



# CONGRESS OF THE SPANISH SOCIETY FOR EVOLUTIONARY BIOLOGY

SEVILLE, 5-7 FEBRUARY 2020





VII BIENNIAL CONGRESS OF SESBE  
SEVILLE, 5-7 FEBRUARY 2020

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 María de Maeztu Unit “Decision Making Cell Collectives” at CABD and the Doñana Biological Station (EBD-CSIC).



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## COMMITTEES AND STAFF

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- Verónica Castaño Sanz, EBD-CSIC



## 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 pollinator-mediated 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 M<sup>a</sup> 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]



## SESSION S2. EVOLUTIONARY GENETICS I

### S2.O.0

#### Transposable element insertions in adaptive evolution

Josefa González<sup>1</sup>

(1) Institute of Evolutionary Biology (CSIC-UPF). Barcelona

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)

Gonzalo Nieto Feliner<sup>1</sup>; Inés Álvarez<sup>1</sup>; Myriam Heuertz<sup>2</sup>; Irene Villa-Machío<sup>1</sup>

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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 Iberian-Corsica-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-by-sequencing (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?**

Marta Barluenga<sup>1</sup>; Ana Santacruz<sup>2</sup>; Gerardo Pérez Ponce de León<sup>2</sup>

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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