counter-adaptation, in this case when the ciliate is present in the community.

S1.S6.P.14

Plasticity evolutionary potential under environmental variation in a population of pied flycatchers, *Ficedula hypoleuca*

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One of the major goals in evolutionary biology is to understand how the interplay between natural selection and genetic variation results in local adaptation. However, microevolutionary responses to selection for advanced laying date in birds are controversial despite a consistent directional selection on early laying date. An alternative mechanism that allows local adaptation without genetic change is phenotypic plasticity. From an evolutionary perspective, phenotypic plasticity can evolve under the presence of genotype-by-environment interaction. In a long-term study in Spain (1987-2016) of a monitored wild population of pied flycatchers (*Ficedula hypoleuca*), we took advantage of the social pedigree information available to use “animal models” in order to explore the genetic basis of phenotypic plasticity and microevolution of laying date. Analyses fund a genotype-by-environment and an individual-by-environment interaction, considering the two most important climatic factors that explain selection on laying date in our population: variation of temperature in spring and mean North Atlantic Oscillation in winter. These results are indicative of the genetic basis of variation in plasticity and of the ability of phenotypic plasticity to be heritable, since our results provide little support for genetic shifts (microevolution). Our results support the notion that more plastic genotypes and individual are favored in our population encountering stochastic environmental conditions, Between-individual variation contribute to the plastic responses at population-level and the evolutionary potential of the phenotypic plasticity suggest a mechanism to promote local adaptation in a population exposed to variable climatic conditions.

S1.S6.P.15

Temperature modulates female harm in wild populations of *Drosophila melanogaster*

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Sexual conflict, the divergence in male and female evolutionary interest over reproduction, is an important determinant of population viability and evolvability. However, the causes why this process varies so much in strength form and outcomes across taxa remain unclear, particularly in relation to its ecological context. In addition, most available studies in *Drosophila* have been conducted in lab populations, questioning the degree to which current knowledge reflects the true operation of sexual conflict in nature. Here, we explore whether temperature modulates sexual conflict in wild/lab *Drosophila melanogaster* populations, and examine underlying behavioural mechanisms. In order to do this, we measured the impact of sexual conflict on female fitness by studying females in a high (i.e. 3 males competing over one female) vs. low (i.e. one male and one female) sexual conflict context, at three different thermal environments: cold (20-21ºC), moderate (24-25ºC) and hot (28-29ºC). We then conducted a series of bioassays to disentangle the effects of temperature on pre- and post-copulatory fitness components. Our results show that temperature can drastically reduce male harm to females via phenotypically plastic responses, with a significant impact on population productivity.

S1.S6.P.16

Niche divergence and limits to expansion in the high polyploid *Dianthus broteri* complex

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Niche evolution in plant polyploids remains controversial and evidence for alternative patterns has been reported. Using the autopolyploid *Dianthus broteri* complex (2x, 4x, 6x and 12x) as a model, we aimed to integrate three scenarios, competitive exclusion, recurrent origins of cytotypes and niche filling, into a single framework of polyploid niche evolution. We hypothesized that high polyploids would tend to evolve towards extreme niches when low ploidy cytotypes have nearly filled the niche space. We used several ecoinformatics and phylogenetic comparative analyses to quantify differences in the ecological niche of each cytotype and to evaluate alternative models of niche evolution. Each cytotype in this complex occupied a distinct ecological niche. The distributions were mainly constrained by soil characteristics, temperature and drought stress imposed by the

Mediterranean climate. Tetraploids had the highest niche breadth and overlap due to their multiple origins, while the higher ploidy cytotypes were found in different, restricted, non-overlapping niches. Niche evolution analyses suggested a scenario with one niche optimum for each ploidy, including the two independent tetraploid lineages. Our results suggest that the fate of nascent polyploids could not be predicted without accounting for phylogenetic relatedness, recurrent origins or the niche occupied by ancestors.

S1.S6.P.17

MHC class II diversity in populations of a neotropical cichlid adaptive radiation

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Morphological and physiological adaptation to divergent environments is a key feature of adaptive radiations. The Midas cichlid species complex (*Amphilophus* spp.), distributed in the Nicaraguan lakes, represents an excellent example of a very recent adaptive radiation through ecological specialization. In this study, we used the Midas cichlid complex to explore whether host-parasite interactions might fuel speciation and adaptive radiation. We characterized the immune response of several Midas cichlid populations by measuring the variability of the Major Histocompatibility Complex (MHC) genes, a key component of the adaptive immune system for its role against parasite infections. We found extensive allele variation at the MHC in the Midas cichlid, with some core alleles present in all individuals, but also a lake specific component and species specific signatures. Isolated crater lakes were the most distinct according to their allele repertoires. We have evidence of lake specific parasite assemblages, which is in agreement with the MHC variation recovered. Therefore, our results suggest that host-parasite interactions have the potential for shaping divergence in the Midas cichlid populations in the Nicaraguan lakes.

S1.S6.P.18

Genetic and environmental components of the colour of mouth, flanges and skin in spotless starling (*Sturnus unicolor*)

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The begging display of avian nestlings includes visual and acoustical signals of their phenotypic condition and needs that parents use to, for instance, decide feeding effort and the individual nestlings to feed. Flamboyant colouration of mouths and flanges, as well as the UV colouration of nestlings' skin, are pivotal characters in parent-offspring communication. Coloration of begging related traits should therefore be phenotypically plastic. However, these traits vary interspecifically in association with species-specific parental visual characteristics and light conditions of nests and, thus, should also have a genetic component allowing its evolution. As far as we know, the genetic component of begging related trait has never been quantified. Here, do so in a spotless starling (*Sturnus unicolor*) population by comparing phenotypes of 10 days old nestlings that were cross-fostered among 15 pairs of nests at the time of hatching. We measured the colour of the mouth, flanges and skin with a spectrophotometer and estimated different chromatic and achromatic colour components, either, considering or not characteristics of the starling colour vision. Results confirm a strong environmental component for most colours and measured traits of nestlings, while evidence of genetic components appeared mainly for coloration of nestling traits that were known to reflect its phenotypic quality (ultraviolet colour of skin, and yellow-red colouration of mouths and/or flanges). Interestingly, we also detected a genetic component of visual contrasts that considered parental visual characteristics, which further suggest that the evolution of these colourations is driven by parents and parental favouritism toward nestlings of particular colouration.

S1.S6.P.19

Bacterial environment of nest cavities influences probability of ectoparasitism of nestling hoopoes

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Parasitism is one of the major selective forces determining the evolution of organisms, while myriads of microorganisms live in close contact with hosts. Parasites might use clues

from symbiotic-bacterial metabolism to detect their hosts and, thus, parasitism selection pressure would be partially mediated by bacterial symbionts. In this study, we intend to test this idea by experimental manipulation of the bacterial community of holes used by European hoopoes (*Upupa epops*) for breeding. The experiment consisted on filling new installed nest-boxes with old nest materials collected from next-boxes where hoopoes breed the previous year. In experimental, but not in control nest boxes, old nest material was previously autoclaved to eliminate the microorganisms from the experimental nest materials. In accordance with the hypothesis that ectoparasites used clues from nest bacterial environment to detect hoopoe nests, we found that (1) intensity of parasitism by *Carnus* flies of nestling was higher in control than in experimental nest-boxes, and (2) that nest bacterial load and parasitism intensity were positively related. Moreover, in accordance with the assumption of our experimental approach, (3) bacteria loads of nest material, soon after hatching, was higher in control than in experimental nest-boxes. All these results therefore suggest that microorganisms play an important role determining the strength of ectoparasitism selection pressure suffered by their host and, thus, on evolutionary outcomes of parasite-host interactions.

S1.S6.P.20

Eggshell biliverdin as an antioxidant maternal effect in birds

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The selective pressures that drive the evolution of avian eggshell pigmentation have long been debated. However, despite efforts in the last decades to improve our current understanding, the adaptive function of blue-green biliverdin-based pigmentation remains unclear. In this communication, I propose that biliverdin pigment could potentially play an antioxidant role in the eggshell due to the molecule's well-known abilities to scavenge free radical species and to reduce mutation. Hitherto, this possibility remains untested. I provide arguments in favour of a direct antioxidant role of eggshell biliverdin and discuss

the main predictions of this hypothesis. I also propose future directions of research to test the idea at the intra- and inter-specific level.

S1.S6.P.21

Where primnoids come from?: historical biogeography of Primnoidae (Cnidaria: Octocorallia)

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Primnoids (Cnidaria: Octocorallia) have worldwide distribution, being common at slope and upper abyssal depths. The ancestral area of the family, as well as the periods of subsequent expansions to the surrounding areas are not fully understood. Competing hypotheses suggesting either an Antarctic or Pacific ancestral area for Primnoidae. Using a molecular calibrated phylogeny, and historical biogeographic methods we test previous hypothesis about the biogeographic origin for the Primnoidae octocoral. The time of divergence estimates of Primnoidae from other octocorals was in 149 Ma (Upper Jurassic). Ancestral range estimations under this best fitting model indicated the Pacific Ocean showed as the most probable ancestral area for primnoids. Bayesian stocastical analyses showed that dispersal events, particularly range expansions, are the principal mode by which members of the family have spread beyond the Pacific Ocean, having a secondary expansion core at the Southern Ocean during the Cretaceous (90 Ma). Primnoids joint to an increasing number of Antarctic marine invertebrates with a preAntarctic Circumpolar Current (ACC) origin. Our analysis demonstrate that Southern and Pacific Oceans could acts as dispersal sources, while the Atlantic and Indian Ocean are rather dispersal sinks. Both Pacific and Southern Oceans have a rather low and net symmetrical dispersal history thought time. Only few dispersal occurs after the established of the Eocene-Oligocene ACC. Although this current constitutes a semipermeable barrier to deep-sea octocorals, in general their onset seems to play a minor role in the evolutionary history of the primnoids, and particularly those belonging to the sub-Antarctic clade.

S1.S6.P.22

Negative frequency-dependent sexual selection maintains a colour polymorphism in the marine snail *Littorina fabalis*

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Previous studies on shell colour (Dark *versus* Light colours) in the marine snail *Littorina fabalis* have shown the polymorphism could be maintained by negative assortative mating and negative frequency-dependent sexual selection via mate choice. In order to confirm this rare mechanism, we studied a new population of *L. fabalis* from Galicia using the same experimental design and methodology as in previous studies. Assortative mating was high and negative (-0.24), similarly to the results obtained in another Galician locality (-0.29). The estimates of sexual selection also corroborated previous estimations, favouring Dark colours in males and showing a frequency-dependent sexual selection in females. Interestingly, when the analysis was carried out for each colour independently (Olive, Yellow, Brown), the frequency-dependent sexual selection was exclusively observed between Yellow and Brown, suggesting that Olive was not involved in the mechanism responsible. This mechanism represents one of the few known cases in which balancing sexual selection via mate choice is responsible for such stable polymorphism.

S1.S6.P.23

Geographic variation in floral traits in two *Linum* species in a contact zone

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Floral trait variation is an ubiquitous characteristic of angiosperms and has played an important role in their evolution. For example, some traits like the spatial separation of sexual organs can affect profoundly the mating patterns and the genetic diversity, by acting directly on the rates of outcrossing and selfing. Others, such as the heterostyly, can promote partial or complete reproductive isolation within populations by increasing non-random mating between complementary floral morphs. In this scenario, a detailed study of both traits is crucial to understand the interaction between flower morphology, mating system, and reproductive barriers, especially in areas where populations of species with different morphology and mating patterns coexist. *Linum suffruticosum* is a distylous SI species that inhabit with *L. tenuifolium*, a SC monomorphic species, a 500 km contact zone. The aim of the study was to characterize the flower variation in both species. During the summer of 2016, 20-30 flowers were collected in allopatric and sympatric populations of the two species and preserved in ethanol 70%. Flowers were photographed and measured with image processing software to estimate intra and interspecific variation. Our results showed significant differences in flower traits between species and populations. The effect of the flower morphology in the mating system and reproductive barriers are discussed.

S1.S6.P.24

Eco-evolutionary effects or ionizing radiation in Chernobyl amphibians

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Ionizing radiation can damage DNA and other organic molecules. As a consequence of human activity, vast amounts of radiation have been released to the environment, as in the accidents in the nuclear power plants of Chernobyl (1986) and Fukushima (2011). Although the negative impact of the acute exposure to radiation is clear, there is still no scientific consensus about the long-term effects of the chronic low-dose radiation for living organisms. Here, we examine the eco-evolutionary responses to the chronic exposure to ionizing radiation in amphibians living inside Chernobyl Exclusion Zone (Ukraine). Using a gradient of radioactive contamination, we analyze the effects of radiation on the life-history, physiology and genomics of Chernobyl frogs. Due to the high mutagenic potential of ionizing radiation, we also examine putative adaptive responses that may allow organisms to persist in highly contaminated environments.

S1.S6.P.25

Sociosexual Networks: sexual selection and population spatial structure from a network perspective

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Currently, network analysis is on the rise in the study of ecology and evolution. In this contribution we reflect on how Network Theory can help us to understand the evolutionary causes and consequences of population spatial structure and sexual selection. Researchers are increasingly studying sexual networks, where relations between individuals are established by reproductive interest. However, the integration between the fields of social evolution and sexual selection within a network perspective has been rarely accomplished. This gap of knowledge is even more evident if we consider the absence of theoretical and empirical work investigating the causes and consequences of sexual conflict from a network analysis perspective. Our current study focuses on the effects of sexual selection and population spatial structure upon sexual network structure using experimental evolution in a seed beetle (*Callosobruchus maculatus*), a system characterised by intense sexual conflict. The beetles have been cultured under a binary gradient of sexual selection (yes or no) and population subdivision (yes or no) and maintained during more than 75 generations. Using this material, we are determining whether selection history in regards to the presence/absence of sexual selection and the presence/absence of population subdivision determine sexual network architectures.

S1.S6.P.26

Reconstructing the evolution of the somatomotor pallial areas: evidences in teleost fish.

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Recent neurobiological evidence shows that, despite salient cytoarchitectonic differences, a structure homologue to the cerebral cortex of mammals is present in the teleost telencephalon. One of the most distinctive characteristics of the cortex is its organization in discrete unimodal sensory areas and in separate motor areas. Nevertheless, important controversies exist on the evolutionary origin of the cortical mechanisms for motor control. Some hypotheses argue that the somatomotor functions of the somatosensorial cortex is a mammalian recent acquisition being absent in marsupials, while others postulate that a somatomotor pallium is an ancient character in non-mammalian vertebrates. We conducted a series of brain lesion, optical recording and electrical microstimulation mapping experiments to evaluate if Dm4 area of the goldfish telencephalon, previously described as containing a primary somatosensory area, is also involved in motor control. Goldfish were trained to acquire a complex sequence of goal-directed movements, achievement that require variable postural adjustments and fine maneuvers of the fins and continuous coordination of axial musculature, fins and mouth. We also analyzed the responses evoked by electrical stimulation of Dm4 in restrained and freely moving fish. The absence of motor impairments in the execution of the learned goal-directed motor sequence following the ablation of the somatosensorial area and the high current intensity thresholds for evoking motor responses suggest that the teleost pallium lacks a somatomotor area. These results have important implications for the question of the evolution of the descendant pallial mechanisms of motor control in vertebrates as they suggest that the ancestral condition could be the absence of a somatomor pallial area.

S1.S6.P.27

Environmental DNA: a novel method to improve knowledge of the diversity of chondrichthyans in Mediterranean seamounts

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Seamounts are underwater elevations of continental margins, commonly located in remote areas. These structures harbor high levels of biodiversity and, because of their isolated location in deep waters, they are refuge sites for marine life including vulnerable species such as chondrichthyans (sharks, rays and chimeras). Despite its ecological importance, the scientific knowledge about seamounts is marked by large gaps. In the Mallorca Channel (Balearic Islands), three seamounts are located: Ses Olives, Ausias March and Emile Baudot. While the first two are of continental origin, the Emile Baudot is of volcanic origin. Here, we assessed the potential of environmental DNA metabarcoding (eDNA) – a novel method based on the retrieval of genetic material naturally released by organisms in their environments – in providing an accurate estimate of diversity of chondrichthyan species on the Emile Baudot seamount. To do so, seawater and sediment samples were collected during a research survey, carried out in the Mallorca Channel during 2018 within the LIFE IP INTEMARES project. Samples of seawater were collected in different bathymetric strata, while the sediment was obtained from the ocean bottom. Chondrichthyan-specific primers of the hypervariable region of the 12S rRNA were used and the samples were sequenced in a single multiplexed Illumina MiSeq run. A total number of 4,754,150 reads was obtained from pooled amplicon libraries, of which 95% were obtained from seawater samples. These reads were pooled and clustered into Molecular Operational Taxonomic Units. Results from eDNA approaches have provided valuable insights about the chondrichthyans diversity in a poorly studied ecosystem.

S1.S6.P.28

Bull's eye patterns in *Anemone palmata* and their relation to pollinator attraction

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In animal-pollinated flowers, colour patterns are important for pollinator attraction. Some species have flowers with a bull's eye pattern, that is, a UV-absorbing central perianth area that contrasts with a UV-reflecting outer perianth area. UV floral patterns show intraspecific variation and mediate floral attractiveness in insect pollination. We tested the effect of bull's eye size on pollinator attraction to flowers of *Anemone palmata*, a species visited mainly by Hymenoptera and Diptera. Our study was carried out in two wild populations growing under pine tree forests in Puebla del Río (Sevilla) and Punta Umbría (Huelva). We characterized the bull's eye relative size in 31 individual per population and assessed pollen grains deposition on their stigmas. To ascertain pollinator response to bull's eye, we manipulated perianth UV-reflecting area so that the whole perianth would be either reflecting or non-reflecting; then, we recorded pollinator attendance on both manipulated and control flowers. Additionally, we assessed how bull's eye pattern is perceived under the visual systems of *Apis mellifera* (bee), *Musca domestica* (fly) and *Eristalis tenax* (hoverfly).

Pollinator behaviour was similar in both types of manipulated flowers, as well as in control flowers. However, we found a significant relationship between bull's eye relative size and pollen grains deposited on stigmas. We found that bees, flies and hoverflies can perceive bull's eyes patterns of *A. palmata*, thus they could use those patterns as cues for foraging. Our study strongly suggests that UV-colour patterns, invisible to human eye, are important in attracting pollinators, thus, enhancing pollen transfer.

S1.S6.P.29

Phenotypic plasticity of the genus *Alytes* sp. under different moisture conditions at metamorphic stage

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Environmental variables are fundamental in niche selection of species. As ectotherm organisms, amphibian physiology is particularly affected by temperature and humidity. In this work, we wanted to determine how environmental moisture is affecting the growth rate, and in consequence fitness, in recent metamorphosed individuals of the five current species of midwife toads (*Alytes* spp.). We evaluated the reactions norms of individuals (N= 30-40/ species) *of A. cisternasii, A. dickhilleni, A. maurus, A. muletensis and A. obstetricans*, as phenotypic response under two experimental moisture conditions: "dry" and "humid". The experiment was carried out during nine weeks, at the same room temperature (24º C), and ad libitum feeding. Our results show marked differences among moisture conditions, being for four of the species significantly larger and heavier the individuals raised in "humid" conditions. Besides, there was a phylogenetic signal in this response, with the most external species, the Iberian midwife toad (*Alytes cisternasii*) growing similarly at both treatments, and thus, showing an apparent adaptation to drier conditions.

S1.S6.P.30

A study of colour patterns leading to mimicry in bumblebees

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Bumblebees represent one of the best examples of Müllerian mimicry, the convergence of colour patterns among species that serve as warning signal to predators. The aim of this study is to identify the colorimetric variables that best indicate similarities in different body parts of these insects. We examined hair colour patterns with spectroscopy analyses and evaluated measurement error (intra-individual variability), inter-individual and inter-specific variation in three cryptic species (*Bombus terrestris*, *B. magnus*, *B. lucorum*) collected in the Cantabrian Mountains (North Western Spain). We obtained 23 reflectance parameters in four different segmental sclerites (collar, scutellum, second abdominal tergite and tail) in 10 individuals per species (totalling 27600 measurements). Our results showed that these species co-occur in 40% - 57% of sampling plots, being significant the positive association between *B. lucorum* and *B. magnus*. The variables that showed lower measurement error were "Mean brightness", "Intensity", "Chroma" and "Contrast" in all segments. With respect to biological differences, a high inter-individual variation in tail and scutellum were found through all species, especially in *B. lucorum* scutellum in the more repeatable variables. Differences between species were often of similar magnitude or only a bit higher than differences within species, especially for the variables associated with brightness and hue. Our study identifies the colour parameters and body segments that best reflect colour biological variability and that may serve to quantify the amount of convergence among species in studies of Müllerian mimicry.

S1.S6.P.31 Alpine meadows: Are there unknown hybrids our there?

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The genus *Gentiana* L. exhibits a remarkable diversification in mountain ecosystems, in which plants tend to diversify more due to the formation of vacant niches and altitudinal zonation, among other factors. *Gentiana* sect. *Calathianae* encompasses several closed-related taxa mainly distributed in Europe. Some of these species (*Gentiana verna* L., *Gentiana brachyphylla* Vill., *Gentiana orbicularis* Schur, *Gentiana bavarica* L.) coexist in sympatry in some areas of the Austrian Alps and bloom simultaneously. However, within this section morphological criteria do not seem to be sufficient to deduce the phylogeny of the group and studies based on chloroplasts and nuclear markers are currently being conducted. These new approaches along with other techniques allow researchers, not only to define better the taxonomy, but also to take a closer look to essential events such as hybridization, which have not been reported in these species yet. Hybridization is one of the main evolving mechanisms in plants and due to the special conditions of the species mentioned above, we also considered the existence of hybrids when phylogenetic analysis was conducted. To carry out our study, several individuals of each species and some possible hybrids were collected and analyzed in order to obtain morphometric data, environmental information, soil samples and some material for the sequencing of two molecular markers (ITS and rpl32F/trnLUAG). Finally, all the information was combined to obtain a clearer view of the relationship that could exist between the studied species and recognize possible hybridization events among them.

S1.S6.P.32

Testing niche conservatism in a cosmopolitan invasive species

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Improve understanding of invasive species pattern is essential to enhance their management in affected regions. In this scope, niche conservatism hypothesis allows predicting areas that are susceptible to be invaded by a species and enable a better protection of the concerned regions. Despite several studies suggesting that niche conservatism is a general rule, the question seems still controversial.

In this study, niche conservatism hypothesis is tested with *Datura stramonium*, an invasive species that accomplished a driven by human migration from the region of Mexico to Europe about 500 years ago, an acceptable time for the species to have completed its fundamental climatic niche. *D. stramonium* occurrences and uncorrelated climatic variables were used to model native and invaded niches of the species with the Maxent algorithm in the Wallace interface. Niche overlap was determined with ecospat package. Niche's projections from one range to the other were realized. Our results show that the native and invaded niches are more similar than two random niches in the same ecological space. Nevertheless, the niches are not identical and the invaded niche encompasses colder climate. The results are discussed and interpreted.

SESSION S2.S7. EVOLUTIONARY GENETICS I AND II

S2.S7.P.1

Metabarcoding characterization of the fecal microbiota of two endemic lizard species from the Balearic Islands

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Podarcis lilfordi and *P. pityusensis* are two lizard species endemic to the Balearic archipelago with a non-overlapping distribution. *P. lilfordi* inhabit the Eastern Gymnesic island group (Mallorca, Menorca, Cabrera and associated islets) and *P. pityusensis* the Western Pityusic group (Ibiza, Formentera and coastal islets), where they are restricted to small, rocky islands marked by the scarcity and unpredictability of food resources. Although many molecular studies have been carried out to investigate their genetic structure and evolution, no attempt has been done to characterize their associated bacterial communities excepting a recent analysis focused in a limited portion of the distribution of the former species through the use of methodologies that implied animal sacrifice. The aim of this study is to perform an analysis of the gut microbiota of both species covering their entire range of distribution through a non-invasive method. A total of 242 fresh faecal samples were collected from 17 locations for high throughput sequencing of the V4 region of 16S rDNA. The reads could be assigned to 2463 OTUs representing 13 phyla, 32 classes, 60 orders, 106 families and 162 genera of microbiome taxa. We could identify core microbiome signatures for each *Podarcis* species. Moreover, PERMANOVA analyses yielded significant microbiome composition, differences at the levels of species ascription, geographical distribution of the samples, population size, skin pigmentation (melanic/non melanic), and the level of human perturbation of their habitats. In addition, we found a significant evolutionary correlation between the phylogeny of *P. lilfordi* and the composition of their hosted microbiota.

S2.S7.P.2

Dioecious plants - the key for understanding the evolution of sex

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Most of the flowering plants are hermaphrodites, bearing male and female reproductive organs within one flower. Dioecious species, which are occurring relatively rarely in nature, have evolved separated sexes - similarly to us, mammals. Since Darwin times, the genus *Silene* L., which possesses great variability between the types of sex determination within its species, has been widely used to investigate this phenomenon. With the help of the best-characterized model species of this genus - *Silene latifolia* Poir. - we are able to elucidate early steps in the evolution of separate sexes, due to its young sex chromosomes, which have evolved much more recently than in mammals.

Interestingly, genus *Silene* serves as a model species for the investigation of ecological aspects, such as population dynamics of invasive species, or endemics. Other dioecious species, however, are of great interest as well and serve as models for the sex chromosome evolution research - such as *Cannabis sativa* L., *Humulus lupulus* L., *Rumex acetosa* L. or *Carica papaya* L. To study the genetic and chromosomal events that model the genome architecture in these species, different approaches are being used, such as the CRISPR-mediated knockout of genes responsible for the expression of certain characteristics, or use of fluorescent probes (Fluor. In Situ Hyb.) to observe the chromosomal reorganizations. By combining these techniques with phylogenetic studies, a global perspective on the evolution of the genome is achieved.

S2.S7.P.3

Patterns of selection and population structure of *Podarcis lilfordi* inferred from RadSeq

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Reduced representation genomic analyses can provide new insights into patterns of diversity within non-model species. We performed a genome scan of single nucleotide polymorphisms (SNPs) obtained with restriction site-associated DNA sequencing (RADseq) of endangered melanic and non-melanic *Podarcis lilfordi* populations found on islands and islets around the main islands of Menorca and Mallorca. Multivariate (DAPC) and admixture analyses were carried out to determine genetic structuring among P. lilfordi populations. We detected greatest divergence among the main island-groupings previously described using mtDNA (Mallorca, Menorca and Cabrera). Within these groups we identified greatest divergence in populations with smallest effective sizes. Loci (o SNPs) that were candidates for selection were detected using Bayescan and nBLAST. Some of these corresponded to sequence regions that are thought to be associated with tail regeneration: an important evolutionary trait because of its association with predation.

S2.S7.P.4

Identification of species of the Fanniidae family (*Diptera*) in the Iberian Peninsula by Barcoding

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The Fanniidae family (*Insecta*, *Diptera*) is made up of 330 species (Couri & Sousa, 2019) distributed in five genera: *Euryomma* (Stein, 1899), *Fannia* (Robineau-Desvoidy, 1830), *Piezura* (Róndani, 1866), *Australofannia* (Pont, 1977) and *Zealandofannia* (Domínguez & Pont, 2014). In the present work we focus on the most abundant genus in number of species of this family, *Fannia*, which contains about 300 species (Couri & Sousa, 2019). This genus is native to South America but currently has a cosmopolitan distribution, probably due to cattle transport (Grzywacz & Prado, 2012). *Fannia* species are morphologically very similar to each other (Grzywacz & Prado, 2012) and, therefore, specific identification methods are needed, such as the "Barcoding" molecular analysis. This genetic analysis is based on a small fragment of mitochondrial DNA, subunit 1 of the cytochrome c oxidase gene (cox1) which contains 658 pb. This region is easy to amplify and sequence, becoming a quick and simple technique (Hebert et al., 2003).

The hypothesis to be tested indicates the fanniids of the sampling that carried out in the Iberian Peninsula (2012-2015) includes different mitochondrial lineages. It is very possible this family has been introduced in Spain through Portugal, since the Portugueses haplotypes are closer to the external group. The results obtained are discussed in the context of the available information on phylogenetic relationships of the genus based on various characters.

S2.S7.P.5

RNA-based phylogenomics, subgenome-detection algorithms and cross-bracing approaches reveal the ancestry of homeologous subgenomes and their hybridization ages in grass *Brachypodium* allopolyploids

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Untapping the evolution of allopolyploids is a major threat for plants missing diploid progenitors. We address this challenge in *Brachypodium* through the reconstruction of its transcriptome-based phylogeny and the inference of the hybridization events that originated six allopolyploid species. We analyse cytogenetic and RNA-seq data from 12 diploid and polyploid *Brachypodium* accessions implementing two novel phylogenomic strategies to uncover the homeologous subgenomes of the allopolyploids. We use crossbracing methods to estimate the hybridization events involved in the origin of each allopolyploid. *B. mexicanum* emerges as the oldest allotetraploid species (7.5 Ma), having ancestral (A) and B. stacei-like (B) subgenomes. *B. hybridum* (1.61 Ma) is composed of B and B. distachyon-type (D) subgenomes. *B. boissieri* and *B. retusum* show three (A, B, E) (6.91-4.39 Ma) and two (A, E-core) (6.53 Ma) ancestral, intermediate and recent subgenomes. *B .rupestre* (2.81 Ma) and *B. phoenicoides* (2.9-2.61 Ma) show two (E, H) relatively recent subgenomes. Chromosome-base numbers x=10, x=5, and x=9 are respectively inferred for the A and B, the E and D, and the H subgenomes. *B. hybridum* is the only polyploid with known extant progenitor species. The A and E subgenomes have been only found in allopolyploid species to date. Our approach could be used to identify ghost subgenomes in allopolyploid plants of unknown diploid and lower-ploidy ancestors.

S2.S7.P.6

How combining nongenetic inheritance with individual agency leads to a generalised theory of adaptive evolution

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In order to increase their ecological performance and thereby expected fitness, individuals often make adaptive changes to their traits and behaviours. When it exists, non-genetic inheritance allows these acquired adaptive changes within generations to be transmitted between generations, thereby causing a change in the population’s composition of heritable traits (i.e. non-genetic evolution). Using a novel causal path diagram, we argue in the context of the Price equation that current theory on adaptive evolution can be generalised to include the evolution of genetic and non-genetic traits (e.g. socially-transmitted traits, epigenetic marks). Most importantly, this generalised theory highlights that individuals can be drivers of evolution due to their selective actions (i.e. they are evolutionary agents), and are not only targets of natural selection. This generalised view also shows the conceptual similarities between phenotypic plasticity, adjustment of the environment (e.g. niche construction or social manipulation), and selection of the environment (e.g. of habitat, social or sexual partners). Finally, I will briefly present recent results of experiments on rapid speciation in captive Zebra finches and optogenetically-manipulated transgenic Drosophila to show how adaptive evolution can occur without the operation of natural selection.

S2.S7.P.7

Lack of genetic structure of the forensically important fly species *Calliphora vicina*, (Diptera: Calliphoridae) in the Iberian Peninsula.

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The study of Diptera in the scene of a crime provides essential information for the interpretation of evidences and for its eventual resolution. Its most known use is the calculation of the minPMI (minimum post mortem interval), but forensic entomology has other applications: cases of neglect and/or abandonment of minors and elderlies, confirming the presence of chemical substances, and even confirming the relocation of a corpse. Phylogeographic reconstruction could help to differentiate haplotypes of a specific species from a geographical area, contributing to the clarification of the possible transfer of the corpse. Besides, reconstruction of ancestral states helps to understand the actual status of the species and its biogeographic history. In this study, 464 specimens of *C. vicina* collected in Spain and Portugal between 2012 and 2015 were used. They were identified with morphological keys and the COI, 16S and ITS2 genes were sequenced. Three matrices were built in GENEIOUS and the sequences were identified with the BLAST tool. The Median Joining algorithm of the PopART program was used for the construction of phylogeographic networks. Reconstruction of ancestral states was done with RASP software. Molecular techniques corroborate the identifications made based on morphology. The phylogeographic networks show that there is no geographical structure, and that the haplotypes are shared among almost all populations. RASP analyses showed a high rate of movement among populations with colonizations crossing the Iberian Peninsula, possibly related to human activity.

S2.S7.P.8

Traditional species concepts fail in a poison frog; evidence from phylogenetic and distribution modelling in *Epipedobates boulengeri*

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Species delimitation is a complicated task in taxonomic groups with low genetic diversity and large phenotypic differences or vice versa, requiring ad hoc analyses for each clade on the phylogeny. Most of the members of *Epipedobates*, the Chocoan poison frogs, are brightly colored and secrete alkaloids as anti-predator defense. A recent phylogenetic analysis revealed very low genetic divergence among species and suggested that at least one species, *Epipedobates boulengeri*, is polyphyletic. Here we clarify the evolutionary relationships in the species complex Epipedobates boulengeri using phylogenetics, morphological analysis, and environmental modelling under the unified species concept. Three mitochondrial and three nuclear markers were sequenced for 104 individuals across 28 populations encompassing the whole range of *E. boulengeri*, from Valle de Cauca, Colombia, to Cotopaxi, Ecuador, including its type-locality (Isla Gorgona, Colombia). We confirmed that some populations of *E. boulengeri* are more closely related to other species than to putative conspecific populations. We identified possible cryptic species, indicating that species limits should be reassessed. *Epipedobates* shows rapid phenotypic diversification in its Southern groups, evidenced by their extremely low genetic diversity and wide morphologic variation. On the other hand, the Northern groups show much higher genetic diversity and lower morphologic variation, making of this genus an interesting case for delimitation of species, population genetics and diversification

processes. Our results contribute to the understanding of speciation in general and rises conservation concerns for undescribed species-level lineages within “*E. boulenger*i”, which faces high rates of habitat destruction in the Chocó regions of Ecuador and Colombia.

S2.S7.P.9

Relevance and molecular evolution of aquaporins in the colonisation of terrestrial environments by fishes

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Aquaporins (AQPs) are a family of integral membrane proteins that exchange water and small solutes and are directly related with osmoregulation processes avoiding desiccation. In this context, they played an important role in the colonisation of terrestrial environments by tetrapod ancestors via the appearance of three exclusive paralogs. Like early tetrapods, other fish groups, such as the mudskippers, mangrove killifishes, or some eels are able to expend large periods out of water, and thus represent independent cases of amphibious lifestyle evolution among vertebrates. Given the lifestyle parallelism and that aquaporins were relevant for early tetrapod terrestrialization, we are examining the relevance and molecular evolution of aquaporins in such amphibious fish groups to investigate whether similar changes in aquaporins could have possibly occurred during their respective water-to-land transitions. Such changes may occur in the form of appearance of new paralogs and/or change/selection at the sequence level. In the first round of our project, we catalogued the aquaporin repertoire in four mudskipper species, detecting signatures of positive selection in AQP10a and AQP11b. This suggests possible alteration of their molecular function (perhaps allowing permeability to new solutes) caused by changes at specific protein sequence positions, some of them located in relatively close proximity to parts of the molecule involved in pore formation and substrate selectivity. We are now expanding the molecular evolution and adaptive selection analyses of aquaporins to other fish groups (apart from mudskippers) that are also capable to live (or at least endure) terrestrial conditions.

S2.S7.P.10

Temporal changes in diversity and signals of balancing selection in Iberian lynx genomes

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Declining populations are expected to lose diversity as the consequence of genetic drift. However, functional diversity is exposed to selection forces, some types of which (i.e. balancing selection) could oppose drift and maintain diversity. Here, we analysed the consequences of population decline in functional variation in the highly endangered Iberian lynx using whole genome data from three ancient (4-2 kya) and 31 contemporary individuals of the two remnant populations, Andújar and Doñana. We characterized genomic diversity and differentiation patterns along these ancient genomes and identified regions with signatures of balancing selection, contrasting these with those observed in contemporary genomes. Preliminary results show that ancient lynx population is genetically closer to Andújar than to Doñana, as expected from their known demographic history. However, and quite unexpectedly, overall diversity of the ancient lynx population is comparable to that of the highly eroded Doñana population and lower than Andújar's. Despite this lower diversity, windows under balancing selection population are enriched for coding regions in the ancient lynx, but not in the contemporary populations, suggesting a partial erosion of balancing selection signatures in the latter. Nevertheless, windows under balancing selection show, both in the contemporary and ancient populations, enrichment for immunological related genes, and olfactory receptors, common candidates for balancing selection. Moreover, windows under balancing selection in the ancient population, maintain intermediate frequencies in the contemporary pops. Overall results suggest that balancing selection has maintained regions of high diversity in the low diversity ancient lynx and that this pattern has partially persisted in drifted contemporary populations.

S2.S7.P.11

Cockroach gut microbiota dynamics in response to a periodic antibiotic treatment

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Gut microbiota is one of the most important microbial communities associated with animals. In insects, it is known that it is involved in different features of the host metabolism, such as vitamin supply, protections against pathogens, food digestion, among others. In general, it has been found that the most predominant phyla are Bacteroidetes, Firmicutes, Spirochaetes, Proteobacteria, and Actinobacteria. Although insects harbor a gut microbiota less diverse that mammals, social insects such as termites, bees or cockroaches are the exception, exhibiting a complex and enriched one, the function of which is still under intense research, mainly in cockroaches.

It is also known that antibiotic's treatment alter the composition and function of the microbial ecosystem. In the present work, we have carried out an extensive experiment in which populations of the German cockroach *Blattella germanica* were treated periodically (three periods of ten days sparsed during one hundred days) with kanamycin during one generation. We evaluated the antibiotic effect in the microbiota composition by sequencing the 16S rRNA gene (Illumina) as well as in several components of host fitness (i.e., weight, fecundity and mortality). We found up to five different behaviors associated to different bacterial taxa throughout the time, some of which can be correlated with changes in the fitness.

S2.S7.P.12

A phylogenomic framework for the study of the role of chromosome number variation in species microevolution (*Carex* gr. *laevigata*, Cyperaceae)

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Carex is one of the most species-rich angiosperm genera and has experienced a relatively rapid diversification. The investigation of such radiation is sometimes hindered by taxonomical problems related to homoplasic morphological features, cryptic species and/or hybridization processes. It is the case of the *Carex laevigata* group (sect. *Spirostachyae*), comprised of *C. laevigata, C. binervis, C. camposii* and *C. paulo-vargasii*. This group is mainly distributed in the Western Mediterranean, with two species reaching NW Europe. Recent molecular phylogenetic studies based on nuclear and plastid DNA regions could not resolve phylogenetic relationships within the group. In order to elucidate the systematics and evolutionary processes underlying Carex gr. laevigata, we have designed a large-scale phylogeographic study. We obtained a phylogenetic tree based on RAD-seq data from more than 160 specimens of all species. We used suggested metrics to evaluate the different dataset, and retained the best matrix after the ipyrad pipeline. All species were retrieved as monophyletic, except for a *C. binervis* lineage, distributed along the British Isles and western Europe, which was placed outside of the core *C. laevigata* group. Moreover, a strikingly strong genetic structure was detected among southern populations of *C. laevigata*, while northern ones displayed weak genetic differentiation, suggesting a recent, northwards postglacial colonization. These findings would have remained unnoticed without a genome wide sequencing approach. Further studies are required to investigate whether chromosome number and bioclimatic niche are correlated in *C. laevigata* group despite correcting by geographic or genetic structure, as suggested by previous studies.

S2.S7.P.13

The role of the Almeria-Oran front in the connectivity between populations of the marine crab *Liocarcinus depurator*

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The gene flow between populations of the marine crab *Liocarcinus depurator* located at the Atlanto-Mediterranean transition depends on the intensity of different oceanographic fronts. These discontinuities are generated by the pattern of marine currents and could change over different seasons and years. In this area, the most important oceanographic discontinuities are the Gibraltar Strait (GS), the Almeria-Oran Front (AOF) and the Ibiza Chanel (IC). To monitor the gene flow variation between the crab populations, we analyzed a 527 pb fragment of COI (Cytochrome oxidase subunit I) mitochondrial gene. The following populations were studied: Cadiz, West Alboran, East Alboran, Alicante, Valencia, Ebro Delta and North Catalonia. They are located at either side of the fronts or well away from them. We studied these populations in a five year period (2014-2018). Depending on the year, GS and IC presented a significant effect which implied a reduction of the gene flow. However, the most important oceanographic barrier is the AOF, although its intensity varies depending on the year. For instance, in 2016 it was displaced to the middle of the Alboran Sea, whereas in 2017 it was strong and located in its classical described position. Finally, in 2018, although it decreased the gene flow its effect was non-significant. Likely, these variations depend on the intensity of the second anticyclonic gyre located in the West Alboran Sea.

S2.S7.P.14

Heterogenity of the effective population size

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The effective population size quantifies the magnitude of genetic drift and inbreeding that have taken place in the populations, and it is usually estimated from genetic markers across the whole genome. However, the variation in recombination rates and the different impact of natural selection lead to a notable heterogeneity in the genetic diversity of the genome of eukaryotes. In fact, the effective size has been found to be heterogeneous along the genome of different species, including humans, though these regional estimates did not consistently correlate with other related variables. In this project, we studied the heterogeneity of the human genome of two populations through the effective size estimated in 2 cM genomic regions, using the linkage disequilibrium between pairs of SNPs. We found a remarkable heterogeneity in the effective size, and some theoretically expected significant correlations: the effective size is positively correlated with the recombination rate, and negatively with the amount of background selection, the number of segregating sites and the inbreeding coefficient. It is also positively correlated, as expected, with the nucleotide diversity, but not always significantly. The quantification of the heterogeneity of the effective population size across the genome allows a fine identification of the combined effect of selective and demographic processes in different genomic regions.

S2.S7.P.15

Conotoxin Diversity in the Magician's Cone, *Pionoconus magus*

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Cone snails are carnivorous marine gastropods well known for their great species, morphological, and ecological diversity and for producing a complex venom cocktail to paralyze their preys (worms. snails, and fish). The venom is composed mainly of peptides, named conotoxins, which block key physiological components in the prey like ion or nicotinic neuromuscular receptors. Conotoxins are extremely variable in sequence and have been hypothesized to have a relevant role in having promoted cone snail species radiation. RNA-seq has become the main technique to characterize the composition of the venoms from the different cone snail species (>900) through the assembly of transcriptomes and the identification of the different conotoxin precursors. Here, we catalogue the conotoxin diversity in the venom gland transcriptomes of three individuals of the magician's cone, *Pionoconus magus*, a fish-hunting cone from the Indo-Pacific region. In the study, we assess inter-individual variability, assign precursors to different superfamilies, and compare the venom composition and conotoxin expression to those of *Chelyconus ermineus*, the only fish-hunting cone from the Atlantic Ocean in order to test whether the diet shift to prey on fish occurred once in the evolutionary history of the group.

S2.S7.P.16

East is East and West is West: population genomics and hierarchical analyses reveal genetic structure and adaptation footprints in the keystone species *Paracentrotus lividus* (Echinoidea)

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The Atlanto-Mediterranean edible purple sea urchin, *Paracentrotus lividus*, is a commercially exploited keystone species in benthic communities. Its browsing activity can deeply modify the littoral landscape and changes in its abundance are of major conservation concern. This species is facing nowadays contrasting anthropogenic pressures and its management requires knowledge of its genetic structure, connectivity, and local adaptation. We used genotyping by sequencing (GBS) of 241 individuals belonging to 11 populations spanning the known range of distribution of this species. We obtained 3,348 loci for population genomics and outlier analyses. We identified significant genetic structure and a gradient matching the longitudinal position of the localities. Two main clusters (Atlantic and Mediterranean) were detected, and a hierarchical analysis revealed subtler patterns of differentiation within them. Candidate markers for selection identified between and within these two main clusters were mostly different, likely indicating different selective pressures. Adaptation to maximum salinity and maximum temperature appeared as an important driver of the transition between Atlantic and Mediterranean basins. Other stressors, such as minimum temperature or range of temperature, seem to define the structuring within the Mediterranean. Our study shows the potential of hierarchical analyses on population genomics to detect fine scale genetic structure and adaptation signatures of marine species with long dispersal capabilities. Although genetic interchange occurs widely in *Paracentrotus lividus*, the species is sensitive to dispersal barriers, displays isolation by distance and faces local selective pressures associated to environmental conditions, all of which can render it more vulnerable than previously thought.

S2.S7.P.17

Detection of purging and estimation of predictive parameters in populations under different management systems

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The consequences of genetic purging on the evolution of inbreeding depression are of great relevance from the evolutionary and conservation point of view. Recently, the software PURGd was developed to detect and estimate purging parameters from pedigreed data by applying the Inbreeding-Purging (IP) model. This program showed good results in simulated populations with random mating and random contributions from parents to progeny, but other types of mating may occur, especially when it comes to captive populations. We evaluated the accuracy of the method in populations under different mating systems: equalization of contributions (EC), circular mating (CM) and partial full-sib mating (PFS). Populations of reduced size were simulated where PURGd is used to estimate the purging coefficient (d) and the rate of inbreeding depression (δ), which were then applied to predict the evolution of fitness. We detected significant purging in all the systems evaluated, but in a lower proportion with EC. The estimates of d and δ allowed to compute predictions of the evolution of fitness considerably close to the simulated results. Our results thus support the applicability of the IP model in populations that do not follow a scheme of random mating and random contributions.

S2.S7.P.18

The genetic architecture of the phenotypic plasticity of *Moricandia arvensis* flowers

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Phenotypic plasticity is the capacity of a genotype to produce alternative phenotypes when exposed to different environments. These phenotypic changes are involved in the expression of most traits, but their evolutionary role is not yet completely understood. *Moricandia arvensis* (Brassicaceae) shows phenotypic plasticity for flowers. This species produces large, dissymmetrical, lilac flowers in spring and small, rounded, white flowers in summer. To explore the genetic basis of floral plasticity, we analyzed the flower bud transcriptomes of five individuals subjected to two experimental conditions simulating spring and summer temperature and photoperiod. We produced a de-novo reference transcriptome and retrieved 171,210 trinity isogenes, although only 47,440 passed the criteria for inclusion in the analyses (at least 10 cpm in spring or summer conditions). The overall expression was different between spring and summer flowers, with a total of 627 differentially expressed genes, with 256 genes down-expressed and 371 overexpressed. We found reduced expression of structural and regulatory genes of the anthocyanin pathway that appears as a coordinated response to environmental signals rather than a secondary or passive response to heat. These differentially expressed genes were significantly enriched in GO terms related to the response to stress, temperature, radiation, and light. Hence, summer flowers overexpressed a diversity of genes related to the buffering of plants against several types of stresses, outstanding those coding for heat shock proteins. This coordinated genetic response allows plants to reproduce in the harsh Mediterranean summer by producing functional but phenotypically different flowers.

S2.S7.P.19

Genomic analysis of inbreeding depression and purging of deleterious mutations in lines of *Drosophila melanogaster*

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Inbreeding depression, the reduction of fitness caused by inbreeding, is a phenomenon observed in almost all experimental, domesticated, and natural populations. The positive aspect of inbreeding, however, is the purging of (partially) recessive deleterious mutations by natural selection. Simulation and analytical studies have shown that in populations of a moderately reduced census size ($40 < N < 100$), the inbreeding generated with panmixia is enough to produce the purging of much of this inbreeding load. From an empirical point of view, the magnitude of inbreeding depression and genetic purging has been estimated using specific experimental designs, which have highlighted their importance in populations of moderate census size. However, detailed information about these processes at the genomic level is lacking. The present study aims to analyze the genomic changes underlying inbreeding depression and genetic purging. To do this, we have used pool sequencing to analyze the genomes of 19 *Drosophila melanogaster* lines maintained with a moderate census size (N = 80) for 40 generations, as well as the base population of origin. Here, we show the first results of the analysis of the fate of the deleterious mutations present in this experimental material using recent advances in metrics to infer the functional effect of genetic variants.

S2.S7.P.20

A large chromosomal inversion explains patterns of polymorphism in common quails

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Structural genomic rearrangements (e.g. inversions) play a relevant role in ecological and evolutionary processes such as local adaptation and diversification, by protecting multiple linked adaptive variants from erosion due to recombination with maladapted alleles. Common quails (*Coturnix coturnix*) show two morphotypes differing in pigmentation, wing shape, body size, and possibly in migratory behaviour, which coexist along their distribution range. Here, we explored the genomic differences among quails from the Iberian Peninsula, the Atlantic coast of Morocco and the Macaronesian Islands. We sequenced 16 individuals' whole genomes and aligned them against the Japanese quail genome (*C. japonica*). PCA and admixture analyses showed that individuals formed very well separated clusters. We evaluated the differentiation of these clusters across the genome using FST. Our results revealed a highly divergent region on chromosome 1, that represents a putative inversion encompassing most of the chromosome, as well as other smaller divergent regions on this and other chromosomes that could be the result of genomic rearrangements. The identification of breakpoints shows that the inverted region measures about 115 Mb and the shape of the FST curve suggests that some recombination may have occurred inside the inverted region. Further analyses are needed to fully understand the phenotypic consequences of the inversion and the mechanisms that contribute to maintain the polymorphism in the population.

S2.S7.P.21

Local adaptation drives within island genomic divergence in a songbird following colonization

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Upon colonization of oceanic islands, organisms are subjected to strong selective pressures often related to dietary shifts. In islands with contrasting habitats and food resources, local adaptation has the potential to drive the formation of within-island independent evolutionary lineages, which should diverge in morphological traits related to feeding behaviour and the genomic regions associated with them. We test this hypothesis in the common chaffinch (*Fringilla coelebs*) on the small island of La Palma (Canary Islands), where the species occupies two drastically different habitats, pine forest and cloud forest. Phenotypic analyses of beak morphology and tarsus length revealed significant differences between both habitats that are consistent with ecomorphological predictions. A genome-wide survey of genetic variation using SNP (single nucleotide polymorphism) loci from a genotyping-by-sequencing approach, revealed marked structure among localities and among habitat types. Analysis of neutral SNP loci showed light structure between localities that was consistent with habitat type but also with geography. To disentangle the roles of drift and selection in driving population structure, we analysed loci under selection, which showed a marked structure strongly associated with habitat type. Preliminary analysis to identify genes associated with peaks of divergence among habitats revealed candidate genes related to bone morphogenesis and metabolism. Our results suggest a strong role for local adaptation in driving lineage divergence in the chaffinch of La Palma, an excellent model for studying the evolutionary mechanisms of phenotypic divergence and speciation.

S2.S7.P.22

The mechanisms of drug resistance in the emergent pathogen *Candida glabrata*

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Advances in medicine (such as chemotherapy, antibiotics or transplants) have allowed extending the life expectancy of patients which used to be doomed to death. Many of these patients have an impaired immune system due to treatment or disease condition, which generates a population of patients that are highly susceptible to infections. Among them, fungal pathogens have become a major source of life-threatening agents, which kill as many people as malaria or tuberculosis. To make it worse, there are very few families of antifungal drugs, and resistance towards them is increasingly reported, particularly for emerging species such as the yeast *Candida glabrata* . A key step towards solving the problem is understanding the molecular mechanisms of resistance, which are likely generated by adaptive mutations. We have investigated this by *in vitro* evolving *Candida glabrata* populations exposed to several of these drugs, followed by whole-genome sequencing. We have performed these experiments with fluconazole, anidulafungin and the serial combination of both, which mimic standard clinical therapy. We find mutational signatures of each drug that are consistent with previous work in pathogenic yeasts. As an example, FKS1/FKS2 mutations are widely associated to anidulafungin resistance, while PDR1/ERG11 changes appear in fluconazole. In addition, we predict a novel phenomenon of cross-resistance between these drugs through mutations in a component of ergosterol biosynthesis. Furthermore, we find events of loss of the resistance trait upon changing the treatment, which are associated with truncation of the proteins that previously conferred the resistance. All in all, this work represents a comprehensive evaluation of the evolutionary processes that confer drug resistance to *Candida glabrata.*

S2.S7.P.23

Development of SNP markers to monitor genetic relationship and hybridisation in natural population of *Abies nebrodensis*

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Abies nebrodensis is an endemic species to the north–central part of Sicily. The Nebrodi fir is classified as critically endangered by the IUCN Red List and included in the list of 50 most endangered plants in the Mediterranean. According to recent estimates, it consists of a single population with 30 adult trees and a fluctuating number of juveniles derived from natural regeneration (170 according to the last census); besides, some thousands of cultivated plants are preserved as ex situ collection. Hybridization between *A. nebrodensis* and both *A. alba* and *A. cephalonica* is one of the most important concerns in the conservation of this endangered fir, and conservation authorities suspect the hybrid origin of some seedlings in the natural population. In the last years, many papers highlighted the power of SNPs markers to study population diversity and parentage assessment, and as few as 100–500 SNPs are sufficient to resolve parentage completely in most situations. We used restriction site associated DNA sequencing (RAD-seq) to identify high-quality and information-rich SNPs in samples of *A. nebrodensis*, A. alba and *A. cephalonica*. We developed a 144 SNP-array for genotyping of *A. nebrodensis* adults and juveniles. This SNP panel will be tested to, (1) evaluate the variability and degree of genetic relationship among the adult mature plants of the original population (2) determine the rate of outcrossing, inbreeding and self-fertilisation and (3) assess the eventual hybridisation due to pollen coming from non-native *Abies* species planted in the park (*A. alba* and *A. cephalonica*).

SESSION S3. PALEOBIOLOGY AND MACROEVOLUTION

S3.P.1

A multilocus phylogeny and timetree of mudskippers shed light on their colonization of terrestrial environments

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Mudskippers (family Gobiidae; subfamily Oxudercinae) are amphibious fishes that are able to spend extended periods out of water (foraging, seeking mates and defending territories for some portion of their daily cycle). They live on mudflats and mangrove swamps, and have colonised peritidal habitats of tropical and subtropical Western Africa, the Indian Ocean, and the whole Indo-West Pacific region. Only half out of the 10 oxudercine genera are strictly considered to be mudskippers, and they present different degrees of adaptation to terrestrial conditions, including species that spend the majority of time out of water. Mudskippers have developed specific adaptations to mudflat life in both aquatic and terrestrial conditions, including aerial respiration, ammonia tolerance, aerial vision, and terrestrial locomotion using modified pectoral fins, among others. We have used a multilocus dataset to reconstruct a robust phylogeny and timetree including all Oxudercinae genera (plus representatives of closely related, mainly aquatic Amblyopinae). Our results disagree with the traditional morphology-based phylogeny that presented reciprocally monophyletic Oxudercinae and Amblyopinae, and arranged oxudecine genera in ascending degrees of terrestriality. In contrast, our results indicate that terrestriality has been achieved several times along the oxudercine + amblyopine tree of life, with both completely aquatic (the majority) and amphibious species appearing admixtured in the phylogeny. The diversification of the group during the Oligocene (as per our timetree) associated to mangroves biogeography likely favoured the recurrent, independent appearance of water-to-land transition scenarios for mudskippers.

S3.P.2

Bioclimatic niche evolution in *Carex* sect. *Phacocystis* (Cyperaceae): a macroevolutionary approach in sedges

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The study of niche evolution in plants helps us to get a better understanding of the biological mechanisms that underlie the adaptation of species to new ecological conditions. We use as a model *Carex* sect. *Phacocystis*, the most diverse of sedges (about 120 spp.). It is distributed worldwide and displays two strikingly contrasting geographical patterns: (1)

widely distributed species vs. restricted endemics; and (2) sympatrically hybridizing closely allied species vs. entirely allopatric counterparts. We used a combined Sanger (nuclear: ETS, ITS; ptDNA: rpl32-trnLUAG, ycf6-psbMR) and NGS (Hyb-Seq) approach to reconstruct an extensive phylogeny of the section (>80% of the accepted species). We investigate the correlation between past and present tempo and mode of ecological evolution of the different lineages, palaeogeological and palaeoclimatic events, and biogeographic patterns. Rate of niche change through time is estimated, as well as the existence of significant shifts in niche requirements along the phylogeny. The aim of this research is crucial in the current context of global climatic change to foresee how organisms will react to increasingly changing environmental scenarios.

S3.P.3

Host-parasite interactions: divergence in neotropical crater lake cihclids

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The Nicaraguan Midas cichlid (*Amphilophus* sp.) is a polymorphic species complex with variable trophic apparatus (pharyngeal jaws) and body shape, distributed in the two Great Nicaraguan lakes (Managua and Nicaragua) and in several crater lakes. The Midas cichlid has diverged in sympatry within some crater lakes as a result of ecological speciation. Recently, parasites have been linked to the divergence and maintenance of genetic diversity in their host in this system. In order to test this hypothesis of parasite mediated divergence we focused on the radiation of Midas cichlid in Crater Lake Asososca León, one of the most isolated volcanic lakes in the region. We find evidence of incipient speciation in this crater lake due to relaxed interspecific competition. We linked morphology and parasite communities with fish physiological and immunological responses. We used geometric morphometric tools to analyze body and pharyngeal jaw shape of fish and found evidence of morphological divergence within the lake. We also found differences in parasite communities associated to each incipient fish species. In addition, we found differences in the relative size of the spleen in each species, which are potentially related

to resistance against parasitic infections. We also measured differential gene expression of relevant immune genes. Differences in spleen size and gene expression suggest immunological differences between incipient species. Our results show signs of speciation based on eco-morphological adaptations and suggest an involvement of the immune system in this diversification.

S3.P.4

The evolution of terrestrial reproductive modes as drivers of diversification in amphibians

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Amphibians have diversified globally and have evolved some of the greatest reproductive mode diversity in tetrapods. Comparative phylogenetic methods have been instrumental for understanding the evolution of reproductive modes as well as for identifying extrinsic factors that may have contributed to differences in lineage diversification across different amphibian clades. For a long time, there has been speculation on a positive association between the evolution of direct development, a form of reproduction in amphibians that is characterized by the loss of the ancestral aquatic larval phase, and increased lineage diversification. The hypothesis put forward is that the ancestors of these lineages would have been freed from the constraints of finding suitable aquatic habitat for reproduction and thus allowed for an 'ecological opportunity' type diversification event as new ecological niches became available to such lineages. Conversely, direct development has been shown to occur only in species constrained to tropical and subtropical areas, hence potentially reducing the effect of the ecological opportunity effect. We use a dataset for all ca. 8000 extant amphibians and a suit of the latest diversification rate models and comparative methods to formally test whether diversification rates are associated with ancestral transitions towards terrestrial reproductive modes, as well as other, extrinsic factors. We find that direct development and other terrestrial modes of reproduction are indeed associated with ecological opportunity patterns of diversification in some cases, but that these trait states are unlikely the sole explanatory factors, painting a complex picture of amphibian diversification.

S3.P.5

Influence of the Mediterranean basin history on the origin and evolution of the halophile tiger beetle genus *Cephalota* (Coleoptera: Cicindelidae)

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The distribution area of the halophile tiger beetle genus *Cephalota* ranges from the Mediterranean Sea to Central Asia, including some endemics restricted to reduced areas in the Iberian Peninsula and Central Asia, such as the critically endangered *Cephalota* (Taenidia) *deserticoloides* in Spain. The origin of this genus has been traditionally related to the closure of the Tethys Ocean and the formation of the Mediterranean Sea. In this work, a phylogenetic tree of nine *Cephalota* species is inferred. The observed phylogenetic relationships between these species challenge the hypotheses previously formulated about the evolution of this group, as the origin of *Cephalota* is dated back 13.5 million years, once the Mediterranean Sea was already formed. Alternative hypotheses concerning the changes on the suitable habitat for this halophile group caused by fluctuating levels of the Mediterranean Sea are proposed. Additionally, the results do not support the established taxonomy of this genus, suggesting that the subgenus Taenidia is not monophyletic.

S3.P.6

Diversity of Sierra de Gredos high mountain: phylogenetic and phenotypic structure

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Mat-grass grassland is an important community in the high mountains and has historically been recognized as a hotspot of biodiversity in Europe and the Mediterranean basin. The restricted distribution of these communities on the biogeographic gradient represents a good example to evaluate the possible correlations between cervunales assemblages and latitudinal, altitudinal and orientation boundaries. We sampled grass community composition at 4 sites in Sierra de Gredos (Spain) in an interval altitudinal (1240-2200 m.a.s.l). We estimated taxonomic, functional and phylogenetic biodiversity of these communities in relation to the environmental conditions and the geomorphological history. Ultimately, we aim to determine in what extent a past climatic history in mountains along a latitudinal gradient and a isolation of these ranges have determined their current evolutionary singularity, as depicted by the phylogenies of these species assemblages.

Climate change decreases environmental optimality which may lead to decreases in taxonomic and phylogenetic diversities in lower latitudes and in lower altitude areas in typical high mountain communities. Preliminary results displayed that mat-grass communities within localities were equally diverse with the exception of the site in the slope low south that displayed less diversity than expected by chance, as well as dendrograms based on beta diversity displayed that the most important factor shaping species assemblages in these communities was the orientation rather than altitude. Our following step in this project is to include mat-grass communities from Iberian Peninsula (Cantabrian range, Sierra Nevada and Pyrenees) and Moroccan high mountains.

S3.P.7

Biogeographical history of the Palearctic genus *Helianthemum* (Cistaceae): timing and ecological patterns

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The Mediterranean Basin represents an attractive area for reliable reconstructions of the spatio-temporal evolution of plant lineages due to its great number of explosive radiations and well-known paleoecological history. The genus *Helianthemum* is one of the most representative plant lineages in the Mediterranean ecosystems due to its abundance, diversity and by exhibiting features of the Mediterranean 'character syndrome'. A well-resolved phylogeny of the genus enabled us to detect the presence of three lineages that radiated during the last 5 Ma in different geographical and ecological contexts. In order to identify possible drivers involved in its diversification, we collected biogeographical and ecological information and applied phylogenetic comparative methods. The biogeographical patterns support the role of the paleoecological events suffered in the Mediterranean Basin during the last 6 Ma (i.e. Messinian Salinity Crisis in the Late Miocene, the onset of the Mediterranean Climate in the Pliocene, and the glacial-interglacial oscillations in the Pleistocene) as trigger for its rapid diversification. In particular, the Late Miocene was dominated by geographical expansions, the Pliocene was characterized by the fragmentation of the ancestral widespread distributions and the Pleistocene define the period of highest ecological shifts and diversification. Mediterranean ecosystems have acted as evolutionary "suppliers" of diversity while the highest diversification rates was recorded in Canary Islands as a result of recent colonization followed by strong geographic isolation. The genus shows a relatively low long-distance dispersal capability and low transition rates between ecological niches which indicate that allopatry seems to have been the prominent mode of speciation.

S3.P.8

Disentangling the fundamental branching patterns of phylogenetic divergence

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Previous studies have shown that phylogenetic divergence (i.e. the average phylogenetic displacement between species in a community) is highly sensitive to the underlying branching patterns of phylogenies, suggesting that there is a need to integrate both facets of phylogenic information to obtain a better understanding of assemblage structure. To fill in this gap, we formally conceptualized the three fundamental branching patterns that can drive phylogenetic divergence, and proposed a method to identify their signature in the communities based on the mean pairwise distance (MPD) metric. Our approach consists of the joint interpretation of two MPD-derived metrics that summarize the differential contribution of individual phylogenetic branches to the observed divergence, which serves to evaluate to what extent the later emerges from contrasting branching patterns. We conducted simulation analyses to compare our two metrics with eight classical descriptors of phylogenetic structure. As expected, our metrics correlated to some extent with the classical descriptors of phylogenetic structure, although the relationships were complex and varied systematically with species richness and the specific combination of metric values considered. Consequently, the information provided by our two indexes was only partially captured by their most correlated classical descriptors. While the sole use of phylogenetic divergence metrics may lead to spurious interpretations in eco-phylogenetic studies, our approach can help to obtain a better understanding of assemblage structure by systematically analyzing phylogenetic divergence in the light of its fundamental branching patterns.

S3.P.9

Speciation processes in annual plants, the genus *Aira* (Poaceae) in the Iberian Peninsula and the Balearic Islands

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The genus *Aira* L. is a relatively small genus with c.12 taxa within the tribe Poeae R.Br., subtribe Airinae Fries of the big family of Paceae. This genus diversified along the Mediterranean Basin and includes only slender, annual plants, which usually occur in dry open habitats. The species concept of *Aira* has been object of controversy. Therefore, due to an exhaustive taxonomical review two new taxa have been distinguished in the Iberian Peninsula and Balearic Islands. These two new diploid species are described, along with chromosome counts, morphology, molecular analyses, risk assessment, distribution and habitat, and their relationships to other taxa are discussed.

S3.P.10 The Selection for Selection: Synthesizing Evolvability with Species-Selection Theory to Explain Adaptive Genetic Variation

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Selection at a level higher than the individual is still considered a suspect notion by many. However, empirical evidence gathered on the mechanisms of genetic variation now strongly suggests that these mechanisms have undergone selection at the species level. Pressure is put on a species to evolve and adapt when their respective environment changes, which is predominantly relaxed through the production of novel genetic variants. Nevertheless, modern theory is ill-equip to explain this phenomenon due to the narrowed and pervasive view of natural selection as a process that operates within-populations on individual organisms. In this talk, I make the argument that the synthesis of evolvability theory with species selection theory could explain this phenomenon. In addition, the literature on this subject also provides a firm evidential basis that these theories could formulate their models around, since both models are currently lacking in empirical support. I begin my argument with a brief summarization of the literature on the evolution of the mechanisms of adaptive genetic variation—i.e., genetic recombination, hypermutation, genetic transposition, horizontal gene transfer, and whole-genome duplication. Secondly, I review the literature on the causation of natural selection, using it as a benchmark to subsequently make the argument that the mechanisms of adaptive genetic variation satisfy all the necessary conditions of adaptations by natural selection, but at the species-level. Lastly, I conclude by arguing that evolvability theory, fused with species selection theory, would allow us to explain and better understand the underlying processes of variation and species extinction.

S3.P.11

Phylogenetic origin of the Iberian *Artemia* (Branchiopoda: Anostraca)

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Brine shrimps (Branchiopoda: Anostraca: *Artemia*) reside exclusively in hypersaline aquatic ecosystems, natural saline lakes or salterns. This genus is almost cosmopolitan (except Antarctica) and integrated by seven bisexual species and several asexual lineages (parthenogenetic) with diverse ploidy (diploids to pentaploids). Parthenogenetic populations extend throughout most of the Old World, including the Iberian Peninsula. *Artemia salina* is distributed in the Iberian Peninsula in solar coastal salterns and in a few southern inland salterns. Parthenogenetic populations, diploid and tetraploid, live in the coast and also in most of the inland salterns and salt lakes. The introduced American species *Artemia franciscana* is expanding its range along the coast due to its main use as fish- breeding food in aquaculture. Although the phylogenetic origin of the Iberian parthenogenetic populations has remained unknown, they are considered natives, together with *A. salina*. In this work, we generate a phylogenetic hypothesis including 6 new complete mitogenomes of Iberian *A. salina*, parthenogenetic populations (diploids, and tetraploids), and one population of *A. franciscana* from Baja California, together with the already available 5 bisexual Asian mitogenomes in GenBank. This data-set provides new perspectives about the evolutive processes within this group and the origin of the Iberian parthenogenetic populations. In addition, we include a phylogeography with Mediterranean populations of *A. salina*, reflecting its high and structured genetic diversity with notable Iberian regional endemism. Our results challenge the basic assumptions for the systematics of *Artemia*, and generate a new perspective for conservation of the native Iberian populations.

S3.P.12

Filogenia e implicaciones taxonómicas de los *Anagallis* del Mediterráneo (actualmente en *Lysimachia*)

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Lysimachia arvensis (= *Anagallis arvensis*) y *L. monelli* (= *A. monelli*) son muy variables morfológicamente y se han descrito un gran número de taxones infraespecíficos. Ambas especies tienen plantas con flores rojas o azules por lo que este polimorfismo del color de las flores añade complejidad taxonómica. Las implicaciones del polimorfismo del color de ambas especies no han recibido suficiente atención en los estudios filogenéticos realizados hasta ahora. En este estudio definimos la identidad filogenética del linaje rojo y azul de cada especie y proponemos implicaciones taxonómicas. Para la construcción filogenética se usaron tres marcadores cloroplásticos (rps16-trnK, rpl32trnL, trnH-psbA) y un marcador nuclear (ITS). Nuestros resultados muestran que los linajes de color de ambas especies aparecen juntos con marcadores cloroplásticos pero separados con ITS. El linaje azul de *L. arvensis* es hermano de *L. talaverae* (= A. parviflora), el linaje rojo de *L. arvensis* es hermano del linaje rojo de *L. monelli*, y el linaje azul de *L. monelli* es hermano de *L. foemina* (= *A. foemina*). El origen común o independiente requiere más estudios pero el aislamiento actual de los linajes de *L. arvensis* y *L. monelli* es evidente. Así, proponemos un nuevo nombre para las plantas con flores azules de *L. arvensis* (*L. loeflingii*) y una nueva combinación para las plantas con flores rojas de *L. monelli* (*L. collina*).

S3.P.13

Using mitogenomes, nuclear ribosomal sequences and RADseqs to infer phylogenetic relationships of Lake Titicaca *Hyalella* (Amphipoda: Crustacea)

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Lake Titicaca, located at high altitude between Perú and Bolivia is an ancient lake although, having a maximum of 5 My, it is relatively young compared to others in this category (e.g. Baikal, Tanganyika, Malawi, etc.). The Lake hosts numerous endemic species including representatives of *Hyalella*, an amphipod genus endemic to the American continent. Previous studies established that Titicacan *Hyalella* are polyphyletic. The geological history of the lake suggests that there have been numerous opportunities for allopatric speciation, population contraction/expansion cycles and possibilities for hybridization between taxa from independent lineages. We have sequenced multiple genetic markers by shotgun NGS to explore the Altiplano *Hyalella* phylogenomics. The samples were selected as key representative taxa among those resulting from the previously Cytochrome Oxidase I (COI)-based species delimitation analyses. We also have obtained congeneric taxa from Ecuador and Chile for comparative purposes. Phylogenies based on the 13 mitochondrial protein-coding genes (PCGs) and nuclear ribosomal sequences confirmed the existence of five major genetic lineages in the Lake and the Altiplano. We also have generated SNP data on a sample of 91 individuals from these five lineages using the NextRAD genotyping by sequencing method. Our aims are (1) to derive a well-supported phylogeny of the *Hyalella* species flock in the High Andes, (2) to estimate tree node ages and date the different colonizations and intra-lacustrine diversifications and (3) to test for mito-nuclear discordances and congruence with morphological characters in a phylogenetic context.

Gustatory and visceral integration in the telencephalic pallium of a teleost fish

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The cerebral cortex of mammals has been frequently described as an evolutionary innovation in this vertebrate group. However, increasing amount of neurobiological comparative evidence suggest that the evolution of the cerebral cortex could have been more conservative than previously thought and that the pallium of different groups of vertebrates share with mammals a common plan of organization. Here we examined the involvement of four subregions of goldfish Dm (Dm1, Dm2, Dm3, Dm4) on taste aversion learning (TAL)using a TAL delayed procedure, which consists of the presentation of two flavors on different days, one followed by the injection of LiCl and the other by NaCl, both after a 10-min delay. Additionally, we studied in vivo the pattern of gustatory evoked activity using the optical recording technique. The results showed that Dm2 and Dm3 lesions impaired the acquisition of TAL, whereas damage to Dm1 and Dm4 animals did not provoke significant changes. The analysis of the spatio-temporal pattern of activity showed that tastant stimulation evoked a depolarization response located in Dm-caudal, suggesting a gustotopic representation. These functional data demonstrate that Dm2 and Dm3 are involved in TAL and provide support to the hypotheses that consider Dm of teleosts as a heterogeneous region including areas not only homologous to the amygdala, but also with the mammalian neocortex and insula. Present data indicate that some features of the functional organization of the telencephalic pallium of teleost fish and the cerebral cortex of amniotes are comparable and could have a common evolutionary origin.

S4.P.2

Floral development of *Eriocaulon* and insights on the origin of nectariferous structures in Eriocaulaceae (Poales)

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Monocotyledons typically have floral nectaries associated to gynoecium, known as septal nectaries, or associated to other floral parts. However, nectaries are absent in most families of the order Poales, with few exceptions. Eriocaulaceae, includes two subfamilies, Eriocauloideae and Paepalanthoideae, and presents three types of floral nectaries that vary in position in the flowers: 1. nectariferous carpellodes, that occur in staminate flowers of both subfamilies; 2. nectariferous branches, that occur in the gynoecium of pistillate flowers of Paepalanthoideae; and 3. petal glands, that occur in both staminate and pistillate flowers of Eriocauloideae. Although the ontogeny of these nectaries has been previously studied in Eriocaulaceae, their evolution is not yet clear. In this work, we analysed the floral development of ten species of *Eriocaulon* (Eriocauloideae) and one of *Paepalanthus* (Paepalanthoideae) using scanning electronic microscopy (SEM) to help solve this question. We observed that the carpellodes of Paepalanthoideae and Eriocauloideae have the same position and develop the same way, indicating that they are probably homologous and originated only once. On the other hand, these carpellodes and the nectariferous branches of pistillate flowers of Paepalanthoideae develop differently, despite their position, indicating two independent origins. Also, the nectariferous branches of Paepalanthoideae and the glands on the petals of Eriocauloideae have distinct position, but they share some developmental pathways, suggesting that similarities are genetically influenced. Finally, we conclude that the most plausible hypothesis is that the three types of nectaries of Eriocaulaceae had three independent origins.

S4.P.3

The *OIKO*eKO project: study of *OIKOpleura dioica* as an “evolutionary KnockOut” model in EvoDevo

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In the advent of the Earth Biogenome Project, it is clear that gene losses are prevalent over gene gains, thus providing a new perspective of gene loss as a pervasive source of genetic variation with a great potential to generate phenotypic diversity. Our work on gene loss has recently led us to propose the novel concept of "evolutionary knockout" (eKO) model, which in contrast to "genetically-engineered knockout" models, consist on species that during its evolution have lost genes and can therefore be investigated as model systems to study the evolution of Gene Regulatory Networks (GRNs), mechanisms of embryo development, or any adaptation in the absence of any given gene of interest. Our lab focuses on the study of the appendicularian urochordate Oikopleura dioica, we have previously shown to be a successful chordate gene loser, including losses related to fundamental signaling pathways (e.g. retinoic acid RA, Fgf and Wnt). Currently, our OikoeKO project has two main lines. First, we investigate how gene losses have impacted the deconstruction of the mechanisms of heart development. And second, we are characterizing the defensome (i.e. set of genes conserved among most organisms that respond against environmental challenges) of O. dioica as RA-eKO, as part of a new EcoEvoDevo adventure trying to understand what developmental genes respond first to biotoxins produced during diatom blooms in the context of climate change. To address these projects our lab uses differential gene expression analysis of RNAseq and single-cell transcriptomic data, as well as the generation of gene knockdowns.

S4.P.4

Serial section Transmission Electron Microscopy (ssTEM) analysis of the acoel Symsagittifera roscoffensis, an early bilaterian representative

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Transmission Electron Microscopy serial sections (ssTEM) of the most anterior half of a *Symsagittifera roscofensis* juvenile body were taken, where the brain and beginning of the nerve cords are located. These sections were aligned in the correct order forming a stack using the ImageJ plugin TrakEM2 (in collaboration with Prof. Hartenstein in UCLA). The software allows us the 3D reconstruction of cells and cell groups. My work in this project consists in analyzing the structure and organization of different cell types present, and how they connect with each other. This is particularly challenging in this group of animals, since the acoel body is not organized as well-delimited organs; the different cell types appear intermingled and their membranes highly folded. As acoels (together with their entire group, the phylum Xenacoelomorpha) are considered the sister group of the remaining bilaterians, this study can help us to shed some light in the evolution of organs' architectures. Our final aim is to see if there are patterns of distribution of these cellular types, how they are connected to each other and very especially to the central nervous system. We also took particular interest in the different sensory receptors and gland necks located in the epidermis, with a focus on their subtype classification, distribution and innervation. This systematic approach gives us a unique opportunity of studying the nervous system in much more detail, and allows us to generate a complete 3D reconstruction of the brain, nerve chords and main peripheral nerve tracks.

S4.P.5

A comparative transcriptomic approach to developmental plasticity evolution in spadefoot toads

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Phenotypic divergence across derived lineages sometimes mirrors phenotypic plasticity in the common ancestor, suggesting that environmentally induced phenotypic changes may precede changes in genotype (i.e. 'flexible stem hypothesis') that can evolve into species divergence through genetic accommodation. Pelobatoids, the spadefoot toads, stand out as a good system for studying the role of plasticity in evolution because this group shows extensive developmental rate variation within and between species with predictable consequences on adult phenotype. Whereas *Pelobates cultripes* has retained the highly plastic developmental rate plesiomorphic of this group, this plasticity has been greatly reduced in *Scaphiopus couchii* as a consequence of adaptation to ephemeral breeding ponds. As a result of this adaptive process, *S. couchii* now presents several features that resemble an accelerated version of *P. cultripes*: from overall morphology to fat storages to metabolic rate and endocrine regulation of development. To understand how the transcriptional regulation may have evolved between these divergent species, we have also characterized the gene regulatory network underlying developmental rate in both *P. cultripes* and *S. couchii*. We have investigated whether the same underlying transcriptional profile is conserved across species, and whether it varies between species in its environmental sensitivity. Spadefoot toads provide a good example of how canalization of ancestrally plastic traits can contribute to adaptive divergence and evolutionary novelty.

S4.P.6

First-Time Cis-Regulatory Interactions between Mammalian-Specific TFs and the Zebrafish Genome: Understanding First Time Encounters in Molecular Evolution

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Biological entities, whether proteins, blue whales, sensory organs or cis-regulatory elements are continuously interacting with other structures, establishing complex networks through which biological information is exchanged. These interaction networks are assembled and maintained during the course of evolution. But, what happens when new elements are incorporated for the first time into these systems? We have expressed highly divergent mammalian-specific homeodomain transcription factors (TFs), such as LEUTX and ARGFX, in the completely foreign chromatin environment of zebrafish embryos. We show that LEUTX mRNA injection disrupts early zebrafish development and embryos are arrested during early gastrulation. In the case of ARGFX, ChIP-seq experiments of injected zebrafish embryos show that the ectopic binding sites in zebrafish are preferentially found in chromatin regions that are open and accessible during zebrafish development, some of them are found in the zebrafish orthologues of ARGFX endogenous target genes in mammals. Our results suggest that biological molecular structures, such as TFs, have inherent capacities to interpret and read the information contained in other biological systems, even when these systems have not co-evolved with and are foreign to these biological structures.

S4.P.7

Genome-wide studies of the dynamic of regulatory information during sea urchin development

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Animals exhibit an astonishing morphological disparity in body plans but also they share many genomic features. Indeed, comparative studies suggest that the several factors composing gene regulatory networks defining developmental tissue layers are conserved in triploblastic animals. A regulatory code of interactions between transcription factors (TFs) and cis-regulatory elements (CREs) determines whether target genes are transcribed in a strict spatial and temporal domain. Therefore, the identification of CREs is crucial to elucidating transcriptional programs across taxa and, because active CREs lay in accessible regions of the chromatin, ATAC-seq method has been exploited to systematically profile regulatory elements associated to open chromatin regions. To better understand modules of regulation during the development of deuterostomes, we generated ATAC-seq libraries of sea urchin, a distant related to vertebrates, at different developmental stages. Then, we identified several clusters of CREs based on the dynamic of the ATAC signal over time. These clusters are characterized by different enrichment in binding motifs of TFs. By combining these temporal data of regulation with the expression level of gene associated to CREs, we aim to define different temporal categories of regulation in sea urchin as a new tool to compare different organisms regardless their anatomy in order to gain insights into the role of regulatory landscape changes in the evolution of gene expression throughout animal development.

S4.P.8

RegAdvisor: an open source web annotation to storage and validate papers for regeneration process.

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Regeneration is a phenomenon whereby damaged or amputated organs can regrow in certain organisms. Diverse animals phyla (such as Cnidaria, Chordata, Platyhelmintes, Arthropoda, Echinodermata, among others) exhibit regenerative capabilities. However, there is also a great heterogeneity in the regeneration process observed across different organs, which makes more difficult to establish a general pattern for this phenomenon. Although there is available information of this process, it is centered at a gene-centric level (http://regene.bioinfo-minzhao.org/), and so far there is not a comprehensive repository of relevant literature. In this line, to maximize the usability of the available information regarding this process, and to facilitating the communication between multidisciplinary teams interested in this topic, we have designed **RegAdvisor.** This tool: 1) requests reviews in the literature based on "topics of interest", 2) endows papers with an specific score of "similarity" using NLP methods with your "queries" (e.g.: regeneration, organ, tissue, animal) and 3) allows to manually adding annotations, and score re-evaluation based on the users knowledge of the specific domain. For the web interface creation we have used agile technologies such as Django (Python-Backend) and Bootstrap(HTML/CSS/JS-Frontend).

S4.P.9

Gene regulatory and expression changes in developing pig limbs hallmark the evolutionary emergence of artiodactyl traits

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During tetrapod evolution, the limb skeleton has undergone multiple types of modifications as part of adaptations to different modes of life and locomotion. Most strikingly, all these diverse anatomies derive from the modification of an ancestral skeletal prototype with five digits. In particular, modern artiodactyls such as pigs or cattle walk on the tip of two hoofed toes, having reduced or eliminated the rest of the digits in both fore- and hindlimbs. We have performed a comprehensive analysis of limb development in the pig (*Sus scrofa*) that shows that the progressive loss of molecular anterior-posterior (AP) polarity is a shared feature between long-diverged artiodactyl lineages. This loss of distal asymmetry is linked to the failure to upregulate the SHH receptor *Ptch1* and is accompanied by the step-wise shutdown of AER-FGF signaling during digit elongation, which provides an explanation for both the loss of the anteriormost digit and the reduction of lateral digits in the pig. Finally, open chromatin profiling of mouse and pig limb buds reveals the functional divergence of approximately one third of the regulome affecting evolutionary conserved regions in the genomic landscapes of multiple genes with essential functions during limb development, including various SHH pathway components and modulators. Our strategy establishes pig as a valuable model in evolutionary developmental biology and uncovers pervasive regulatory changes that are likely part of the molecular machinery underlying the morphological diversification of the artiodactyl limb.

S4.P.10

Impact of the expression of human CTCF protein on the S*accharomyces cerevisiae* genome

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In contrast to other eukaryotes, transcriptional regulation is particularly complex in animals, where it depends on long-range interactions between multiple distal enhancers and their target promoters. This is specially so in developmental genes, which usually have very complex expression patterns that require the control of many *cis*-regulatory elements.

Thus, 3D chromatin organization is critical to guarantee proper *cis*-regulatory interactions and to avoid spurious ones. In different groups of animals, such as humans and other vertebrates, the protein CTCF works as an essential factor to control the 3D structure of the genome, regulating cohesin-mediated chromatin interactions and the formation of loops between distal enhancers and their target promoters. In contrast, this type of long-range *cis*-regulation and its associated 3D chromatin organization have not been observed in other eukaryotic lineages such as plants and fungi. Interestingly, CTCF is also absen t from the genome of these non-animal species. To investigate how CTCF can contribute to the establishment of long-range chromatin interactions in animals, we use the model organism *Saccharomyces cerevisiae* to study the effects that CTCF expression may have on the 3D organization of a fungal genome that does not have distal *cis*-regulation. We have successfully generated a yeast strain expressing human CTCF in which we have also introduced several transgenes of human-derived boundary elements containing CTCF binding sites. Using this model we are studying the ability of CTCF to establish 3D structures on the yeast chromatin, and its potential impact on the transcriptional regulation of this unicellular species.

SESSION S5. MICROBIAL EVOLUTION

S5.P.1 Phylogenomic analysis of the zoonotic pathogen *Vibrio vulnificus*

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Vibrio vulnificus (Vv) is a multi-host pathogenic species whose geographic distribution is spreading due to global warming. The species has been classically subdivided into three biotypes (Bts) defined by phenotypic traits and host range. The three Bts are human pathogens, but only Bt2 is also a fish pathogen, a capacity that is conferred by a transferable virulence plasmid (pVvbt2). Previous work using the core genome of 80 Vv strains belonging to the three Bts invalidated the subdivision of the species into Bts and proposed a subdivision into five phylogenetic groups or lineages (L) plus a pathovar defined by the possession of pVvbt2 and the ability to infect fish. The objective of this work has been to gain insights on the evolution of Vv as a species, significantly increasing the number of genomes and analyzing them in depth with a special emphasis on the core genome and the virulence plasmid. Preliminary results confirm that the species is subdivided into five phylogenetic lineages and highlights the great diversity of the virulence plasmid, which has been transmitted between the lineages and other Vibrio species.

S5.P.2

Virosphere, ecological and evolutionary contributions driving host-virus-virophage coexistence

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Virosphere ecological and evolutionary forces are becoming increasingly important to understand community changes. Viruses can influence microbial communities driving ecological and evolutionary changes of their hosts, which may result in ongoing ecoevolutionary dynamics. Parasites of viruses, virophages can alter the interaction of viruses and their hosts by integrating into the host genome and by preventing the spread of the virus in the host population. We aim to understand the evolutionary and ecological mechanisms that allow coexistence of such tripartite systems, so then to comprehend which of the forces drive community dynamics. As a first step we performed a chemostat experiment where host, virus and virophage could co-evolve for 57 days (~130 host generations). We assessed community dynamics and tested for viruses (infectivity) and host (resistance) fitness changes. Results show that virophage presence has a significant effect on long-term community dynamics favouring host survival. Furthermore, in a selection experiment, we manipulated whether virophage, virus or both could evolve to test how the virus and virophage interaction evolves. We assessed viruses (infectivity) fitness changes. We found that the virus lost infectivity while virophage seems to become harmful to the host. All together, these results indicate coevolution of host and virus as well as virus and virophage within a few generations influencing community dynamics.

S5.P.3 Taxonomic vote: assigning taxonomy after similarity searches

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In many applications of high-throughput sequencing, BLAST searches are used to assign taxonomy to reads/contigs. To overcome some of the limitations of this approach, we propose an alternative method, denoted Taxonomic Vote (TV). TV allows obtaining the most probable taxonomy for each query sample and evaluating how many queries in a sample are well identified. Also, it gives information about the taxonomy of the sample for each taxonomic level, contributing to create a very approximate idea of the closest relative organism to that in the sample of interest. There are several differences between the TV procedure and traditional identifications based on BLAST searches. Firstly, in most traditional projects based on BLAST results, only the first hit is retained. In TV, all the hits with a significant score (90% of the best-hit score) are evaluated. Secondly, it is assumed that traditional BLAST accuracy reaches the species level for each best hit. The TV algorithm performs a vote (counting the number of occurrences of each taxon) in each taxonomic level and estimates at what taxonomic level a robust taxonomic identification has been produced. This is indicated with different proposed Taxonomic Vote classes dependent on how well a gene is identified at each taxon level. Although Taxonomic Vote was developed to understand the taxonomic content of the samples, it can be applied to many other situations, such as identification of contamination in high-throughput sequencing studies, characterizing horizontal gene transfer events, or identifying the taxonomic contents of metagenomic samples.

S5.P.4 How to help *Bartonella quintana* grow more and better... and what for

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Obligatory endosymbiotic organisms, whether parasitic or mutualistic, tend to have reduced genomes compared to their free-living relatives, as a result of the evolutionary process called 'genomic reduction syndrome'. Although many genes get lost, these streamlined genomes maintain those genes involved in essential functions, getting close to the definition of a minimal genome. Therefore, their characterization, as well as the possibility of optimizing them, by eliminating superfluous genes or by adding genes to complete impaired metabolic pathways, is highly relevant in synthetic biology. However, most endosymbionts cannot be cultured in the laboratory, making it difficult to manipulate them. *Bartonella quintana* is a parasitic endosymbiont of humans that can grow *in vitro*, but it has a very slow growth rate due to its complex nutritional requirements. In our research group, we have generated a metabolic model of *B. quintana* from genomic data and, through flux balance analysis (FBA), we have determined which compounds are limiting factors for its growth and are deficient in commercial media. We have established a protocol for culturing this bacterium using media supplemented with these compounds in different concentrations, to define the ideal medium composition that improves its growth efficiency. This has also an impact on the ease of performing genomic manipulation experiments for a better characterization of the model prior of its use as an endosymbiont chassis.

S5.P.5 The effect of rifampicin on the symbiotic systems of *Blattella germanica*

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Two symbiotic systems have been described, endosymbiosis and ectosymbiosis, and generally insects harbour one of the two. However, *Blattella germanica* is an omnivorous insect in which both systems coexist: *Blattabacterium cuenotii*, an endosymbiont located in specialised cells (bacteriocytes) in the fat body, and a rich microbiota located in the hindgut. *Blattabacterium* is an obligate endosymbiont with an essential role in the nitrogen recycling and essential amino acids biosynthesis, as it has been proposed after its genome sequencing. The gut microbiome is a complex population similar to the human gut microbiome, with many potential functions that still have to be elucidated. To assess if there is a crosstalk between both symbiotic systems in *B. germanica*, despite being located in separate compartments, we planned to reduce the *Blattabacterium* population by antibiotic treatment, but affecting as little as possible to its microbiota. To do that, we treated adults with rifampicin (antibiotic that attacks *Blattabacterium* as well as Gram-negative and some Gram-positive bacteria) in short periods of time (12 days, when *Blattabacterium* is extracellular to infect the nextgeneration oocytes), during three generations. We have measured in adult females the amount of *Blattabacterium* by qPCR and the changes of the bacterial community of the gut microbiota by sequencing the 16S rRNA gene. We have also determined several fitness parameters (developmental time, sexual maturation time, reproductive rate and mortality) to assess the effect on the host of the reduction of the endosymbiont. Results indicate that the gut microbiota is not able to carry out *Blattabacterium*'s role.

S5.P.6

Four novel genomes from unicellular opisthokonts for a better understanding of the genomic footprints behind the origin of Metazoa, Fungi and their multicellularity

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Multicellularity is a major evolutionary transition, responsible of the emergence of complex living forms such as animals. Despite it occurred roughly 20 times in life history, it is in eukaryotes where multicellularity achieved highest levels of complexity. Opisthokonta represents a great phylogenetic framework to study the genomic footprints behind this transition, as it includes two distinct multicellular lineages, animals and fungi, both surrounded by early-branching unicellular relatives. In theory, the comparison between the genomes of the last unicellular and the first multicellular ancestors would reveal which innovations were crucial for the appearance of multicellularity. As these genomes are not accessible, we need to reconstruct them from a well-sampled representation of their descendants. This implies that not only genomic data from animals and multicellular fungi is needed, but also from their immediate unicellular relatives. Unfortunately, the acquisition of genomic data from unicellular Opisthokonta is problematic as there are few cultured species, which most of them usually grow on a large and heterogeneous population of contaminant species. A methodological protocol and bioinformatics pipeline used to generate good quality genomes from polyxenic cultures of three filastereans and one nucleariid species will be presented. Preliminary results from comparative genomics analyses including these four genomes will also be shown.

S5.P.7

Natural selection in the evolution of a bacterial pathogen, *Treponema pallidum*

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Treponema pallidum subsp. *pallidum* (TPA) is the etiological agent of syphilis, a sexually transmitted disease that has been resurgent in the last decades. TPA genome is highly conserved and very similar to that of the closely related *T. pallidum* subsp. *pertenue* (TPE) and *T. pallidum* subsp. *endemicum* (TEN), which cause the human treponematoses yaws and bejel, respectively. We have analyzed 75 complete genome sequences from the three *T. pallidum* subspecies looking for potential recombination events and to establish the role of natural selection in their evolution. We found 12 genes with 21 different recombination events. Only one recombination event per gene was detected except for genes of tp0136 and tp0326, which showed 7 and 4 events, respectively. All but one events (in tp0136) corresponded to inter-subspecies transfers (TPE/TEN to TPA). Clear evidence for natural selection acting on the recombinant genes was provided by significantly higher values of the non-synonymous/synonymous substitution rate in the recombinant regions than in the non-recombinant zones of those genes. Additionally, 14 non-recombinant genes with evidence of positive selection, and 23 non-recombinant genes with significantly more SNPs than expected were identified. These signals of natural selection were confirmed by additional tests in ten of the recombinant genes, 2 of the non-recombinant genes with abundant SNPs and in 1 of the other nonrecombinant genes with positive selection signal. The phylogenetic location of some of these events and their functional role suggest that both recombination and selection may have had an important role in the evolution of *T. pallidum*.

S5.P.8

Unveiling the evolutionary relationships within the cluster Natrinema-Haloterrigena based on phylogenomics and comparative genomics

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The genera *Natrinema* and *Haloterrigena*, belonging to the family Natrialbaceae within the class Halobacteria, were described in 1998 and 1999, respectively, and currently contain eight and ten species, respectively. Since the two genera were proposed with only 3-month time difference, the article describing the genus *Haloterrigena* did not included the recently described (at that time) genus *Natrinema* and, 20 years later, a detailed study dealing with the evolutionary history of both genera remains to be done to elucidate if they should be maintained as separate genera or joined in a single taxa. With this purpose we have obtained the genome sequences of type and representative strains of species of those genera to carry out phylogenomic and comparative genomic analyses. The phylogenomic tree based on 975 translated orthologous core gene sequences together to overall genome relatedness indexes (Average Nucleotide Identity, Average Amino acid Identity, Percentage of Conserved Proteins) showed that most of the species of the genus *Haloterrigena* must be transferred to the genus *Natrinema*. Nevertheless, *Haloterrigena turkmenica* (type species of the genus) and *Haloterrigena salina* will remain as the only species of the genus *Haloterrigena*. Futhermore, the species *Haloterrigena daqingensis* is, actually, a member of a different genus, *Natronorubrum*. Synteny analysis also indicate a high level of conservation in the physical co-localization of genetic loci among the members of the genus *Natrinema* and the species of the genus *Haloterrigen*a that should be reclassified into the former genus **S5.P.9**

Impact of reference selection on the inference of evolutionary parameters from bacterial short-read sequence data

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Alignment (mapping) of high throughput sequencing (HTS) reads to a single arbitrary reference genome is a frequently used approach in microbial genomics. However, the choice of a reference may represent a source of errors that may affect genome assembly and subsequent analyses such as the detection of single nucleotide polymorphisms (SNPs) and phylogenetic reconstruction. In this work, we evaluated the effect of reference choice on short-read sequence data from five clinically and epidemiologically relevant bacterial species (*Neisseria gonorrhoeae*, *Treponema pallidum*, *Klebsiella pneumoniae*, *Legionella pneumophila* and *Pseudomonas aeruginosa*). Publicly available whole-genome assemblies covering the species' genomic diversity were selected as reference sequences. Then, we compared and assessed the resulting differences in read alignment statistics, SNP calling, recombination rates, inference of natural selection, topology of phylogenetic trees and epidemiological outcomes. The choice of different reference sequences proved to have an impact on almost all parameters considered in the five species. Furthermore, the biases detected due to reference choice had potential evolutionary and epidemiological implications, including the assignment of isolates to transmission clades, estimates of genetic distances between genome sequences and natural selection analyses. These findings suggest that the single reference approach could introduce systematic errors beyond genome assembly, affecting subsequent evolutionary analyses and epidemiological conclusions, especially for datasets with isolates from genetically diverse backgrounds.

SESSION S8. EVOLUTION OF AND BY HUMANS

Validation of the KEE (Theory of Evolution knowledge) and MATE (Theory acceptance) questionnaires in students of the University of Granada

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Evolutionary theory is a central dogma in biology, but certain social groups have shown some reluctance to accept it. Here, we use MATE and KEE questionnaires, together with demographic-personal information, in third-year university courses of four degree majors (Chemistry, English philology, History and Biology) from ten different universities in Spain (Vigo, Autónoma de Madrid, Complutense de Madrid, Alicante, Sevilla, Granada, Valencia, Salamanca, Santiago and Iles Balears), to measure the degree of acceptance and knowledge of evolutionary theory in a sample of undergraduate students (N= 978-981). The KEE inquiry and other demographic questions were validated at the University of Granada (N=268). The degree of acceptance was relatively high (87.2%) whereas the degree of knowledge was moderate (5.4 out of 10), similar to what has been found in other countries. The latter statistic was higher in Biology (6.5), followed by Chemistry (5.2), History (4.8) and English Philology (4.4), and in general, variable among different universities (KEE range across universities: 4.71-5.81). In fact, the degree of knowledge in Biology among universities was partially explained by the frequency of evolutionary themes within the syllabus, suggesting that increasing the relative importance of evolutionary theory in the curricula would have a direct impact in the students' education. Interestingly, we found that people who define themselves as churchgoers showed on average a reduction of about 5% in level of evolutionary acceptance. The moderate knowledge of evolution in our undergraduate students together with the potential problem of acceptance in certain groups suggests that a revision of the evolutionary concepts in the curricula of our students since primary school is necessary.

S8.P.2

Madadapted personalities may be sexually selected

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Extreme variants of personality (personality disorders) cause harm in most aspects of life, but may be maintained in the population because of their advantages for fitness. In a sample of 959 outpatients, we examined whether, and how, sexual selection acts on the main dimensions of personality pathology, taking into account mating success, reproductive success, and the mediating role of status. We find that, to varying extents, all personality dimensions are under sexual selection. Far from being predominantly purifying, selective forces push traits in diverging, often pathological, directions. These pressures differ moderately between the sexes. Sexual selection largely acts in males through the acquisition of wealth, and through the duration (rather than the number) of mates. This gives a reproductive advantage to males high in persistence–compulsivity. Conversely, because of the decoupling between the number of mates and offspring, the promiscuous strategy of psychopaths is not so successful. Negative emotionality, the most clinically detrimental trait, is slightly deleterious in males but is positively selected in females, which can help to preserve variation. Our study supports the growing conviction that personality takes part in the competition over resources, mating opportunities, and reproductive success, and is therefore a product as well as a driver of evolution. However, a sole evolutionary mechanism is unlikely to apply to all traits.

S8.P.3

The first peopling of Western Europe: a review on subsistence patterns during Early Pleistocene times and new insights on the hominin population of Guadix-Baza Basin (SE Spain)

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A number of Early Pleistocene localities from Spain, France and Italy record the most ancient evidence of human presence in Western Europe. This is the case of Barranco León (BL) and Fuente Nueva-3 (FN-3), two Late Villafranchian localities dated to ~1.4 Ma and placed near the town of Orce (Guadix-Baza basin, Southeastern Spain). At these sites, huge assemblages of Oldowan tools (mostly flint flakes and cores) and evidence of defleshing, butchering and marrow processing of large mammal bones have been unearthed together with a deciduous tooth of Homo sp. in level BL-D. Here we report on the anthropic marks found in the cortical surface of the bone remains, which allows to discuss on the subsistence strategies of the first hominins that inhabited the European subcontinent. Moreover, we use cartographic data for reconstructing the paleogeographic extent of the sedimentary environments of the basin (i.e., outcrop areas of the lacustrine system, flood plains with alluvial fans and glacis surface), which allows to estimate the size of the hominin population that inhabited it. The results obtained suggest that this population was small, ~350 individuals distributed in seven to twelve hunter-gatherer groups. This probably compromised its viability in the medium to long term due to inbreeding depression, as documented in the wild dog *Lycaon lycaonoides*. This helps to explain the discontinuous nature of the archaeopaleontological record in the basin, a situation that could also be largely extrapolated to the sporadic record of hominin presence for these ancient chronologies in Western Europe.

S8.P.4

Modeling mammalian food webs in the Orce sites: A quantitative reconstruction of prey-predator relationships in the first hominin settlements of Western Europe

Guillermo Rodríguez-Gómez[1]; Paul Palmqvist[1]; Jesús A. Martín-González[2]; M. Patrocinio Espigares[1]; Sergio Ros-Montoya[1]; Manuel Salvador de Lara[3]; Bienvenido Martínez-Navarro[4] (1) Department of Ecology and Geology, University of Málaga; (2) Departament of Mathematics and Computation, University of Burgos; (3) SynBio lab, University of Surrey; (4) Institut Català de Paleoecologia Humana i Evolució Social, IPHES grodgom@uma.es

Meat was a relevant resource for the first hominins that dispersed in Europe during Early Pleistocene times and competition with other carnivores could have conditioned their presence. This makes interesting to test the conditions immediately before and after the earliest hominin presence. The Late Villafranchian sites of Orce (Guadix-Baza Basin, SE Spain) offer a unique opportunity to analyze the food webs of mammalian paleocommunities in these conditions. With an age of 1.6-1.5 Ma, the site of Venta Micena (VM) provides the ecological scenery before the initial peopling, while Barranco León (BL) and Fuente Nueva-3 (FN-3), dated at ~1.4 Ma, preserve the oldest evidence of hominin presence in the basin. All these sites have provided huge assemblages of large mammals with an excellent state of preservation, which has allowed to carry out a number of taphonomic, biogeochemical and paleoecological analyses useful for contextualizing the environmental context of the first hominin settlements in Western Europe. In this study, we apply a mathematical approach based on Leslie matrices to quantify the biomass of large mammals available to the carnivore guild, including hominins in BL and FN-3. The model determines: (i) the stable age structure of each prey species; (ii) the distribution of individuals among body mass categories; and (iii) the average biomass that could be extracted in the long term from these populations. Finally, it distributes the ungulate meat among the carnivore guild, estimates the sustainable densities of each species and measures the intensity of intraguild competition. The results show that meat was not a limiting factor to hominin presence in Europe before 1.4 Ma.

S8.P.5

Acceptance and knowledge of evolutionary theory among 3rd-year university students from Spain

Emilio Rolán-Alvarez[1]; Juan Gefaell[1]; Tamara Prieto[1]; Mohamed Abdelaziz[2]; Inés Álvarez[3]; Josefa Antón[6]; Juan Arroyo[4]; Jose Luis Bella[5]; M. Botella[2]; Anxela Bugallo[7]; Vicente Claramonte[8]; José Gijón[2]; E. Lizarte[2]; R.M. Maroto[2]; Manuel Megías[1]; Borja Milá[9]; Cori Ramón[10]; Marta Vila[7]

(1) Universidade de Vigo; (2) Universidad de Granada; (3) Real Jardín Botánico, CSIC; (4) Universidad de Sevilla;(5) Universidad Autónoma de Madrid; (6) Universidad de Alicante; (7) Universidade da Coruña; (8) Universitát de Valéncia; (9) Museo Nacional de Ciencias Naturales,
CSIC; (10) Universitat de les Illes Balears rolan@uvigo.es

Evolutionary theory is a central dogma in biology, but certain social groups have shown some reluctance to accept it. Here, we use MATE and KEE questionnaires, together with

demographic-personal information, in third-year university courses of four degree majors (Chemistry, English Philology, History and Biology) from ten different universities in Spain, to measure the degree of acceptance and knowledge of evolutionary theory in a sample of undergraduate students (N= 978-981). The KEE inquiry and other demographic questions were validated at the University of Granada (N=268). The degree of acceptance was relatively high (87.2%) whereas the degree of knowledge was moderate (5.4 out of 10), similar to what has been found in other countries. The latter statistic was higher in Biology (6.5), followed by Chemistry (5.2), History (4.8) and English Philology (4.4), and in general, variable among different universities (KEE range across universities: 4.71-5.81). In fact, the degree of knowledge in Biology among universities was partially explained by the frequency of evolutionary themes within the syllabus, suggesting that increasing the relative importance of evolutionary theory in the curricula would have a direct impact in the students' education. Interestingly, we found that people who define themselves as churchgoers showed on average a reduction of about 5% in level of evolutionary acceptance. The moderate knowledge of evolution in our undergraduate students together with the potential problem of acceptance in certain groups suggests that a revision of the evolutionary concepts in the curricula of our students since primary school is necessary.

SOCIAL ACTIVITIES

COFFEE BREAKS

Wednesday, 5th February, 16:30 to 17:00, Thursday 6th February 11:00 to 11:30 and from 16:00 to 16:30, Friday 7th February 10:45 to 11:15 Coffee, tea and refreshment, Hall, School of Biology

MEETING

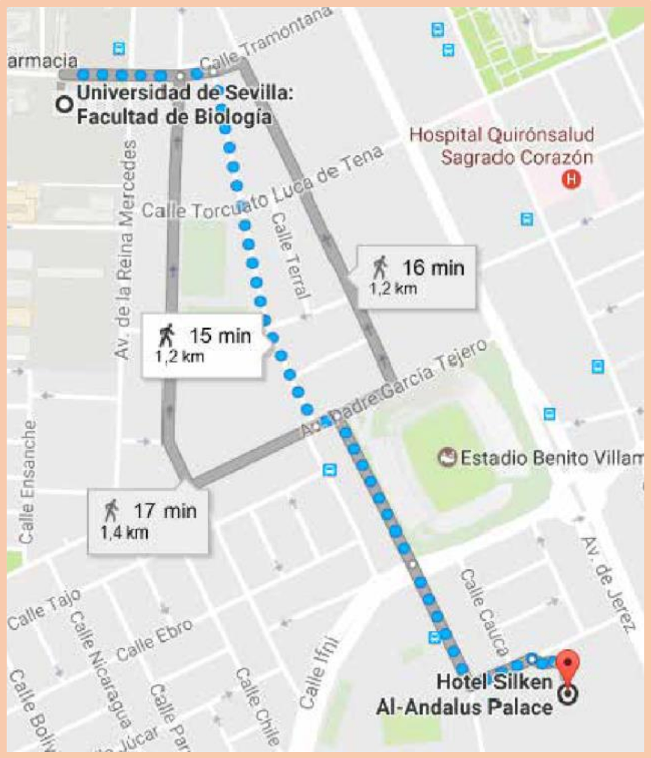
Thursday 6th Feb, 15:00-16:00 **SESBE General Assembly**, at Conference Hall, School of Mathematics.

POSTER SESSIONS

During poster sessions soft-drinks, beers and wines will be served. Poster authors will offer you some special wine just to encourage discussion of their results and to "convince" you to vote for awards

WELCOME RECEPTION & SESBE VII-TAPAS

Wednesday, 5th February, from 20:45 to 22:00, Join us and enjoy a drink or a refreshment and try some typical Spanish “Tapas”, at the Hall of Silken Al-Andalus Palace Hotel. (La Palmera Ave., S/N, junction Paraná street. 41012 Seville).



AWARDS. SPONSORS: SESBE, AEET, PEERJ

Friday, 7th February, from 13:15 to 13:30, at Conference Hall, School of Mathematics.

BEST POSTER AWARDS

SESBE 2020 will award the three PhD student best posters (First, Second and Third prizes). Student posters will automatically be considered for the Poster Awards. All participants are invited to vote for the best poster during the meeting. Winners will be formally announced during the closing ceremony. The three winners of the Poster Awards will receive official certificates, a SESBE book set and a cash prize (€50, €100 and €150). In addition, the SESBE 2020 scientific committee will select the PeerJ Award for the Best Poster. All the posters are eligible for this prize. The posters will be evaluated in terms of: design and layout, attractiveness, scientific content, verbal interaction with the presenter and overall impression. In addition to the official certificate, the SESBE book set and a €150 cash prize, the winner will receive a voucher for a free PeerJ paper (upon submission and acceptance through our normal peer review system – a $1095 value) and an interview on the PeerJ site about their research.

SOCIAL NETWORKING

Follow the meeting on Twitter, Instagram and Facebook at @sesbe2020 and the hashtag

#sesbe2020

ADVISE FOR SPEAKERS AND CHAIRPERSONS

GUIDELINES FOR ORAL PRESENTATIONS Presentations

times:

1. Invited symposium presentation slots: 25 minutes + 5 minutes for discussion.

2. Regular oral presentation slots: 13 minutes + 2 minutes for discussion.

3. Reduced oral presentation slots: 8 minutes + 2 minutes for discussion.

Technical details:

1. Presenters must follow the assigned times to ensure the correct development of the congress. Please keep in mind the importance of tightly adjusting to the available time and ensure your talk does not overrun the time it has been allocated. The session chair will let you know when you have 1 minute of speaking time remaining, prior to questions.

2. To enable the staff to handle the technical aspects in an efficient way, it is strongly recommended to prepare all presentations in Microsoft PowerPoint (.pptx format advised), although pdf will also be accepted and encouraged as a backup.
3. Please upload and check out your presentations at the registration area of the congress venue as soon as possible upon your arrival. There will be a congress volunteer with a computer to help you.
4. Presentations cannot be uploaded directly in the session room.
5. You cannot use your own laptop for your presentation.
6. We recommend you make your slides as concise as possible by keeping texts short and avoiding too many bullet points, so text will be readable. Do not use any material owned by someone else or under copyright protection.
7. For those presenters who do not want to have their presentation on social media, please use the following 'do not share' image at the beginning of your presentation and/or on each slide.

Please respect that in case the image is present.

Audio-Visual Guidelines

The session rooms will be equipped with a PC (Windows) running Microsoft PowerPoint 2010 + Office 2013. PDF and Prezi presentations are also supported.

To prevent unforeseen failures and assure proper functioning, please bring a second (backup) copy, a pdf version of your presentation to the Speakers’ Room.

XGA 1024 X 768 is recommended for desktop-size screen resolutions, as it is the lowest resolution available in the room. Please use common fonts in presentations.

Format of available screens are:

•Conference Hall, School of Mathematics: 3/4 & 16/9

GUIDELINES FOR POSTER PRESENTATIONS

During SESBE 2020, there will be poster sessions on two days at the Biology School Hall, at coffee breaks and after the oral sessions:

Wednesday, 5 February, 16:30-17:00 and 19:00-20:30

Thursday, 6 February, 11:00-11:30, 16:00-16:30 and 18:30-20:00

Evening poster sessions will be held in conjunction with social mixers that include light food, beer, wine and non-alcoholic beverages. Presenters are requested to be by their poster during the time of their designated poster session.

Posters may not exceed the maximum dimensions of 100 cm (height) x 85 cm (width) and double-sided adhesive tape will NOT be provided. Please, take into account that surface is hard and pushpins cannot be used. All posters must be written in English. Poster boards will be numbered and presenters should use the space assigned to them in the published program. Please note that poster presenters are responsible for removing their posters at the end of the meeting. Posters will not be stored or sent back to their owners after SESBE 2020.

For those presenters who do not want to have their presentations on social media, please use the following 'do not share' image to add to your poster presentation. Please respect that in case the image is present.

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- For those coming by plane, there is a bus service to downtown and taxi to fixed prices
- For coming by train, the "Santa Justa" terminal train station is close to old town and serviced by regular city.
- Buses and taxi. There is a commuter train (C1, C4) to Virgen del Rocío Hospital train stop, then 15 min walking to Science Campus. Buses 03, 06 and 34 stop at Reina Mercedes (Escuela Ing. Edificación) N° 157, 62. Please check Google Maps to "Facultad de Biología, Universidad de Sevilla" for further details.

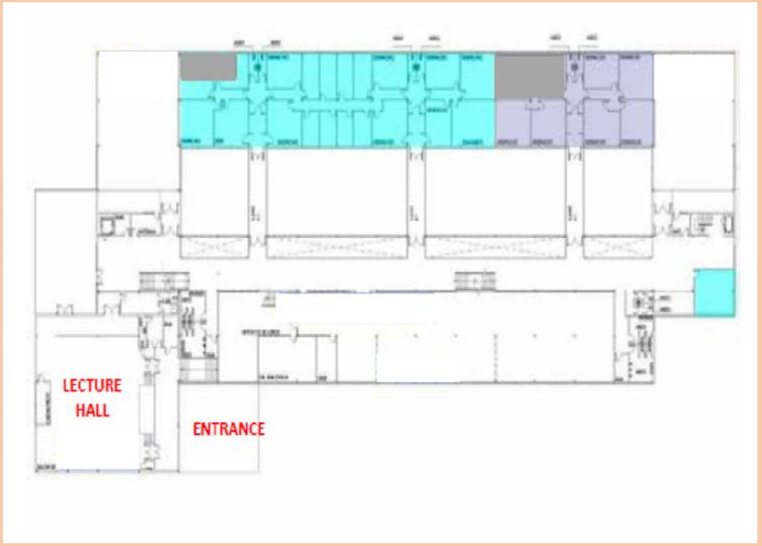
CAMPUS REINA MERCEDES – UNIVERSIDAD DE SEVILLA

1 School of Mathematics First Floor. Conference hall

2 School of Biology Ground Floor. Registration and information desk, poster hall, Coffee break.

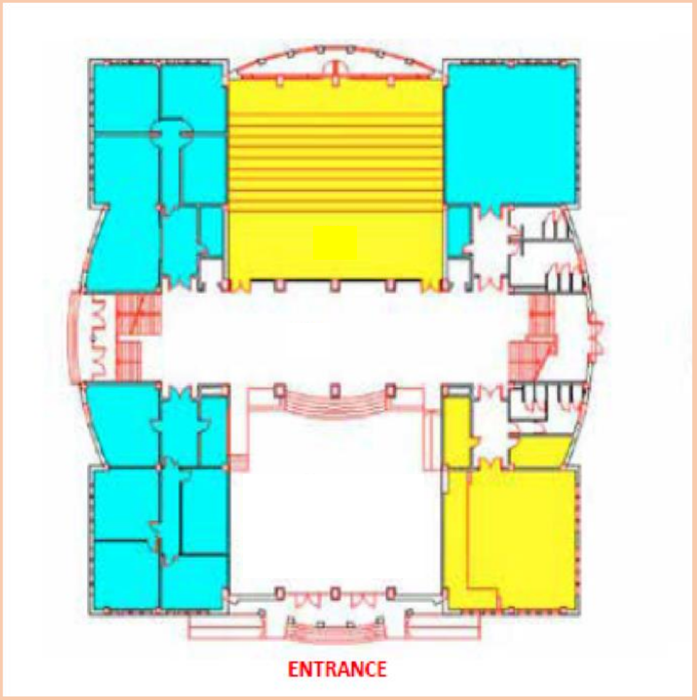
SCHOOL OF MATHEMATICS

First Floor. Conference hall



SCHOOL OF BIOLOGY

Ground Floor. Hall



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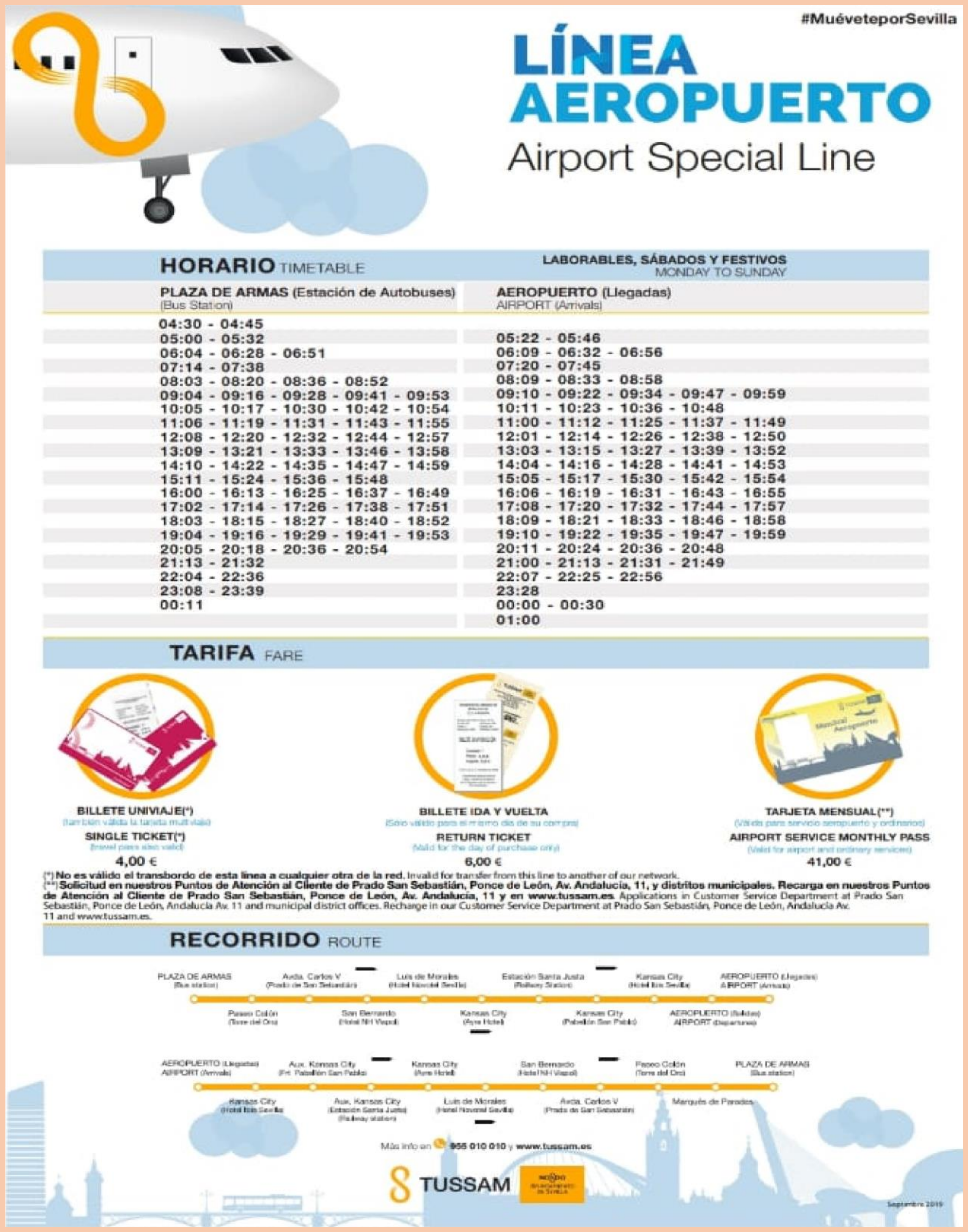

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HORARIO TIMETABLE

LABORABLES, SÁBADOS Y FESTIVOS
MONDAY TO SUNDAY

PLAZA DE ARMAS (Estación de Autobuses) (Bus Station)	**AEROPUERTO** (Llegadas) AIRPORT (Arrivals)
04:30 - 04:45	
05:00 - 05:32	05:22 - 05:46
06:04 - 06:28 - 06:51	06:09 - 06:32 - 06:56
07:14 - 07:38	07:20 - 07:45
08:03 - 08:20 - 08:36 - 08:52	08:09 - 08:33 - 08:58
09:04 - 09:16 - 09:28 - 09:41 - 09:53	09:10 - 09:22 - 09:34 - 09:47 - 09:59
10:05 - 10:17 - 10:30 - 10:42 - 10:54	10:11 - 10:23 - 10:36 - 10:48
11:06 - 11:19 - 11:31 - 11:43 - 11:55	11:00 - 11:12 - 11:25 - 11:37 - 11:49
12:08 - 12:20 - 12:32 - 12:44 - 12:57	12:01 - 12:14 - 12:26 - 12:38 - 12:50
13:09 - 13:21 - 13:33 - 13:46 - 13:58	13:03 - 13:15 - 13:27 - 13:39 - 13:52
14:10 - 14:22 - 14:35 - 14:47 - 14:59	14:04 - 14:16 - 14:28 - 14:41 - 14:53
15:11 - 15:24 - 15:36 - 15:48	15:05 - 15:17 - 15:30 - 15:42 - 15:54
16:00 - 16:13 - 16:25 - 16:37 - 16:49	16:06 - 16:19 - 16:31 - 16:43 - 16:55
17:02 - 17:14 - 17:26 - 17:38 - 17:51	17:08 - 17:20 - 17:32 - 17:44 - 17:57
18:03 - 18:15 - 18:27 - 18:40 - 18:52	18:09 - 18:21 - 18:33 - 18:46 - 18:58
19:04 - 19:16 - 19:29 - 19:41 - 19:53	19:10 - 19:22 - 19:35 - 19:47 - 19:59
20:05 - 20:18 - 20:36 - 20:54	20:11 - 20:24 - 20:36 - 20:48
21:13 - 21:32	21:00 - 21:13 - 21:31 - 21:49
22:04 - 22:36	22:07 - 22:25 - 22:56
23:08 - 23:39	23:28
00:11	00:00 - 00:30
	01:00

TARIFA FARE

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(travel pass also valid)	(Valid for the day of purchase only)	(Valid for airport and ordinary services)
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TUSSAM

Septiembre 2019

ACKNOWLEDGMENTS

We would like to express our gratitude to all those who has given us the possibility to configure and prepare this exciting program: Scientific and Working Committees, Special invited speakers, Session Chairmen, Symposium organizers, volunteer assistants and to all Sponsors and Collaborators and finally to all people who has submitted a contribution and to all attendees.

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AUTHOR INDEX

(Only first authors are listed)

CONGRESS OF THE SPANISH SOCIETY FOR EVOLUTIONARY BIOLOGY

SEVILLE, 5-7 FEBRUARY 2020

UNIVERSIDAD DE SEVILLA

SESBE
Sociedad Española de Biología Evolutiva

DECISION MAKING IN CELL COLLECTIVES
UNIDAD DE EXCELENCIA MARÍA DE MAEZTU (2017-2021)

Centro Andaluz de Biología del Desarrollo

Estación Biológica Doñana
CSIC

LAST MINUTE CHANGES

1- ADDED POSTER CONTRIBUTIONS, OUT OF SESSIONS

Add. 1. Parsimonious scenario for the emergence of viroid-like replicons de novo

Pablo Catalán[1,2]; Santiago F. Elena[3,4]; José A. Cuesta[1,2,5,6]; Susanna Manrubia[1,7*]

(1) Grupo Interdisciplinar de Sistemas Complejos (GISC), Madrid, Spain; (2) Departamento de Matemáticas, Universidad Carlos III de Madrid, 28911 Leganés, Spain; (3) Instituto de Biología Integrativa de Sistemas (I2SysBio), CSIC-Universitat de València, Paterna, 46980 València, Spain; (4) The Santa Fe Institute, Santa Fe, NM 87501, USA; (5) Instituto de Biocomputación y Física de Sistemas Complejos (BiFi), Universidad de Zaragoza, 50018 Zaragoza, Spain; (6) Institute of Financial Big Data (IFiBiD), Universidad Carlos III de Madrid Banco de Santander, 28903 Getafe, Spain; (7) National Biotechnology Centre (CSIC), 28049 Madrid, Spain

*smanrubia@cnb.csic.es

Viroids are small, non-coding, circular RNA molecules that infect plants. Different hypotheses for their evolutionary origin have been put forward, such as an early emergence in a precellular RNA World or several de novo independent evolutionary origins in plants. Here, we discuss the plausibility of *de novo* emergence of viroid-like replicons by giving theoretical support to the likelihood of different steps along a parsimonious evolutionary pathway. While Avsunviroidae-like structures are relatively easy to obtain through evolution of a population of random RNA sequences of fixed length, rod-like structures typical of Pospiviroidae are difficult to fix. Using different quantitative approaches, we evaluated the likelihood that RNA sequences fold into a rod-like structure and bear specific sequence motifs facilitating interactions with other molecules, e.g., RNA polymerases, Rnases, and ligases. By means of numerical simulations, we show that circular RNA replicons analogous to Pospiviroidae emerge if evolution is seeded with minimal circular RNAs that grow through the gradual addition of nucleotides. Further, these rod-like replicons often maintain their structure if independent functional modules are acquired that impose selective constraints. The evolutionary scenario we propose here is consistent with the structural and biochemical properties of viroids described to date.

Add. 2. Four major milestones of human evolution

Hernán Pérez Ramos[1*]

(1) Avda. de la Costa Blanca, 14, Playa San Juan, Alicante 03016.
*puchoramos0562@yahoo.es

Generalization of the hominid condition. Predictably through the females that leave their clan after puberty, hybridization would occur between a group carrying the hominid condition (their cognition worked throughout life) with another in which there would have been a growth of the neuro-associative tissue. This would cause the hominid condition to generalize. 2. The Referential Communication 1Behavior appears. With him, the subjects begin to feel the need to communicate to their peers everything that they find interesting. And this makes parents want to actively teach their children. 3. Language arises. The arcuate fascicle is modified so that the system that associates sound and movement with which it associates sound and visual images is synchronized. This is what allows us to transmit our thoughts through sounds. 4. Cognitive function specializes. The genetic information that deactivated cognition would reappear, but this would now act from the very beginning of life, only partially eliminating some of the systems that associate images to elaborate our knowledge. Causing the appearance, in some subjects, of disorders such as autism, attention deficit syndrome, dyspraxia, lack of language, executive dysfunction, etc., at the same time as in other individuals would generate extraordinary talents for social intelligence (leaders and politicians renowned), for the making of theories, for empirical research, for motor activities (great athletes), for artistic creation, etc. This poster is based on the article by the same author published in the magazine eVOLUTION (of the SESBE), Vol 13. and of Epistemology from the perspective of evolutionary biology

Add. 3. Nociception processing in the teleost telencephalon: insights into the evolution of the neural signature of pain in vertebrates

Tamara Águila[1*]; Patricia Nevado[1]; Antonia Gómez[1]; Francisco Ocaña[1]; Fernando Rodríguez[1]; Cosme Salas[1]

(1) Laboratory of Psychobiology, University of Seville, Sevilla (Spain)
* tdelaguila@us.es

The issue of pain in fish has instigated a vivid debate in the last years. Pain requires the processing of nociceptive inputs by both sensory and emotional-related brain areas. Although there is agreement about shared anatomical and physiological mechanisms among all vertebrates, there is also a widespread idea that fish's responses to nociceptive stimuli are mediated by simple reflexive circuits at spinal level. There has been a generalized disregard of telencephalic mechanisms potentially implicated. Previous functional and behavioral studies suggest a segregated role for different areas of the dorsomedial telencephalic pallium (Dm) of the goldfish (*Carassius auratus*) Dm2 and Dm4 - in the sensory and emotional processing . The aim of the present work is to analyze this role by means of behavioral procedures in combination with electrical microstimulation, lesion and brain imaging techniques. The results support a role for Dm2 in the emotional-processing of nociceptive stimulus, as opposed to Dm4, that appears to be more related to sensory processing, and therefore the existence of a network for complex processing of nociception in the teleost telencephalon. The thorough study of the basic functional and organizational features of the brain in regarding nociceptive processing in phylogenetically distant species can shed light into out understanding of the evolution of the neural signature of pain in vertebrates. The present results has, therefore, far reaching implications, as supports the view that the pallial mechanisms for pain processing might have long preceded the mammalian radiation.

2- ERRATUM

Oral communication S.3.O.1

The correct title, authors and abstract is:

Ancient tropical extinctions contributed to the latitudinal diversity gradient

Andrea S. Meseguer[1] & Fabien L. Condamine[1]

(1) CNRS UMR Institut des Sciences de l'Evolution Université de Montpellier France

Global biodiversity currently peaks at the equator, and decreases toward the poles. Growing fossil evidence suggest this hump-shaped latitudinal diversity gradient (LDG) has not been persistent through time, with similar diversity across latitudes flattening out the LDG during past greenhouse periods. However, when and how diversity was lost at high latitudes to generate the current LDG remains an open question. Unfortunately, diversity-loss scenarios have been repeatedly proposed but not yet clearly

demonstrated. Here, we use phylogenies and fossils to study the LDG of Testudines, Crocodilia and Lepidosauria We outline the asymmetric gradient of extinction and dispersal framework that contextualizes previous ideas behind the LDG under a time-variable scenario. We find that the humpshaped LDG could be explained by disproportionate extinction of tropical-adapted clades from Neogene temperate regions, together with the equator-ward dispersal of organisms tracking their climatic preferences when tropical biomes became restricted to the equator. Conversely, high speciation rates and pole-ward dispersals can account for the formation of an ancient flat LDG. This study underscores the time- and space-variable roles of climate transitions on the evolutionary processes shaping the LDG, and that the 3mail3ión of fossils in macroevolutionary studies allows revealing time-dependent extinction rates hardly detectable from phylogenies only.

Poster S1.S6.P.31
The correct title and order of authors is:

Alpine meadows: are there unknown hybrids out there?

Alba Sotomayor Alge[1]; Juan Luis García Castaño[1]; María Ángeles Ortiz Herrera[1]; Andreas Tribsch[2]

(1) Department of Plant Biology and Ecology, University of Seville, Seville; (2) Department of Biosciences, University of Salzburg, Austria

3- ADDED ORGANIZING INSTITUTION

The **University Pablo de Olavide** (UPO, Sevilla) is now included as **Organizing Institution** of SESBE VII 2020. We thank UPO for this support.