ANNUAL REPORT

2015

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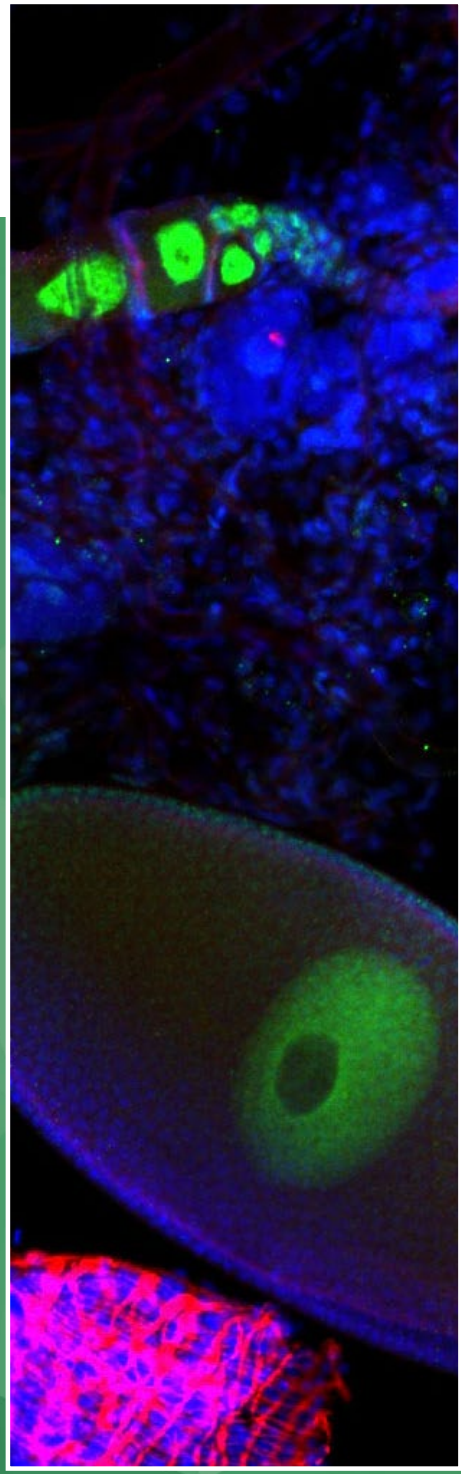
ANNUAL REPORT

2015



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CMIMA building: Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Spain
PRBB building: Dr. Aiguader 88, 08003 Barcelona, Spain

Scientific Coordinator and Layout: Carles Lalueza-Fox
Technical Coordinator and Layout: Anna Pérez-Lezaun and Jordi Lanuza-Masdeu
Text and Photography: IBE Researchers
Graphic Design: Rosa Romeu
Printing: Marc-Martí

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Photo Cover Image: *Ovarioles from a* Blattella germanica *6-day-old last instar nymph. F-Actins were stained with Phalloidin-TRITC (red), somatic nuclei were stained with DAPI (blue). Nuclei from germinal cells were labelled with eya10H6 antibody.*

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FOREWORD

By Xavier Bellés, Director of the IBE

I would venture to guess that Anon, who wrote so many poems without signing them, was often a woman.

Virginia Woolf, *A Room of One's Own* (1929)

Nothing in science has any value to society if it is not communicated, and scientists are beginning to learn their social obligations.

Anne Roe, *The Making of a Scientist* (1953)

Two important facts implemented in 2015 deserve especial mention. One is the formalization of the Commission of Diversity in the IBE, and the other is the foundation of the IBE Unit of Communication. The Commission of Diversity exists thanks to the efforts of Elena Casacuberta and Iñaki Ruiz Trillo, who are currently heading it. The Commission aims at helping the Executive Board to promote and manage diversity among IBE people with particular attention to gender balance. We do not need to remind the dismaying extent to which gender inequalities still exists in science. An incisive editorial in *Nature* in March 2013 summarized the problem with significant data. Just an example: in the United States and Europe around half of those who obtain a doctoral degree in science and engineering are women, but… barely one-fifth of full professors belong to this gender. Childcare might be one major factor that blocks the career of many women, but that is a practical issue that might be addressed with political decisions. There is a second more insidious problem that does not obviously depend on policy makers: it is the overt or unconscious gender bias, which can be noticed even in female scientists. This suggests that raising awareness of gender bias (also among women) at all levels is possibly the first step to overcome it. Other more operational ways to achieve gender assumptions are the promotion of efforts to offer women mentoring and other support, or use gender-blind review. Setting quotas can be another operational, although more controversial, strategy. Recently, the European Commission committed to reaching 40% female participation in its advisory structures for Horizon 2020. However, statistics obtained by the European Research Council suggest that quotas are no magic wand to solve the problem. Quotas might even make matters worse by overburdening the few women who

already hold top positions. The IBE is aware of all these problems, and aims at contributing to improve the situation, at least in-house. We applaud, thus, the foundation of the Commission of Diversity.

The other important fact implemented in the IBE is the foundation of the Unit of Communication, which will be coordinated by Jordi Lanuza, recently appointed for this purpose. The tasks of this unit will be very diverse, but can be summarized into two main aspects. One is to increase the visibility of the Institute by using every tool available, from improving the web page to the preparation of press releases of the most relevant papers emerging from our researchers, the edition of the Annual Report, or the dissemination of our news through the social media. Increase of visibility might appear unimportant per se, but in the short-term may result, for example, in more opportunities for funding or for attracting top students and post-docs. The second aspect is dissemination of science. This is a key point that should motivate every researcher, especially those of us that are civil servants and have thus the obligation of explaining what we are doing with our salaries that are paid with citizens' taxes. It is not a kind of altruism, but a strict obligation, that, by the way, can also result in better funding, as it is the society, in the end, who should decide what to do with public funds. The IBE has always had a deep commitment in favour of public engagement, and Jordi Lanuza comes to give structure to this commitment, to promote outreach activities in the IBE, and to help and coordinate outreach activities emerging from research groups.

The Administrative Unit has experienced significant changes during 2015. The administrative officer Emiliano González retired towards the end of the year (replacement is already planned), and the accountant Rita Arias moved to another institution and was replaced by Vicente Vives, who is warmly welcomed. Concerning institutional and social activities, we celebrated the IBE retreat on the 1st and 2nd of October in a new, and pleasant, place (L'Ametlla de Mar), and we keep good memories of the popular barbecue organized in Les Planes on the 21st of December, to celebrate Christmas.

A great new of 2015 was that Josefa González was awarded with a Consolidator Grant of the European Research Council (ERC) for the project entitled "New approaches to long-standing questions: adaptation in *Drosophila*", which will be developed in the IBE. It is also worth noting that the IBE passed the CSIC evaluation related to the Strategic Plan 2014-2017 with very good marks. As usual, financial support from grants and projects followed the oscillations determined by the schedules of the national and international calls; and in 2015, in contrast with 2014, has relied mostly on international rather than in Spanish funds. As far as scientific production is concerned, the number of publications by IBE researchers has significantly increased with respect to that of 2014, with a parallel increase the quality as well, following a tendency sustained since the foundation of the Institute.

Finally, a few words in memory of Margarita Metallinou and Johannes Engelken, two young researchers that spent in the IBE part of their energetic young lives and who sadly left this world too soon. To quote the beautiful epitaph of the tomb of Nikos Kazantzakis at Heraklion, Margarita and Johannes will not have to fear anything anymore, they will be free forever.

INTRODUCTION TO THE IBE

Scope and General Goals

The Institute of Evolutionary Biology (IBE) was formally founded in July 2008, as a joint Institute of the Spanish National Research Council (CSIC) and the Pompeu Fabra University (UPF). Nowadays, IBE activity involves more than a hundred people and 19 research groups distributed in five scientific programs related to Evolutionary Biology research. The scope and general research goals of the IBE focus on biological evolution.

Indeed, one of the great challenges of the 21st century, after the publication of the Human Genome Sequence and many other species, is the description and understanding of biodiversity, either within species (variation, polymorphism) and/or between species (divergence), as an important element to understand the essential mechanisms of life. In this context, evolutionary biology provides the key tools and concepts. Thus, the main IBE mission is to promote knowledge and research excellence in evolutionary biology. The basis of the IBE, and its main peculiarity, is to address biodiversity studies describing functional and evolutionary genomics at all levels of observation: molecular, biochemical, physiological, and morphological.

The IBE project vision, defined as the projection of the long-term future of the institute, is to be a centre of international reference in the study of biodiversity, in the broadest sense, and its evolution, from a molecular and genomic perspective. Establishing the foundations of a multidisciplinary approach, not limited to the evolution from a mere biological approach, but extended to the human sciences in the broadest sense.

General Structure

In addition to the classical figures of Director, Vice director, and the Executive Board, the IBE also relies on the important structures of the Board of Trustees and the External Scientific Committee.

Board of Trustees

The IBE main managing structure is the "Board of Trustees" composed of two representatives of both partner Institutions (CSIC and UPF). It is competent in the direction, composition, research lines, structure, and functioning rules of the IBE.
Members of the Board of Trustees during 2015:

Anton Bosch, UPF Vice chancellor for Economy and Strategic Projects
Lluis Calvo, CSIC Institutional Coordinator in Catalonia
Francesc Posas, UPF Vice chancellor for Scientific Policy
José Ramón Urquijo Goitia, CSIC Vice president of Institutional Relationships and Organization

External Scientific Committee (CCE)

The IBE External Scientific Committee (CCE) is a group of scientific experts external to the IBE, with international recognition in the Evolutionary Biology field whose main task is to help the IBE in the definition of new research lines and strategies, and to recruit talent and widen the scientific strength of the Institute.

The Composition of the External Scientific Committee was approved by the Board of Trustees in 2011. The first meeting and *in situ* evaluation of IBE activity by this commission took place on 1st and 2nd March 2012.

The composition of the CCE is as follows.

Chairman:

Andrés Moya
Universitat de València
València, Spain

Members:

Brian Charlesworth
University of Edinburgh
Edinburg, UK

Gonzalo Giribet
Harvard University, Cambridge
MA, US

Stuart Reynolds
University of Bath
Bath, UK

Luis Serrano
Centre de Regulació Genòmica
Barcelona, Spain

Eske Willerslev
University of Copenhagen
Copenhagen, Denmark

Executive Board

The IBE Executive Board is composed by 7 members:

IBE Director, Xavier Bellés
IBE Vice director, David Comas
Current Members

Jaume Bertranpetit, Coordinator of the "Population Genetics" Program

José Castresana, Coordinator of the "Animal Biodiversity and Evolution" Program

Carles Lalueza-Fox, Coordinator of the "Comparative and Computational Genomics" Program

Maria-Dolors Piulachs, Coordinator of the "Functional Genomics and Evolution" Program

Ricard Solé, Coordinator of "Complex Systems" Program

Anna Pérez-Lezaun, General Manager and Board Secretary

Scientific Structure

The IBE research activity is organized in five Programs:

Animal Biodiversity and Evolution
Comparative and Computational Genomics
Complex Systems
Functional Genomics and Evolution
Population Genetics

Service Units

In support of the IBE scientific structure there are two service units; one administrative "Central Management Unit" and the other one technical: "Experimental Techniques Unit". The former IBE "Bioinformatics Unit" has been merged into a bigger core service (SAT-UPF) managed though the Department of Experimental and Health Sciences at UPF that will give service to a bigger scientific community ensuring sustainability in time and a more efficient use of resources.

IBE Organisation Chart

BOARD OF TRUSTEES (CSIC/UPF)

DIRECTOR
Xavier Bellés

VICE DIRECTOR
David Comas

EXTERNAL SCIENTIFIC COMMITTEE

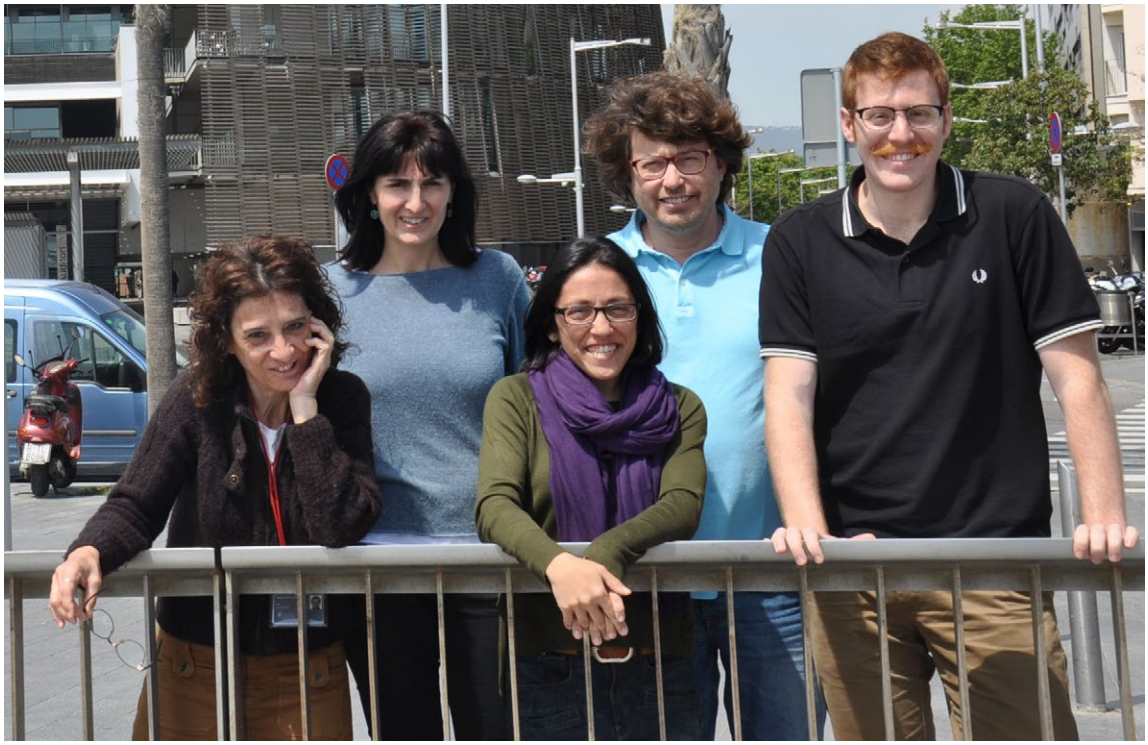
EXECUTIVE BOARD

ADMINISTRATIVE MANAGEMENT

Animal Biodiversity and Evolution Program José Castresana *Coordinator*	**Comparative and Computational Genomics Program** Carles Lalueza-Fox *Coordinator*	**Complex Systems Program** Ricard Solé *Coordinator*	**Functional Genomics and Evolution Program** Maria-Dolors Piulachs *Coordinator*	**Population Genetics Program** Jaume Bertranpetit *Coordinator*
Butterfly Diversity and Evolution Roger Vila *Group Leader*	**Comparative Genomics** Tomàs Marquès-Bonet *Group Leader*	**Evolution of Complex Systems** Ricard Solé *Group Leader*	**Evolution and Developmental Biology** Xavier Franch-Marro *Group Leader*	**Evolutionary Population Genetics** Elena Bosch *Group Leader*
Herbivore Beetle Evolution Jesús Gómez-Zurita *Group Leader*	**Evolutionary and Functional Genomics** Josefa González *Group Leader*	**Language Evolution** Luc Steels *Group Leader*	**Insect Physiology and Molecular Biology** Xavier Bellés *Group Leader*	**Evolutionary Systems Biology** Jaume Bertranpetit *Group Leader*
Phylogeny and Phylogeography of Mmammals José Castresana *Group Leader*	**Evolutionary Genomics** Arcadi Navarro *Group Leader*		**Insect Reproduction** Maria-Dolors Piulachs *Group Leader*	**Genomics of Individuality** Francesc Calafell *Group Leader*
Systematics, Biogeography and Evolution of Reptiles and Amphibians Salvador Carranza *Group Leader*	**Paleogenomics** Carles Lalueza-Fox *Group Leader*		**Multicell Genome** Iñaki Ruiz-Trillo *Group Leader*	**Human Genome** David Comas *Group Leader*
Water and Cave Beetle Evolution Ignacio Ribera *Group Leader*				

Management Unit

The IBE management unit is composed by 6 people and covers at a micro scale level all basic institute running processes: purchasing and accounting, human resources, logistics and safety, support to projects, communication and outreach.



From left to right: Blanca Álvarez, Anna Pérez-Lezaun, Judit Sainz, Vicente Vives, Jordi Lanuza

group members

General Manager:
- Anna Pérez-Lezaun (UPF)

Vice Manager and Accountant:
- Rita Arias (CSIC) until April 2014
- Vicente Vives (CSIC) thereafter

Communications Manager:
- Jordi Lanuza (UPF)

Administrative Support:
- Emiliano González (CSIC)
- Blanca Álvarez (CSIC)
- Judit Sainz (UPF)

Experimental Techniques Unit

There are some long-term laboratory technicians that give key scientific support to different IBE programs. These include the coordination and maintenance of the insect colonies and the specialized technical instrumentation and facilities.

It is planned that the personnel and functions of this unit should be enlarged in the near future to give support to other programs and technological needs.

From left to right: Mònica Vallés, Cristina Olivella

group members

Mònica Vallés, Technical staff (UPF), Supporting the Population Genetics and the Comparative and Computational Genetics Programs
Cristina Olivella, Technical staff (CSIC), Supporting the Functional Genomics and Evolution Program

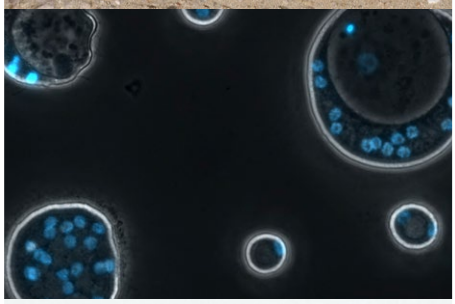
Localisation

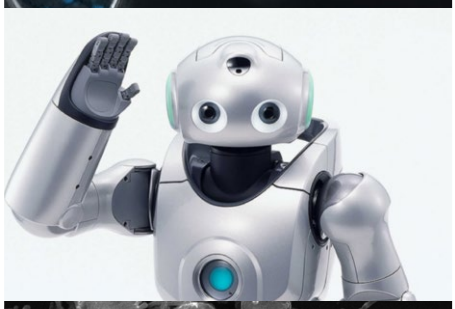
While it does not have a specific building, the IBE has two different headquarters:

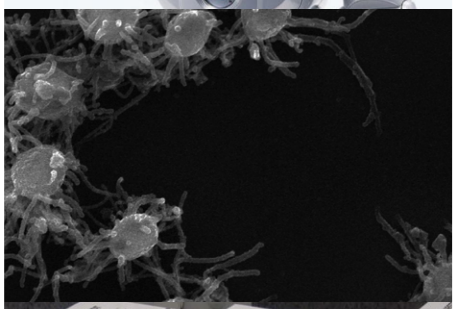
- **IBE at the PRBB building:**
  C/ Dr. Aiguader, 88.
  08003 Barcelona, Spain.

- IBE at the CMIMA building:
  Passeig Marítim de la Barceloneta, 37-49. 08003 Barcelona, Spain.

IBE
RESEARCH PROGRAMS







PROGRAM

ANIMAL BIODIVERSITY AND EVOLUTION

Research Groups

Butterfly Diversity and Evolution
Roger Vila, *Group Leader*

Herbivore Beetle Evolution
Jesús Gómez-Zurita, *Group Leader*

Phylogeny and Phylogeography of Mammals
José Castresana, *Group Leader*

Systematics, Biogeography and Evolution of Reptiles and Amphibians
Salvador Carranza, *Group Leader*

Water and Cave Beetle Evolution
Ignacio Ribera, *Group Leader*

Members of this research program carry out research on animal biodiversity from a phylogenetic perspective with the aim of gaining further insight into the tree of life. The program's specific research interests include the origin and distribution of biodiversity (whether morphological, genetic, ecological or functional), systematics, speciation, hybridization, diversification, biogeography, evolutionary ecology, genomics, proteomics, bioinformatics, morphometry and phylogenetic methodology. Program members work on the systematics and phylogenetic relationships among certain groups of organisms, but also on the evolutionary processes that gave rise to current biodiversity patterns. The main groups studied are mammals, reptiles, amphibians, butterflies and beetles, thus including a broad variety of animal taxa.

An important activity of the program members consists in the maintenance of extensive research collections of specimens, tissue samples and DNA extractions of these groups. A wide range of techniques is covered, from fieldwork and morphological analysis to genetic studies, genomic data mining and software development. The use of genomic data and large-scale phylogenetic analyses (both in terms of species considered and sequenced data) is helping to obtain more robust phylogenies and evolutionary conclusions. Phylogenetic trees are a common framework for many evolutionary studies and therefore this research program provides many points of contact with other programs at the IBE.

group BUTTERFLY DIVERSITY AND EVOLUTION

From left to right: Sämi Schär, Andrei Deulofeu, Lucas Kaminski, Gerard Talavera, Marga Marín, Roger Vila, Raluca Vodă, Vlad Dincă, Joan Carles Hinojosa, Patricia Giménez, Leonardo Dapporto

group members

Roger Vila, *Group Leader*
Tenured Scientist, CSIC

Leonardo Dapporto, Postdoctoral Researcher, Marie Curie Fellowship
Vlad Dincă, Postdoctoral Researcher, Marie Curie Fellowship
Lucas Kaminski, Postdoctoral Researcher, CAPES Fellowship
Sämi Schär, Postdoctoral Researcher, Early Postdoc Mobility
Gerard Talavera, Postdoctoral Researcher, Marie Curie Fellowship
Raluca Vodă, PhD Student, FPU Scholarship, MEC
Joan Carles Hinojosa, MSc Student
Andrei Deulofeu, Undergraduate Student
Patricia Giménez, Undergraduate Student
Marga Marín, Laboratory Technician

Research Outline

We study butterfly diversity patterns in time and space, as well as their evolutionary causes. Our final goal is to answer longstanding questions regarding the limits between species, chromosomal evolution, and the link between phylogeography and ecology. When did a group of tiny butterflies colonize the New World and what route did they follow? How did parasitism evolve from a friendly association between species? Is a given population a new species worth protecting? These are examples of questions we address.

Research Lines

1. Characterization of butterfly diversity with DNA barcoding

We are leading the implementation of DNA barcoding studies for butterflies, including DNA barcoding in Romania (which has been the first country with all butterfly species barcoded), the Iberian Peninsula and Italy. We have recently started the challenging project of obtaining a library of DNA barcodes for all the species of butterflies in Europe. Our main goals are to test the efficiency of the method on a large scale, and to develop tools based on barcoding technology in order to characterize diversity.

2. Uncovering of cryptic butterfly biodiversity in Europe

Potential cryptic species are highlighted as a result of DNA barcoding studies. We are using a wide array of techniques (e.g., ddRADseq, nuclear and mitochondrial markers, geometric and linear morphometry, analysis of karyotype, and ecological niche modelling) to deeply analyze each case, and to shed light on the origin and status of highly diverged taxa.

3. Ecological factors determining butterfly biogeography

Our aim is to unravel the historical biogeography of some groups of butterflies. To do so, we combine phylogenetic methods with ecological niche modelling. We are mostly interested in understanding what ecological factors lie behind current and past distributions. One of our flagship projects focuses on the migratory routes of the cosmopolitan butterfly Vanessa cardui, thanks to funding from the EU, Catalan government and National Geographic.

4. Chromosomal evolution in Polyommatus and Leptidea

Some butterfly groups have remarkably unstable chromosomes and display unusual patterns in

their karyotypes. They constitute an ideal group to study chromosomal evolution in action. We are trying to understand the origin and evolutionary consequences of karyotype instability in Polyommatus and Leptidea.

Fig. 1: Lycaena virgaureae. *The ostentatious appearance of a* Lycaena virgaureae *male is meant to attract the interest of a less conspicuous female counterpart. They can be rather abundant in the midst of summer in many lush meadows throughout Europe. This fiery male was photographed during a field expedition in the Alps, in 2015.*

Photo: *Raluca Vodă*

Publications 2015

De Freina, J.J.; Monasterio-León, Y.; Antonietty, C.A. and Vila, R. (2015). Notes on the biology, distribution and taxonomy of Chondrostega LEDERER, 1857 in the Iberian Peninsula with a description of the southern Spanish *Chondrostega escobesae sp. nov.* (Lepidoptera: Lasiocampidae, Chondrosteginae). *Deutsche Entomologische Zeitschrift* 125(4): 195-207.

Dincă, V.; Montagud, S.; Talavera, G.; Hernández-Roldán, J.; Munguira, M.; García-Barros, E.; Hebert, P. and Vila, R. (2015). DNA barcode reference library for Iberian butterflies enables a continental-scale preview of potential cryptic diversity. *Scientific Reports* 5: 12395.

Espeland, M.; Hall, J.; DeVries, P.; Lees, D.; Cornwall, M.; Hsu, Y-F.; Wu, L.-W.; Campbell, D.; Talavera, G.; Vila, R.; Salzman, S.; Ruehr, S.; Lohman, D. and Pierce, N. (2015). Ancient Neotropical origin and recent recolonisation: Phylogeny, biogeography and diversification of the Riodinidae (Lepidoptera: Papilionoidea). *Molecular Phylogenetics and Evolution* 93: 296-306.

Gonçalves-Souza, T.; Araujo, M.; Barbosa, P.; Lopes, S.; Kaminski, L.; Shimizu, G.; Santos, A. and Romero, G. (2015). Fine-scale Beta-diversity Patterns Across Multiple Arthropod Taxa Over a Neotropical Latitudinal Gradient. *Biotropica* 47(5): 588-594.

Kaliszewska, Z.A.; Lohman, D.J.; Sommer, K.; Adelson, G.; Rand, D.B.; Mathew, J.; Talavera, G.; and Pierce, N.E. (2015). When caterpillars attack: biogeography and life history evolution of the Miletinae (Lepidoptera, Lycaenidae). *Evolution* 9(3): 571-88.

Kaminski, L.; Dell'Erba, R.; Barbosa, E.P. and Freitas, A. (2015). New distribution records and notes on the habitat of *Magneuptychia flavofascia* Zacca & Siewert, 2014 (Lepidoptera: Nymphalidae). *Check List* 11(4): 1692.

Kaminski, L.; Iserhard, C. and Freitas, A. (2015). *Thisbe silvestre* sp. nov. (Lepidoptera: Riodinidae): a new myrmecophilous butterfly from the Brazilian Atlantic Forest. *Australian Entomological Society* 55, 138-146.

Oliveira, K.; Coley, P.; Kursar, T.; Kaminski, L.; Moreira, M. and Campos, R. (2015). The Effect of Symbiotic Ant Colonies on Plant Growth: A Test Using an Azteca-Cecropia System. *PLoS ONE* 10(3): e0120351.

Fig. 2: *Altopiano di Montasio is a spectacular and well-known pastoral area in the Giulian Alps. Vlad and our collaborator Sylvain Cuvelier, in the distant foreground, exploring the diversity of butterflies..*

Photo: *Raluca Vodă*

Fig. 3: *During 2015, Gerard Talavera surveyed the North American continent (Mexico, USA and Canada) to investigate the seasonal migratory movements of the butterfly* Vanessa cardui. *This species largely migrates between Central Mexico and Canada, sometimes as north as Alaska, by successive generations throughout the year. Along the way, this species can find suitable habitat where to breed even in remote places as the deep canyons of the far west.*

Photo: *Gerard Talavera*

Šichová, J.; Voleníková, A.; Dinca, V.; Nguyen, P.; Vila, R.; Sahara, K. and Marec, F. (2015). Dynamic karyotype evolution and unique sex determination systems in Leptidea wood white butterflies. *BMC Evolutionary Biology* 15: 89.

Talavera, G.; Espadaler, X.; and Vila, R. (2015). Discovered just before extinction? The first endemic ant from the Balearic Islands (*Lasius balearicus* sp. nov.) is endangered by climate change. *Journal of Biogeography* 42: 589-601.

Talavera, G.; Kaminski, L.; Freitas, A. and Vila, R. (2015). One-note samba: the biogeographical history of the relict Brazilian butterfly *Elkalyce cogina*. *Journal of Biogeography* 43(4): 727-737.

Voda, R.; Dapporto, L.; Dinca, V. and Vila, R. (2015). Why do cryptic species tend not to co-occur? A case study on two cryptic pairs of butterflies. *PLoS ONE* 10(2): e0117802.

Volkmann, L.; and Kaminski, L. (2015). Orugas de mariposas & hormigas. Maravillas de la Evolución. *Revista de Educación y Ambiente* Año I, nº1.

Funded Projects

- **Project Title:** Eco-PhyloGeo - Linking phylogeography to ecology: extracting rules for butterfly biodiversity at large spatial scale.
  Financed by: Marie Curie Actions—European Fellowships (EF) (H2020-MSCA-IF-2014-EF_658844)
  Years: 2015–2017
  PI: Roger Vila. Research Fellow: Leonardo Dapporto

- **Project Title:** Dynamics of Mediterranean butterflies in a phylogeographic framework: mapping genetic diversity across time and space (DynaGen)
  Financed by: Ministerio de Economía y Competitividad (CGL2013-48277-P)
  Years: 2014–2017
  PI: Roger Vila

- **Project Title:** Deep Africa project: The mystery of the European butterflies vanishing into the Sahara
  Financed by: Committee for Research and Exploration. National Geographic Society (9528-1)
  Years: 2014–2015
  PI: Roger Vila

- **Project Title:** EUGENMAP— Genetic map of European butterflies: Continental-scale cryptic species assessment and comparisons to North America and Australia
  Financed by: Marie Curie Actions—International Outgoing Fellowships (IOF) (FP7-PEOPLE-2013-IOF_625997)
  Years: 2014–2017
  PI: Roger Vila. Research Fellow: Vlad Dincă

Fig. 4: Colias palaeno. *Many butterfly species like flowery meadows, but some are linked to other special habitats. It is the case of* C. palaeno, *usually flying in open bogs and swamps. This female is resting on its larval food plant,* Vaccinium *spp.*

Photo: *Raluca Vodă*

- **Project Title:** MIGRATION— The most cosmopolitan animal migration: phylogeography and population genomics of the butterfly Vanessa cardui
  Financed by: Marie Curie Actions— International Outgoing Fellowships (IOF) (FP7-PEOPLE-2013-IOF_622716)
  Years: 2015–2018
  PI: Roger Vila. Research Fellow: Gerard Talavera

- **Project Title:** El código de barras genético como aproximación a la biodiversidad de insectos de Huinay
  Financed by: Fundaciones Endesa y San Ignacio del Huinay (2014CL0015)
  Years: 2014–2015
  PI: Roger Vila

- **Project Title:** Species Recovery Program (SRP) for 4 of the 15 threatened endemic species of butterflies in continental Europe - phase I
  Financed by: MAVA Foundation Pour la Nature
  Years: 2012–2015
  PI: Miguel López Munguira

- **Project Title:** How climate change and extreme drought events disrupt Mediterranean food webs: an eco-evolutionary analysis
  Financed by: Netherlands Organization for Scientific Research (NWO)
  Years: 2012–2015
  PI: Jofre Carnicer

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014–2016
  PI: Salvador Carranza

Fig. 5: *The Argentinian Chaco is an ideal environment for Lucas Kaminiski's research on the Neotropical* Aricoris *butterflies. A fast evolutionary radiation of these myrmecophylous butterflies have occurred in sympatry through complex mutualisms with multiple ant and plant species. Our expedition was focused on identifying and studying these interactions.*
From left to right: *Gerard Talavera, Roger Vila, Luis Volkmann and Lucas Kaminski.*
Photo: *Gerard Talavera*

group HERBIVORE BEETLE EVOLUTION

From left to right: Nguyen Thi Dinh, Helena Vizán, Anabela Cardoso, Gissela De la Cadena, Jesús Gómez-Zurita, Diego Santana, Josep Roca

group members

Jesús Gómez-Zurita, *Group Leader*
Tenured Scientist, CSIC

Gissela De la Cadena, PhD Student, SENESCYT Scholarship
Nguyen Thi Dinh, PhD Student, CSIC Scholarship (International Cooperation)
Diego de Santana Souza, PhD Student, CSIC Scholarship (International Cooperation)
Helena Vizán, PhD Student, MICINN Scholarship
Anabela Cardoso, Lab Manager and PhD Student, MICINN
Josep Roca, Research Assistant, MICINN

Research Outline

We have a broad spectrum of interests ranging from the systematics and community structure of leaf beetles to the study of geographic speciation and the analysis of the spatial structure of genetic diversity within a temporal framework (phylogeography), as well as the investigation of biological processes such as hybridization, unisexuality or insect-host plant associations from an evolutionary perspective.

Research Lines

1. Evolution of male-specific genes in thelytokous species

Calligrapha has several thelytokous species and we are using testis-specific RNA-Seq from closely related bisexual species to find male-biased candidate genes which can be studied in female-only lineages.

2. Pattern association of genetic structure of beetle populations and *Wolbachia* strains

Thelytoky appeared several times in *Calligrapha* via interspecific hybridization events, whereby lineages of different beetle species with a particular mtDNA type were always involved. The project tries to ascertain if *Wolbachia* or a strain of the endosymbiont were responsible for this pattern, which has the signature of a selective sweep.

3. DNA-based species delimitation

From the analysis of leaf beetle communities to the validation of morphospecies, we use DNA sequence data from single universal loci and phylogenetic approaches to hypothesize species limits.

4. Characterization of insect-plant associations in tropical dry forests

We are using DNA-based approaches to study the leaf beetle communities of seasonally dry forests in Nicaragua and Vietnam, as well as their trophic ecology. In Nicaragua we look at a regional scale, and seek to understand the community structure from taxonomic and ecologic perspectives. In Vietnam we look at a local scale with the aim of understanding the effect of subtle ecological transitions on beta-diversity.

5. Beetle systematics

The work being undertaken in ongoing and previous projects always results in interesting samples, some representing new species for science. We describe this diversity.

Fig. 1: *Sampling leaf beetles in Vietnam. We have analysed the change in the community of Chrysomelidae in a short elevation gradient in the Núi Chúa National Park. With up to 300 species estimated in an area smaller than 10 km², the diversity of leaf beetles staggering, as it is confirming that this diversity appears structured, i.e. the communities seem to change ascending a few hundred meters along the mountain slopes.*

Photo: *Nguyen T. Dinh.*

Publications 2015

Gómez-Zurita, J. (2015). Systematic revision of the genus *Calligrapha* Chevrolat (Coleoptera: Chrysomelidae, Chrysomelinae) in Central America: the group of *Calligrapha argus* Stål. *Zootaxa* (Monograph) 3922: 1-71.

Gómez-Zurita, J. (2015). What is the leaf beetle *Calligrapha scalaris* (LeConte)? *Breviora* 541: 1-19.

Montagna, M.; Gómez-Zurita, J.; Giorgi, A.; Epis, S.; Lozzia, G. and Bandi, C. (2015). Metamicrobiomics in herbivore beetles of the genus *Cryptocephalus* (Chrysomelidae): towards the understanding of ecological determinants in insect symbiosis. *Insect Science* 22: 340-352.

Montelongo, T. and Gómez-Zurita, J. (2015). Non-random patterns of genetic admixture expose the complex historical hybrid origin of unisexual leaf beetle species in the genus *Calligrapha*. *American Naturalist* 185(1): 113-134.

Papadopoulou, A.; Chesters, D.; Coronado, I.; De la Cadena, G.; Cardoso, A.; Reyes, J.C.; Maes, J.-M.; Rueda, R.M. and Gómez-Zurita, J. (2015). Automated DNA-based plant identification for large-scale biodiversity assessment. *Molecular Ecology Resources* 15: 136-152.

Fig. 2: Calligrapha alnicola *Brown is a thelytokous species that we find always associated with alder in northeastern North America. We have unequivocally shown that its origin can be traced back to an interspecific hybridisation event between ancestors of* C. ignota *Brown (associated with birch,* Betula*) and another species feeding on alder, in the lineage of* C. alni *Brown and* C. confluens *Schaeffer.*

Photo: *Tinguaro Montelongo.*

Funded Projects

- **Project Title:** Análisis a escala genómica de las consecuencias evolutivas del abandono del sexo: Explorando el destino de la función masculina.
  Financed by: Ministerio de Ciencia e Innovación (CGL2011-23820)
  Years: 2012–2015
  PI: Jesús Gómez-Zurita

- **Project Title:** Phylogeny and biogeography of Polyrhaphidini and their placement among the Lamiinae (Coleoptera: Cerambycidae)
  Financed by: CSIC (i-COOP+)
  Year: 2015
  PI: Jesús Gómez-Zurita

- **Project Title:** ¿Tienen los endosimbiontes de herencia materna algún papel en el origen y mantenimiento de la unisexualidad en *Calligrapha* (Coleoptera: Chrysomelidae)?
  Financed by: Ministerio de Economía (CGL2014-52937-P)
  Years: 2015–2017
  PI: Jesús Gómez-Zurita

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014–2016
  PI: Salvador Carranza

group PHYLOGENY AND PHYLOGEOGRAPHY OF MAMMALS

From left to right and top to bottom: José Castresana, Marina Querejeta, Lídia Escoda, Oliver Hawlitschek, Alfonso Balmori de la Puente, Karla García

group members

José Castresana, *Group Leader*
Research Scientist, CSIC

Oliver Hawlitschek, Postdoctoral Researcher, DFG Fellowship, Germany
Alfonso Balmori de la Puente, PhD Student, FPI Fellowship, MINECO
Lídia Escoda Assens, PhD Student, FI AGAUR Fellowship, Generalitat de Catalunya
Marina Querejeta, PhD Student, FPI Fellowship, MINECO
Karla García, Visiting PhD Student from the Universitat de Barcelona

Research Outline

Our main goal is the application of phylogenetic and genomic analyses to study animal biodiversity and evolution. We use next-generation sequencing techniques and advanced bioinformatic tools to understand the phylogeographic patterns and the population history of several species of mammals, some of them of great conservation importance. We also analyze the speciation process in different species complexes to obtain a better description of our biological diversity.

Research Lines

1. Speciation

The reconstruction of species trees of closely related species based on multiple genomic markers can help to estimate speciation times, study gene flow, delimit species and, in general, better understand the speciation process. To be able to effectively use these techniques in mammals, we have developed a large set of intronic markers. In addition, we are using next-generation sequencing techniques to obtain a large number of genomic markers. We are sequencing these markers in several groups of small mammals such as *Neomys*

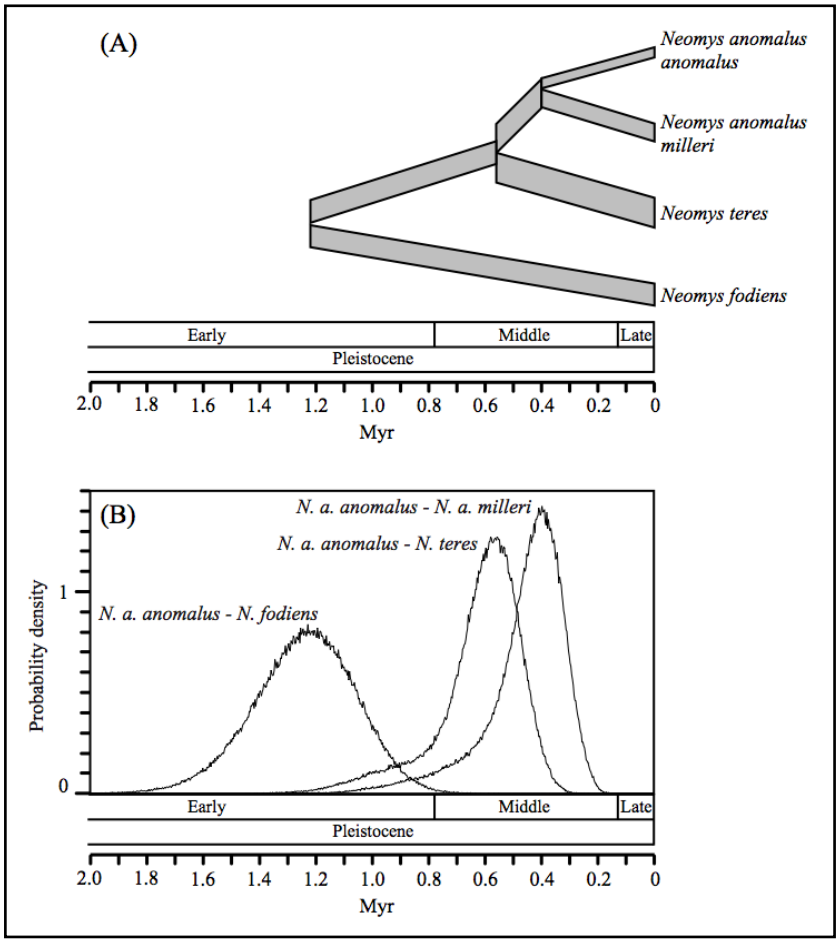


Fig. 1: *Scheme of the dating analysis of* Neomys *species modified from Igea et al. (2015).*
(A) Species tree of Neomys *species based on a coalescence analysis of 13 introns and cytochrome b with mutation rates specifically estimated for each marker.*
(B) Posterior probability density distributions for estimated split times between the studied species. Obtaining accurate split times and associated confidence intervals in the species tree allows distinguishing between different Pleistocene ages, which can provide important information for studies on recent speciation.

(see figure), *Sorex*, *Microtus* and *Arvicola*. To obtain material for these studies we are making extensive use of noninvasive samples such as skulls obtained from owl pellets. The rigorous characterization of speciation in these species complexes is expected to lead to a better understanding of our biological diversity.

2. Conservation genomics

The Pyrenean desman (*Galemys pyrenaicus*) is a small semi-aquatic mammal endemic to the northern half of the Iberian Peninsula and is endangered in a large part of its distribution range. We are currently studying several aspects of the phylogeography and population history of this unique species using mitochondrial data as well as SNPs obtained by next-generation sequencing techniques. Much of the material that we use for genetic studies comes from the droppings that desmans deposit on rocks emerging from rivers. To get additional samples and carry out this research we are collaborating with different scientists and administrations. The results we are obtaining may have crucial implications for the conservation of this species.

3. Methodological aspects of phylogenetic reconstruction

Phylogenetic trees are essential in evolutionary biology and therefore it is important to understand their potentials and limitations. With this aim, we are working on different aspects of tree reconstruction and on the detection of artifacts that may affect phylogenetic analysis. We are interested in all steps of these analyses, including the generation of alignments, the reconstruction of phylogenetic trees and the comparison of these trees. We are also interested in coalescence-based multilocus species trees and in the estimation of accurate speciation times in closely related species (see figure). We are currently trying to use these methods with large amounts of sequences obtained by next-generation sequencing techniques.

Publications 2015

Igea, J.; Aymerich, P.; Bannikova, A.A.; Gosálbez, J. and Castresana, J. (2015). Multilocus species trees and species delimitation in a temporal context: application to the water shrews of the genus *Neomys*. *BMC Evolutionary Biology* 15, 209.

Funded Projects

- **Project Title:** Studies of genomic divergence and contact zones of populations of small mammals in the Iberian Peninsula using next-generation sequencing techniques
  Financed by: Ministerio de Economía y Competitividad (CGL2014-53968-P)
  Years: 2015–2017
  PI: José Castresana

- **Project Title:** Reconstruction of species trees with genomic markers and its application to the study of mammalian speciation
  Financed by: Ministerio de Economía y Competitividad (CGL2011-22640)
  Years: 2012–2015
  PI: José Castresana

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014–2016
  PI: Salvador Carranza

group SYSTEMATICS, BIOGEOGRAPHY AND EVOLUTION OF REPTILES AND AMPHIBIANS

Top, from left to right: Emilio Valbuena, Joana Mendes, João Campos
Left from top to down: Joan Garcia-Porta, Pedro Tarroso
Group photo, from left to right and top to down: Phiilip de Pous, Salvador Carranza, Josep Roca, Margarita Metallinou, Luis Machado, Duarte Gonçalves, Raquel Vasconcelos, João Maia, Marc Simó, Santiago Montero

group members

Salvador Carranza, *Group Leader*
Tenured Scientist, CSIC

Joan Garcia-Porta, Postdoctoral Researcher, Contracted
Pedro Tarroso, Postdoctoral Researcher, FCT Scholarship, Portugal
Raquel Vasconcelos, Postdoctoral Researcher, FCT Scholarship, Portugal
Marc Simó, PhD Student, FPI Scholarship, MEC
Emilio Valbuena Ureña, PhD Student, Teaching Assistant UAB, Barcelona
João Campos, PhD Student co-supervised with Dr. José Carlos Brito, CIBIO, Portugal, FCT Scholarship, Portugal
Duarte Gonçalves, PhD Student co-supervised with Dr. J.C. Brito, CIBIO, Portugal, FCT Scholarship, Portugal
Luis Machado, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
João Maia, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Joana Mendes, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Philip de Pous, PhD Student co-supervised with Delfi Sanuy, UDL, FI AGAUR Scholarship, Generalitat de Catalunya
Dragan Arsovski, MSc in Biology, Erasmus Mundi Program in Evolutionary Biology (MEME)
Josep Lluís Roca, Technician, Contracted

Research Outline

Our research focuses on the application of phylogenetic analyses of reptiles and amphibians to understand how biodiversity is generated and maintained. Moreover, we are also interested in inferring the biogeographical and evolutionary patterns of the different groups studied, to revise their taxonomy and to use all this information to address conservation issues. Although our investigations include the study of many different reptile and amphibian groups, our central research lines focus mainly on the faunas of the Mediterranean Basin and Arabia, including some oceanic and continental islands, such as the Canary and Cape Verde islands in the Atlantic Ocean and, since 2010, the unique archipelago of Socotra in the Indian Ocean.

Research Lines

1. Historical biogeography and evolution of the reptiles and amphibians around the westernmost Mediterranean

Our main objectives are: 1) infer the geographical history and evolution of the reptiles and amphibians around the westernmost Mediterranean Basin; 2) characterize and compare the molecular evolutionary rates of reptiles and amphibians; and 3) test the current taxonomy of the groups concerned.

2. Uses of phylogenies to study evolutionary, ecological and biogeographical processes: the North African and Arabian arid reptile faunas

In this project, we are using molecular phylogenies from multiple reptile taxa to address a whole range of evolutionary, ecological and biogeographical questions. The main objectives of the project are: 1) to understand how deserts gain and maintain their endemic faunas; 2) to infer the age of the Sahara and Arabian deserts; 3) to compare the diversification rates of several desert lineages; and 4) to test and improve the current taxonomy of the groups concerned.

Fig. 1: *Asaccus caudivolvulus Adult Female*
Fig. 2: *Diplometopon zarudnyi*
Fig. 3: *Cerastes gasperettii*
Fig. 4: *Teratoscincus keyserlingii*
Photos: *Salvador Carranza*

3. Island biogeography and evolution

The main goal of this research line is to take advantage of the excellent experimental conditions of the island systems to try to understand how biodiversity is generated and maintained. Island systems offer great opportunities to study evolution, and are especially attractive environments for several reasons: 1) they present discrete geographical entities within defined oceanic boundaries; 2) gene flow between individual islands is reduced by oceanic barriers; 3) their often small geographical size has made the cataloguing of flora and fauna easier than continental systems; 4) despite their small geographical size they can contain a diversity of habitats; and 5) they are often geologically dynamic with historical and contemporary volcanic and erosional activity. At the moment we are investigating both oceanic and continental islands' reptilian fauna from several places in the world including the Canary Islands and Cape Verde in the Atlantic Ocean and the Socotra archipelago in the Indian Ocean.

Publications 2015

Amat, F.; Oromí, N.; Sanuy, D. and Carranza, S. (2015). Sexual dimorphism and age structure of the Montseny newt (*Calotriton arnoldi*). *Amphibia-Reptilia* 36: 245-252.

Bellati, A.; Carranza, S.; Garcia-Porta, J.; Fasola, M. and Sindaco, R. (2015). Cryptic diversity within the *Anatololacerta* species complex (Squamata: Lacertidae) in the Anatolian Peninsula: evidence from a multi-locus approach. *Molecular Phylogenetics and Evolution* 82: 219-233.

Metallinou, M.; Cervenka, J.; Crochet, P.A.; Kratochvíl, L.; Wilms, T.; Geniez, P.; Shobrak, M.Y.; Brito, J.C. and Carranza, S. (2015). Species on the rocks: Systematics and biogeography of the rock-dwelling *Ptyodactylus* geckos (Squamata: Phyllodactylidae) in North Africa and Arabia. *Molecular Phylogenetics and Evolution* 85: 208-220.

Smid, J.; Martinez, G.; Gebhart, J.; Aznar, J.; Gallego, J.; Göçmen, B.; de Pous, P.; Tamar, K. and Carranza, S. (2015). Phylogeny of the genus *Rhynchocalamus* (Reptilia; Colubridae) with a first record from the Sultanate of Oman. *Zootaxa* 4033: 380-392.

Smid, J.; Moravec, J.; Kratochvíl, L.; Nasher, A.K.; Mazuch, T.; Gvozdik, V. and Carranza, S. (2015). Multilocus phylogeny and taxonomic revision of the *Hemidactylus robustus* species group (Reptilia, Gekkonidae) with descriptions of three new species from Yemen and Ethiopia. *Systematics and Biodiversity* 13: 346-368.

Tamar, K.; Carranza, S.; in den Bosch, H.; Sindaco, R.; Moravec, J. and Meiri, S. (2015). Hidden relationships and genetic diversity: Molecular phylogeny and phylogeography of the Levantine lizards of the genus *Phoenicolacerta* (Squamata: Lacertidae). *Molecular Phylogenetics and Evolution* 91: 86-97.

Other Publications

Arribas, O. and Carranza, S. (2015). Lagartija leonesa – *Iberolacerta galani*. In: Enciclopedia Virtual de los Vertebrados Españoles. Salvador, A., Marco, A. (Eds.). Museo Nacional de Ciencias Naturales, Madrid.

Fig. 5: *Field expedition to Oman*
Photo: *Salvador Carranza*

Funded Projects

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014–2016
  PI: Salvador Carranza

- **Project Title:** Olvidados en el océano: los reptiles del Archipiélago de Socotra como modelo para el estudio de la Biogeografía, Evolución y conservación en islas
  Financed by: Ministerio de Economía y Competitividad MINECO (CGL2012-36970)
  Years: 2013–2015
  PI: Salvador Carranza

- **Project Title:** Population study, habitat management and programming for introduction of captive-born individuals of one critically endangered amphibian, the Montseny newt
  Financed by: Mohamed bin Zayed Species Conservation Fund (Ref: 14258012)
  Year: 2015
  PI: Fèlix Amat

- **Project Title:** Dragon's blood tree's gecko – a flagship for Socotra fauna
  Financed by: Mohamed bin Zayed Species Conservation Fund (Ref: 14259910)
  Years: 2015–2016
  PI: Raquel Vasconcelos

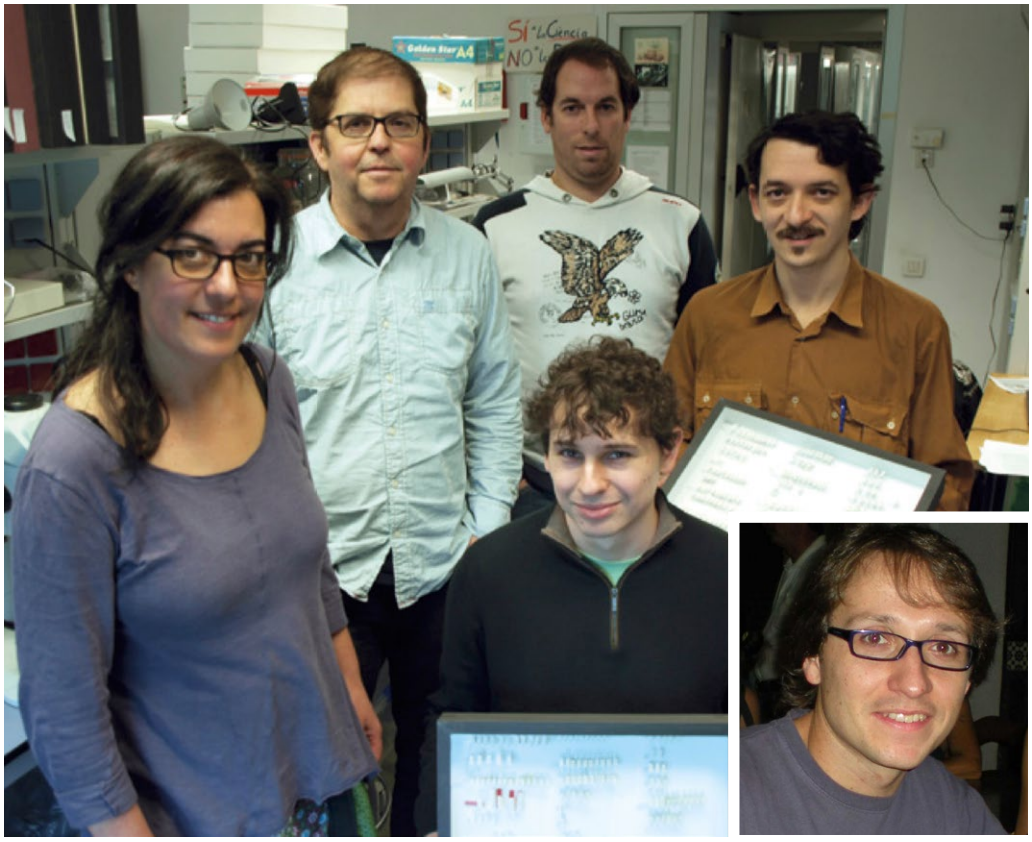
Fig. 6: Omanosaura jayakari
Photo: *Salvador Carranza*

Fig. 7: *Ferry to Al-Hallaniyah*
Photo: *Jiri Smith*

Fig. 8: *Taking a picture of a* Scincus *in the desert*
Photo: *Salvador Carranza*

Fig. 9: *Searching for lizards*
Photo: *Jiri Smith*

group WATER AND CAVE BEETLE EVOLUTION



Clockwise from left to right: Anabela Cardoso, Ignacio Ribera, David García-Vázquez, Andrey Rudoy, David Sánchez-Fernández (insert) and Adrián Villastrigo

group members

Ignacio Ribera, *Group Leader*
Research Scientist, CSIC

David Sánchez-Fernández, Postdoctoral Researcher,
Juan de la Cierva Program
David García Vázquez, PhD Student, MICINN Scholarship
Andrey Rudoy, PhD Student, JAE Scholarship, CSIC
Adrián Villastrigo Carbajo, PhD Student, MICINN Scholarship
Anabela Cardoso, Lab Manager, MICINN Contract

Research Outline

We study evolutionary processes using beetles, the world's most diverse group of animals. 250 MY of evolutionary history and a vast ecological and morphological variation enables us to use them to address virtually every problem in evolutionary biology. We use water and cave beetles to address different questions centred on the origin and distribution of biodiversity. Our current focus is the study of the causes and consequences of range expansions, and the evolution of adaptations to new habitats and ecologic conditions: the subterranean life in cave beetles and hypersaline waters in different lineages of aquatic beetles.

Research Lines

1. Thermal tolerance and Pleistocene range expansions

Most species have narrow geographic ranges, but many groups also include some widespread species. In most cases why and how these widespread species have reached their current ranges is unknown. One possibility is that they have wider thermal tolerances, allowing them to withstand a wider range of conditions. We test this in different lineages of aquatic and subterranean beetles, using phylogeographies, physiological experiments and proteomics.

Fig. 1: Pheggomisetes bureshi, *a groundbeetle of the tribe Trechini from Ledenika cave, in the Balkan mountains in Bulgaria, showing all typical characters of extreme troglobiont species: blind, unpigmented, and with elongated body and appendages.*

Photo: *A. Faille*

2. Origin of widespread species of European lotic water beetles

A particularly intriguing case is that of species with continental-scale distributions despite belonging to lineages with generally poor dispersal abilities. This is the case of some species of beetle typical of running waters that are widespread in central and northern Europe. We investigate the origin of these species, in an attempt to understand how they have reached their current distributions.

3. Evolution of the complex male genitalia in Hydraenidae

The extraordinary complexity of the male genitalia of some arthropods has always intrigued evolutionary biologists. Some genera of Hydraenidae combine an extremely uniform external morphology with a magnificent repertoire of aedeagal extravaganza. Using a comparative phylogenetic and morphometric approach we study the selective forces shaping the evolution of male genitalia in this group of beetles.

4. Conservation of Iberian water beetles

Inland waters are one of the most diverse but endangered ecosystems in Europe. Freshwater fauna is often neglected and poorly known, a situation we try to reverse. 2014 marks a milestone towards this objective, with the publication in collaboration with the Aquatic Ecology group of the University of Murcia of an Atlas of the ca. 500 species of Spanish water beetles.

5. Evolution of the tolerance to salinity

Life in water with salt concentrations many times that of seawater requires extreme physiological adaptations, which only few organisms have managed to acquire - among them several lineages of beetles. In a project in collaboration with the Aquatic Ecology group of the University of Murcia, we study the evolution of these adaptations in order to determine the mechanisms involved and how they originated.

Fig. 2: *An undescribed new species of* Hyphalus *from Rodrigues Island, in Mauritius. The minute species of this genus of Limnichidae live in the intertidal area, and lock themselves in small holes on the surface of fossil coral rocks when covered by sea water.*

Photo: *Ignacio Ribera*

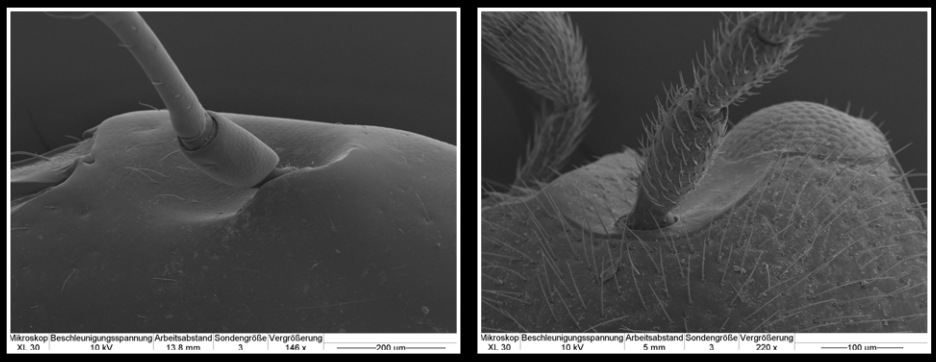


Fig. 3: *Some very specialized subterranean beetles can present a highly deviating morphology, especially in all sensorial organs. Above, the head of* Leptodirus hochenwartii *from Slovenia, the first species of subterranean invertebrate to be formally described in 1832; below, the head of a typical species of the same family (Leiodidae), living in forest litter, with what is likely the ancestral phenotype.*

Photo: *Ignacio Ribera*

Publications 2015

ISI Articles

Abellán, P. and Sánchez-Fernández, D. (2015). A gap analysis comparing the effectiveness of Natura 2000 and national protected area networks in representing European amphibians and reptiles. *Biodiversity and Consevation* 24: 1377-1390.

Aragón, P.; Sánchez-Fernández, D.; Abellán, P. and Varela, S. (2015). Effects of temporal bias on the assessment of an ecological perturbation: a case study of the Prestige oil spill. *Environmental Research Letters* 10: 094006.

Gutiérrez-Cánovas, C.; Sánchez-Fernández, D.; Velasco, J.; Millán, A. and Bonada, N. (2015). Similarity in the difference: changes in community functional features along natural and anthropogenic stress gradients. *Ecology* 96: 2458-2466.

Rizzo, V. and Comas, J. (2015). A new species of *Troglocharinus* Reitter, 1908 (Coleoptera, Leiodidae, Cholevinae, Leptodirini) from southern Catalonia, with a molecular phylogeny of the related species group. *Zootaxa* 3946: 104-111.

Fig. 4: *The river Sushitsa, in the Rhodopes mountains of Bulgaria, a typical low mountain stream flowing through a well preserved Mediterranean mixed forest*
Photo: *Ignacio Ribera*

Rizzo, V.; Sánchez-Fernández, D.; Fresneda, J.; Cieslak, A. and Ribera, I. (2015). Lack of evolutionary adjustment to ambient temperature in highly specialized cave beetles. *BMC Evolutionary Biology* 15: 10.

Sánchez-Fernández, D. and Abellán, P. (2015). Using null models to identify under-represented species in protected areas: a case study using European amphibians and reptiles. *Biological Conservation* 184: 290-299.

Sánchez-Fernández, D.; Millán, A.; Abellán, P.; Picazo, F.; Carbonell, J.A. and Ribera, I. (2015). Atlas of Iberian water beetles (ESACIB database). *Zookeys* 520: 147-154.

Other Publications

Fresneda, J.; Alfambra, F.; Bourdeau, C.; Faille, A. and Ribera, I. (2015). Nuevas capturas de *Aphaenops mensioni* Lagar, 1976, con un inventario de la fauna hipogea terrestre del parque nacional de Ordesa y Monte Perdido. *Exploracions* 21: 60-67.

In 2015 the Proyecto IDE@ was launched, a web portal intended to provide access to taxonomic and faunistic data of all 108 Orders of Arthropods present in the Ibero-macaronesian area: http://www.sea-entomologia.org/IDE@/

Alexander, K.A.; Melic, A. and Ribera, I. 2015. Orden Psocoptera. *Revista IDE@-SEA* 50: 1-13.

Melic, A.; Ribera, I. and Torralba, A . 2015. El proyecto IDE@. *Revista IDE@-SEA* 1: 1-14.

Ribera, I. and Melic, A. 2015. Orden Neuroptera s.s. (Planipennia). *Revista IDE@-SEA* 58: 1-12.

Ribera, I.; Melic, A. and Torralba, A. 2015. Introducción y guía visual de los artrópodos. *Revista IDE@-SEA* 2: 1-30.

Funded Projects

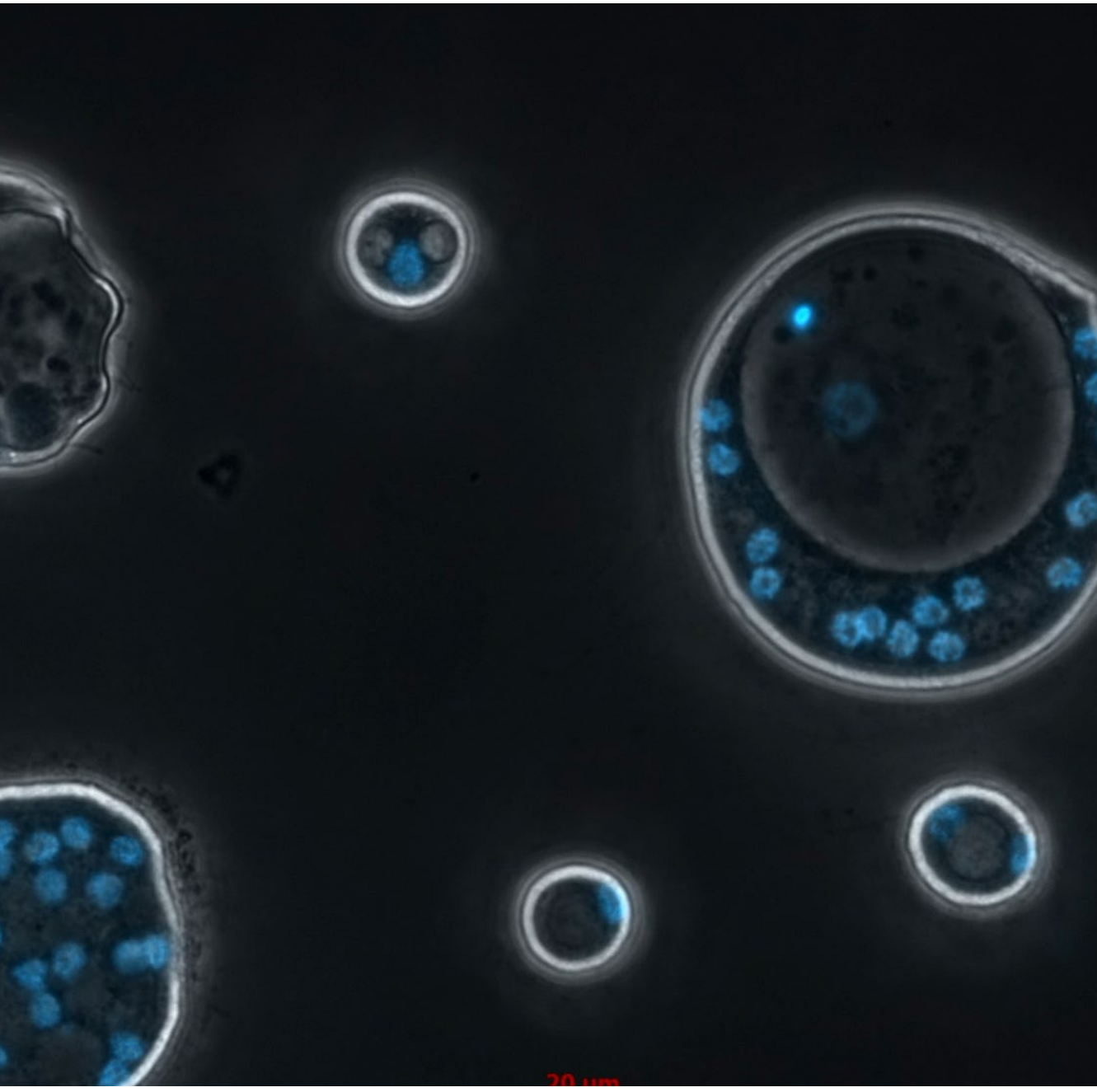
- **Project Title:** Evolution of habitat transitions in aquatic Coleoptera.
  Financed by: Ministerio de Ciencia e Innovación
  Years: 2014–2016
  PI: Ignacio Ribera

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014–2016
  PI: Salvador Carranza

Fig. 5: *Micro-hydroelectric power station in the oued Laou, in the Rif mountains. Despite the increasing anthropic pressure on its water resources, Morocco still harbours a rich an interesting aquatic fauna.*
Photo: *Ignacio Ribera*

PROGRAM

COMPARATIVE AND COMPUTATIONAL GENOMICS



Research Groups

Comparative Genomics
Tomàs Marquès-Bonet, *Group Leader*

Evolutionary and Functional Genomics
Josefa González, *Group Leader*

Subgroups
Evolutionary and Functional Genomics
Josefa González, *PI*

Drosophila Telomeres
Elena Casacuberta, *PI*

Evolutionary Genomics
Arcadi Navarro, *Group Leader*

Paleogenomics
Carles Lalueza-Fox, *Group Leader*

Genomes contain a wealth of information, not only about how phenotypes are shaped in interaction with the environment, but also about the evolutionary history of species. Thus, studying full genomes is key to answer the basic questions posed eight decades ago by the research paradigm created by the Synthetic Theory of Evolution: how much adaptation can we detect in nature?

In addition to the study of adaptation, genomics allows us to answer questions about other crucial evolutionary phenomena such as chromosomal evolution, speciation or the dynamics of transposable elements. Understanding these phenomena is fundamental in shedding light in issues as varied as hominization or the genetic architecture of complex phenotypes.

In the Comparative and Computational Genomics program, genes and genomes are compared at the intra and inter-specific levels with the general aims of understanding genome dynamics, reconstructing the evolutionary processes that generate biodiversity and linking genome diversity and function, with a recent emphasis on phenotypic differences between individuals and species. To achieve these goals, we deploy state-of-the-art techniques at both the experimental and numerical level.

group COMPARATIVE GENOMICS

From left to right and top to down: Marc de Manuel Montero, Tiago Carvalho, Aitor Serres, Claudia Fontsere, Jessica Hernadez, Irene Lobón, Raquel Garcia, Lukas Kuderna, Tomàs Marquès-Bonet

group members

Tomàs Marquès-Bonet, *Group Leader*
ICREA Research Professor

Martin Kuhlwilm, Postdoctoral Researcher
Inna Povolotskaya, Postdoctoral Researcher
Marc de Manuel, PhD Student
Claudia Fontsere, PhD Student
Raquel Garcia, PhD Student
Sojung Han, PhD Student
Jessica Hernadez, PhD Student
Lukas Kuderna, PhD Student
Irene Lobón, PhD Student, (co-directed with Eduardo Soriano, IRB)
Aitor Serres, PhD Student

Research Outline

Our main line of research is centered on the discovery of the extent of all kinds of genome variation within phenotypically different genomes. Specifically, we study genome variation (centered on CNVs), gene expression and epigenetic differences in the human species in the context of great ape evolution and other mammalian genomes such as canids. Our goal is to create an integrated view of genome evolution by studying changes in the composition, frequency, size and location at every major branch point of recent human evolution.

Research Lines

1. Genomic variation in ape genomes

Characterizing the variation of thousands of human genomes is standard today. However, primates (our closest relatives) are the ideal set of species for studying the evolution of these features from both mechanistic and adaptive points of view. In this line of research, we use genomic approaches in humans and primates to understand the impact of variants in the evolution of every species to provide a proper perspective to the differences among species.

2. Epigenetics and transcriptomics of non-human primates

DNA methylation is an epigenetic modification involved in regulatory processes such as cell differentiation during development, X-chromosome inactivation, genomic imprinting and susceptibility to complex disease. However, the dynamics of DNA methylation changes between humans and their closest relatives is still poorly understood. In this project, we evaluate methylation patterns in recent human evolution. We identified a significant positive relationship between the rate of coding variation and alterations of methylation at the promoter level.

3. Canid evolution

The domestic dog has been widely recognized as an important organism for studying the relationship between selection, genome variation and phenotypic diversity. Both dogs and wolves have been extensively surveyed using mtDNA, microsatellites and SNPs, but structural variation, including variation in multicopy gene families, has not been fully characterized in canines.

Publications 2015

Der Sarkissian, C.; [29 authors]; Marquès-Bonet, T.; Ryder, O.A.; McCue, M.; Rieder, S.; Leeb, T.; Slatkin, M. and Orlando, L. (2015). Evolutionary genomics and conservation of the endangered Przewalski's horses. *Current Biology* 25(19): 2577-83.

Dobrynin, P.; Liu, S.; Komissarov, A.; [16 authors]; Marquès-Bonet, T.; [3 authors]; Zijun, X.; Zhang, G. and O'Brien, S.J. (2015). Genomic Legacy of the African Cheetah, Acinonyx jubatus. *Genome Biology* 16: 277.

Gallego Romero, I.; [15 authors]; Marquès-Bonet, T.; Laurent, L.C.; Loring, J.F. and Gilad, Y. (2015). A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. *eLife* 23;4: e07103.

Hernando-Herraez, I.; Garcia-Perez, R.; Sharp, A.J. and Marquès-Bonet, T. (2015). DNA methylation: insights into human evolution. *Plos Genetics* 10;11(12): e1005661.

Hernando-Herraez, I.; Heyn, H.; Fernandez-Callejo, M.; Vidal, E.; Fernandez-Bellon, H.; Prado-Martinez, J.; Sharp, A.J.; Esteller, M. and Marquès-Bonet, T. (2015). The interplay between DNA methylation and sequence divergence in recent human evolution. *Nucleic Acid Research* 43(17): 8204-14.

Koepfli, K.-P.; Paten, B.; G10K consortium; O'Brien, S.J. (2015). The Genome 10K Project: A Way Forward. *Annual Review of Animal Biosciences* 3(1), 57-111.

Librado, P.; [34 authors]; Marquès-Bonet, T.; Nielsen, R.; Willerslev, E.; Kantanen, J.; Prokhortchouk, E. and Orlando, L. (2015). Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. *Proceedings of the National Academy of Sciences* 112(50): E6889-97.

Nam, K.; Munch, K.; Hobolth, A.; Dutheil, J.Y.; Veeramah, K.R.; Woerner, A.E.; Hammer, M.F.; Great Ape Genome Diversity Project; Mailund, T. and Schierup, M.H. (2015). Extreme selective sweeps independently targeted the X chromosomes of the great apes. *Proceedings of the National Academy of Sciences* 112(20): 6413-8.

Olalde, I.; Schroeder, H.; Sandoval-Velasco, M.; [14 authors]; Marquès-Bonet, T.; Gilbert, M.T.P.; Lalueza-Fox, C. (2015). A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures. *Molecular Biology and Evolution* 32(12): 3132-3142.

Ruiz-Orera, J.; Hernandez-Rodriguez, J.; Chiva, C.; Sabidó, E.; Kondova, I.; Bontrop, R.; Marquès-Bonet, T. and Albà, M.M. (2015). De novo gene emergence in human and chimpanzee. *Plos Genetics* 2015 11(12):e1005721.

Ruiz, S.; Lopez-Contreras, A.J.; Gabut, M.; [7 authors]; Marquès-Bonet, T.; Serrano, M.; Blasco, M.A.; Batada, N.N. and Fernandez-Capetillo, O. (2015). Limiting replication stress during somatic cell reprogramming reduces genomic instability in induced pluripotent stem cells. *Nature Communications* 6: 8036.

Sonay, T.B.; Carvalho, T.; Robinson, M.; Greminger, M.; Krützen, M.; Comas, D.; Highnam, G.; Mittelman, D.; Sharp, A.; Marquès-Bonet, T. and Wagner, A. (2015). Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. *Genome Research* 25(11): 1591-9.

Stevison, L.S.; Woerner, A.E.; Kidd, J.M.; Kelley, J.L.; Veeramah, K.R.; McManus, K.F.; Great Ape Genome Project, Bustamante, C.D.; Hammer M.F. and Wall, J.D (2015). The Time-Scale Of Recombination Rate Evolution In Great Apes. *Molecular Biology and Evolution* 33(4): 928-45.

Veeramah, K.R.; Woerner, A.E.; Johnstone, L.; Gut, I.; Gut, M.; Marquès-Bonet, T.; Carbone, L.; Wall, J.D.; Hammer, M.F. (2015). Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. *Genetics* 115.174425.

Warren, W.C.; [51 authors]; Marquès-Bonet, T.; Dewar, K.; Weinstock, G.M.; Wilson, R.K. and Freimer, N.B. (2015). The genome of the vervet (Chlorocebus aethiops sabaeus). *Genome Research* 25(12): 1921-33.

Xue, Y.; [20 authors]; Marquès-Bonet, T.; Tyler-Smith, C. and Scally, A. (2015). Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. *Science* 348(6231), 242-245.

Funded Projects

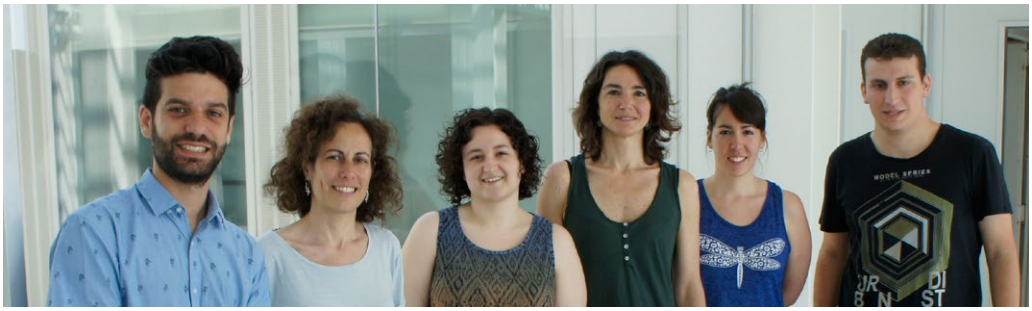
- **Project Title:** Somatic mutations in autism spectrum disorders (ASD): single neuron analysis
  Financed by: NIH
  Years: 2015–2020
  PI: Nenad Sestan and Christopher Walsh

- **Project Title:** Evolucion de la diversidad estructural del cromosoma y humano (BFU2014-55090-P)
  Financed by: MICINN (Spain)
  Years: 2015–2017
  PI: Tomàs Marquès-Bonet and Oscar Fornas

- **Project Title:** Structural variation and impact on gene expression of the human y chromosome (BFU2015-7116-ERC)
  Financed by: MICINN (Spain)
  Year: 2016
  PI: Tomàs Marquès-Bonet

- **Project Title:** Ebola genetics in gorilla (PRIC)
  Financed by: Fundació Zoo Barcelona
  Year: 2016
  PI: Tomàs Marquès-Bonet

group EVOLUTIONARY AND FUNCTIONAL GENOMICS



Top, from left to right: Quirze Rovira, Vivien Horváth, Jaione Arrizabalaga, Maite Barrón, Josefa González, Lain Guio, Jon Frías, Miriam Meneciano, Hung Le
Down, from left to right: Nicola di Stasi, Cristina Aresté, Silvia Chafino, Elena Casacuberta, Maria Rubio, Adrià Chorro

group members

Josefa González, *Group Leader*
Ramón y Cajal Researcher

Subgroups

Evolutionary and Functional Genomics

Josefa González, Ramón y Cajal Researcher
Maite G. Barrón, Postdoctoral Researcher, CSIC Contract
Hung Le Manh, Postdoctoral Researcher, VAST-CSIC Fellowship
Lain Guio, PhD Student, FI Fellowship
Anna Ullastres, PhD Student, FPI Fellowship
Jaione Arrizabalaga, Master Student
Vivien Horváth, Master Student, Erasmus Fellowship
Miriam Merenciano, Master Student
Jon Frias, Undergraduate Student
Quirze Rovira, Undergraduate Student

Drosophila Telomeres

Elena Casacuberta, Tenured Scientist, CSIC
Cristina Aresté, Postdoctoral Researcher, Moore Foundation
Sílvia Chafino, PhD Student, FPI Fellowship
Adrià Chorro, Master Student
Maria Rubio, Research Technician, Moore Foundation

Research Outline

1. The Evolutionary and Functional Genomics group uses transposable elements as a tool to unravel genome function and evolution.

2. The EvolMet group is interested in understanding the molecular mechanisms that govern insect metamorphosis, specifically the regulation of those players involved in reaching adulthood.

In addition, my group is also interested in understanding the diverse organization and evolution of different genomes. In this context we are currently involved in the study of some marine holozoa; Ministeria vibrans, Abeoforma whisleri, Pirum gemmata, Sphaeroforma arctica and Corallochytrium limacisporum.

Research Lines

Subgroup: **Evolutionary and Functional Genomics**

The key question in genomics is how genomes vary and evolve at both large and fine scales. In our lab, we are particularly interested in understanding the molecular processes underlying adaptive evolution and the functional consequences of adaptive mutations. Towards this end, we combine -omics strategies with detailed molecular and functional analyses of the candidate adaptive mutations in order to arrive at a comprehensive picture of adaptation. We study both transposable element (TE)-induced adaptations and point mutations in the model organism Drosophila melanogaster.

We are also interested in the population dynamics of TEs. TEs are the most active, diverse, and ancient components in a broad range of genomes. As such, a complete understanding of genome function and evolution cannot be achieved without a thorough understanding of TE impact and TE biology.

Subgroup: **Evolution of Insect Metamorphosis**

1. Despite dramatic differences between hemimetabolous and holometabolous insects, the metamorphic process in both types of insects is controlled by a series of conserved genes whose expression is linked to the action of the two principal metamorphic hormones, 20- hydroxyecdysone (20E) and juvenile hormone (JH).

These transcription factor-encoding genes, E93, Krüppel-homolog 1 (Kr-h1) and Broad-complex (Br-C), form a highly specific metamorphic gene network that we have defined as the "metamorphic toolkit". However, many gaps remain in our current knowledge about the different regulation and functioning of the toolkit in both types of insects. In this regard, our group works towards analyzing in detail what genetic and developmental innovations and changes in the metamorphic toolkit were required to allow the evolution of holometabolous metamorphosis.

2. In addition, part of my group is investigating different molecular tools to develop new model organisms from marine holozoans. We investigate in detail the life cycle of Ministeria vibrans, Abeoforma whisleri, Pirum gemmata, Sphaeroforma arctica and Corallochytrium limacisporum. We screen for antibiotic or selection agents, generating recombinant plasmids with endogenous promoters and fluorescent proteins. We are trying different molecular techniques to optimize the methodology to genetically transform these organisms, which are of key importance for subsequent investigations.

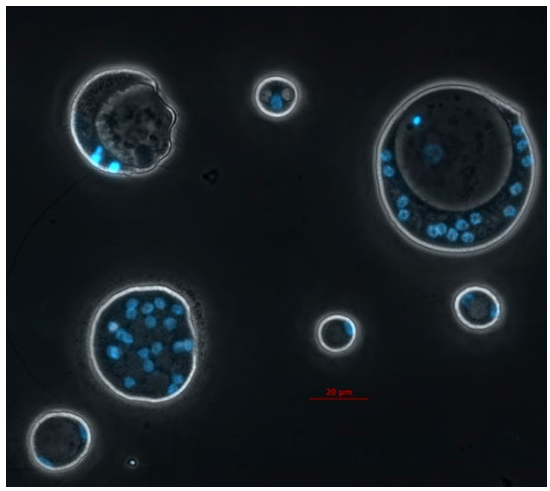


Fig. 1: *Colony of* Abeoforma whisleri *(Ichthyosporea) stained with Hoechst (nuclei in blue) in vivo.*
Image: *Maria Rubio and Cristina Aresté*

Publications 2015

Fiston-Lavier, A.-S.; Barrón, M.G.; Petrov, D.A. and González, J. T-lex 2: genotyping, frequency estimation and re-annotation of transposable elements using single or pooled next-generation sequencing data. *Nucleic Acids Research* 43(4): e22.

González, J.; Martinez, J. and Makalowski, W. (2015). Lack of population differentiation patterns of previously identified putatively adaptive transposable element insertions at microgeographic scales. *Biology Direct* 10: 50.

Guio, L. and González, J. (2015). The dominance effect of the adaptive transposable element insertion *Bari-Jheh* depends on the genetic background. *Genome Biology and Evolution* 7(5): 1260-1266.

López-Panadès, E.; Gavis and Casacuberta, E. (2015). Specific localization of the Drosophila telomere transposon proteins and RNAs, give insight in their behavior, control and telomere biology in this organism. *PLoS ONE* 8 e0128573.

Ullastres, A.; Petit, N. and González, J. Exploring the phenotypic space and the evolutionary history of a natural mutation in *Drosophila melanogaster*. *Molecular Biology and Evolution* 32(7): 1800-1814.

Funded Projects

- **Project Title:** Origen of metamorphosis: Molecular and evolutionary dissection of the metamorphic toolkit. CGL2014-55786
  Financed by: Plan Nacional I+D+I. Ministerio de Economía y Competitividad. Spain.
  Years: 2015–2017
  PI: Elena Casacuberta Suñer and David Martín

- **Project Title:** Screening Marine Holozoans, the closest relatives to Eukaryotes
  Financed by: Betty and Gordon Moore Foundation
  Years: 2015–2016
  PI: Iñaki Ruíz-Trillo; Elena Casacuberta Suñer co-IP

- **Project Title:** AdaptNET. Genomics of adaptation network (CGL2015-71726-REDT).
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2015–2017
  PI: Josefa González

- **Project Title:** Origin, diversification and diversity of metazoans, fungi and their unicellular relatives; an ecological and evolutionary approach (BFU2014-57779-P).
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2015–2017
  co-PI: Josefa González and Iñaki Ruiz-Trillo

- **Project Title:** El proceso molecular y las consecuencias funcionales de la adaptación (BFU2011-24397)
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2012–2015
  PI: Josefa González

- **Project Title:** The molecular process and functional consequences of adaptation (FP7-PEOPLE-2011-CIG-293860)
  Financed by: European Commission
  Years: 2011–2015
  PI: Josefa González

- **Project Title:** The process of adaptation and its functional consequences (RYC-2010-07306)
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2011–2015
  PI: Josefa González

- **Project Title:** Grup de Recerca en Evolució Genòmica Comparada (ECG, Evolutionary Comparative Genomics) (2014 SGR 1311)
  Financed by: Generalitat de Catalunya
  Years: 2011–2015
  co-PI: Elena Casacuberta and Josefa González

Outreach Projects

- **Project Title:** Melanogaster Catch The Fly
  Financed by: Fundación Española para la Ciencia y la Tecnologia
  Year: 2015
  PI: Josefa González

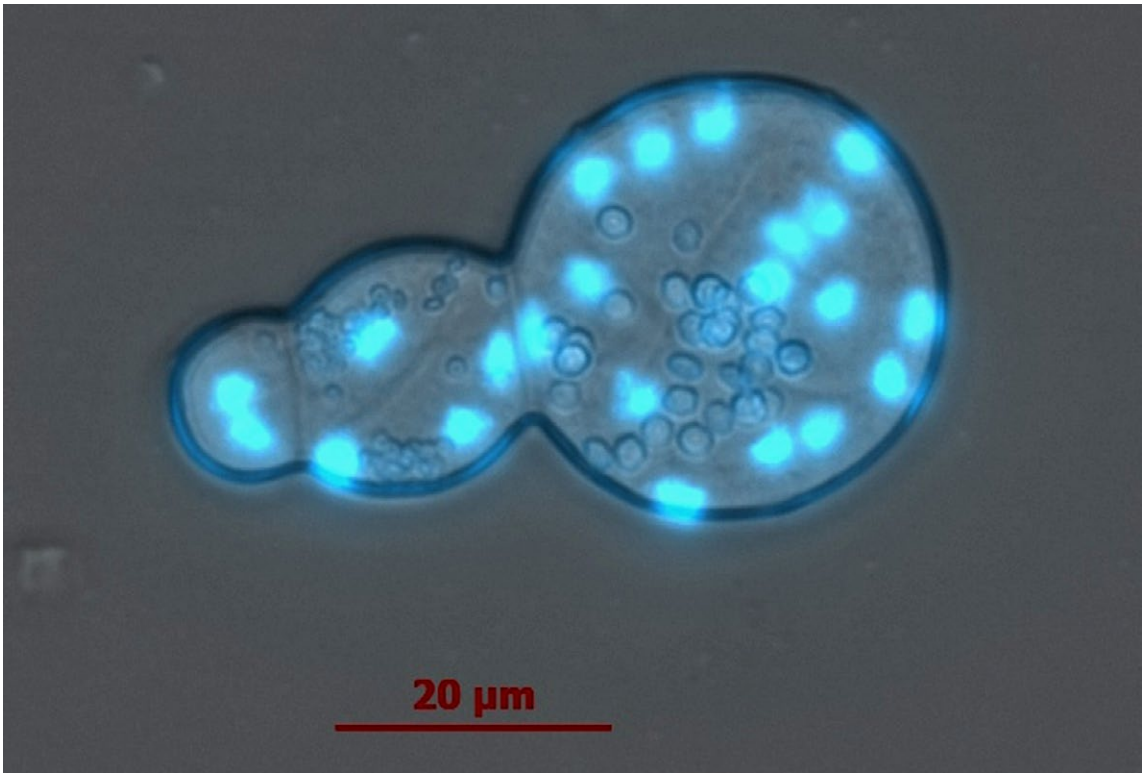
- **Project Title:** Jugant amb robots: la teoria evolucionista i els misteris del llenguatge
  Financed by: Professors i Ciència. Fundació Catalunya-La Pedrera
  Year: 2015
  PI: Josefa González

- **Project Title:** Com els organismes s'adapten a l'ambient
  Financed by: Joves i Ciència. Fundació Catalunya-La Pedrera
  Year: 2015
  PI: Josefa González

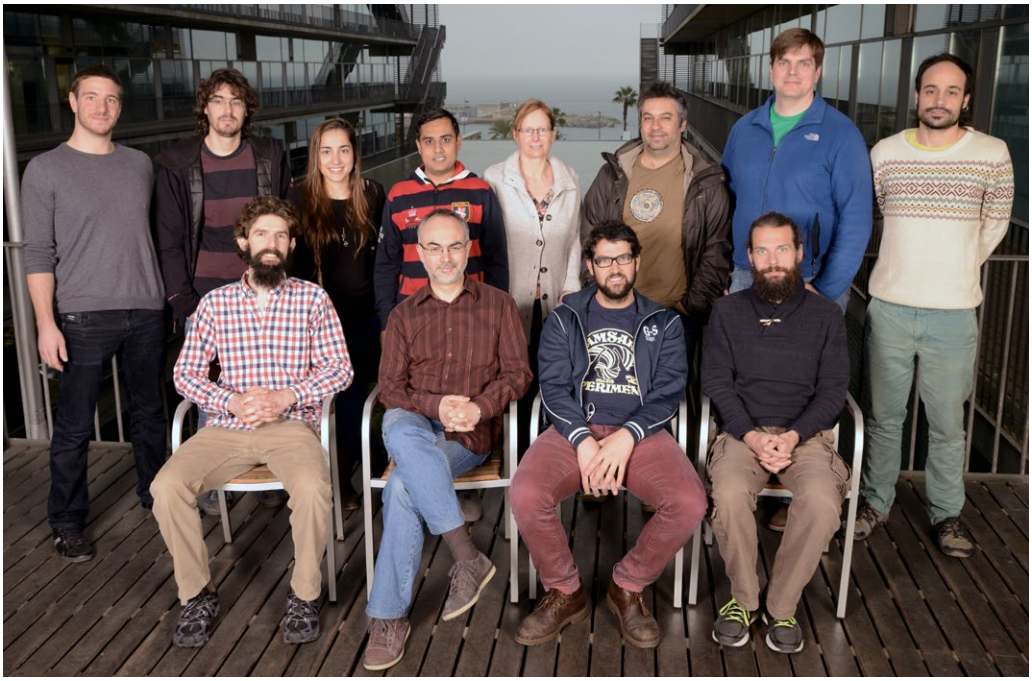
- **Project Title:** La genètica posada en pràctica
  Financed by: Joves i Ciència. Fundació Catalunya-La Pedrera
  Year: 2015
  PI: Elena Casacuberta

Fig. 2: Sphaeroforma arctica *(Ichthyosporea), nuclei stained in blue with DAPI*

Image: *Maria Rubio and Cristina Aresté*



group EVOLUTIONARY GENOMICS



From left to right and top to bottom: Marco Telford, Gabriel Santpere Baró, Marina Brasó Vives, Rajendra Haribau Mandage, Josephine Daub, Rui Miguel Faria de Maceira, David Hughes, Gerard Muntané Medina, Diego Andres Hartasánchez Frenk, Arcadi Navarro Cuartiellas (GL), Juan Antonio Rodriguez-Pérez, Txema Heredia Genestar

group members

Arcadi Navarro, *Group Leader*
Professor, UPF and Research Professor, ICREA

Josephine Daub, Postdoctoral Researcher, SNSF Fellowship (Swiss National Science Foundation)
Rui Faria, Postdoctoral Researcher, FCT Fellowship (Fundaçao Para a Ciência e a Tecnologia, Portugal)
David A. Hughes, Postdoctoral Researcher, Marie Curie Fellowship
Gerard Muntané, Postdoctoral Researcher, Project Contract
Gabriel Santpere, Postdoctoral Researcher, Project Contract
Marina Brasó, PhD Student, Project Contract
Diego Hartasánchez, PhD Student, JAE Fellowship (CSIC)
Txema Heredia, PhD Student, Project Contract
Rajendra Mandaje, PhD Student, Project Contract
Juan Antonio Rodríguez-Pérez, PhD Student, UPF PhD Grant
Marco Telford, PhD Student, Project Contract
Xavier Ferré, IT Technician, Project Contract
Edgar Pavel Salazar Fernández, Master Student
Irune Ruiz-Garcia, Undergraduate Student

Research Outline

Life on our planet today has been shaped by many different biological processes over billions of years. These processes leave a signature on our genomes in the form of differences between species, or between individuals of the same species. By investigating these patterns of genome diversity we can infer what forces affect living organisms, how and when they act, and how they affect such things as biodiversity, human emotions or people's different susceptibilities to disease. All this knowledge empowers us to control our future and, more importantly, is fun to obtain.

In practical terms, there are two main kinds of research we carry out in our group. First, we develop and analyze models that help to answer questions concerning natural selection, genome dynamics, speciation, comparative gene expression and the genetic architecture of complex human traits (including disease). The tools we use for these research lines include analytical and simulation studies, together with data mining and analysis. Second, we also carry out wet-lab research. We have recently focused on sequencing full viromes, and on studying viral gene expression levels in LCLs to analyze the evolution of virus-host interactions.

Research Lines

Currently, the main research goals of the group focus on elucidating how evolution, and particularly natural selection, has shaped genome and phenotypic diversity in our lineage. To this end, we combine experiments, models and data analysis. Some specific research lines are as follows:

1. Chromosomal evolution and speciation
We study how large chromosomal rearrangements affect many aspects of genome structure and evolution, including how they may drive the generation of new species.

2. Segmental duplications and copy-number variation in primates
The genomes of humans and other primates show enrichment in Segmental Duplications (SDs) with high sequence identity, plus they present many Copy-Number Variants (CNVs), large genome fragments of which different individuals present different copies. SDs and CNVs are fundamental for the creation of novel genes and may have been key in the evolution of our lineage. We study not only the frequencies and genome locations of these variants, but also the molecular evolution of their sequence content.

3. Detecting the genomic signature of natural selection
We try to detect the signature of adaptive changes in single-copy protein-coding regions. We focus on how natural selection may have shaped variability patterns in introns and regulatory regions of genes.

4. Human disease and its evolutionary implications
We study world-wide patterns of disease susceptibility distribution to ascertain how these may have been influenced by recent human evolution. In addition, we investigate the possible origins of Multiple Sclerosis and its possible relationship with very recent natural selection events in humans.

5. Genoeconomics
Complex human traits that are exclusive to our lineage are the basis of our societies and have great socio-economic impact. We deploy the latest tools in genomics for the dissection of human economic traits.

Publications 2015

Bustamante, M.F.; [22 authors]; Navarro, A.; Montalban, X. and Comabella, M. (2015). Pharmacogenomic study in multiple sclerosis patients responders and non-responders to IFNb. *Neurology: Neuroimmunology & Neuroinflammation* 2(5):e154.

Gil, E.; Spataro, N.; Malhotra, S.; Navarro, A.; Bosch, E.; Montalban, X. and Comabella, M. (2015). Search of causal variants in risk genes for multiple sclerosis by means of DNA-sequencing. *Multiple Sclerosis Journal* 21: 438 - 439.

Hartasánchez, D.A.; Brasó-Vives, M.; Fuentes-Díaz, J.; Vallès-Codina, O. and Navarro, A. (2015). SeDuS: segmental duplication simulator. *Bioinformatics* 32(1): 148-50.

Lappalainen, I.; [21 authors]; Navarro, A.; Paschall, J and Flicek, P. (2015). The European Genome-phenome Archive of human data consented for biomedical research. *Nature Genetics* 47: 692-695.

Montes, A.; Roca, G.; Sabate, S.; Lao, J.I.; Navarro, A. and Cantillo, J. Canet for the GENDOLCAT Study Group. (2015). Genetic and Clinical Factors Associated with Chronic Postsurgical Pain after Hernia Repair, Hysterectomy, and Thoracotomy. A Two-year Multicenter Cohort Study. *Anesthesiology* 122: 1123-1141.

Santpere, G.; Carnero-Montoro, E.; Petit, N.; Serra, F.; Hvilsom, C.; Rambla, J.; Heredia-Genestar, J.M.; Halligan, D.; Dopazo, H.; Navarro A. and Bosch, E. (2015). Analysis of five gene sets in chimpanzees suggests decoupling between the action of selection on protein-coding and on non-coding elements. *Genome Biology and Evolution* 7(6): 1490-505.

Spataro, N.; Calafell, F.; Cervera-Carles, L.; Casals, F.; Pagonabarraga, J.; Pascual-Sedano, B.; Campolongo, A.; Kulisevsky, J.; Lleó, A.; Navarro, A.; Clarimón, J. and Bosch, E. (2015). Mendelian genes for Parkinson's disease contribute to the sporadic forms of the disease. *Human Molecular Genetics* 24(7): 2023-34.

Book Chapters

Marigorta, U.M.; Rodriguez, J.A. and Navarro, A. (2015). GWAS replicability across time and space. In: Genome-Wide Association Studies: From Polymorphism to Personalized Medicine. Ed: Krisnarao Appasani. Cambridge University Press (Cambridge).

Marigorta, U.M.; Rodriguez, J.A. and Navarro, A. (2015). GWAS: a milestone in the road from genotypes to phenotypes. In: Genome-Wide Association Studies: From Polymorphism to Personalized Medicine. Ed: Krisnarao Appasani. Cambridge University Press (Cambridge).

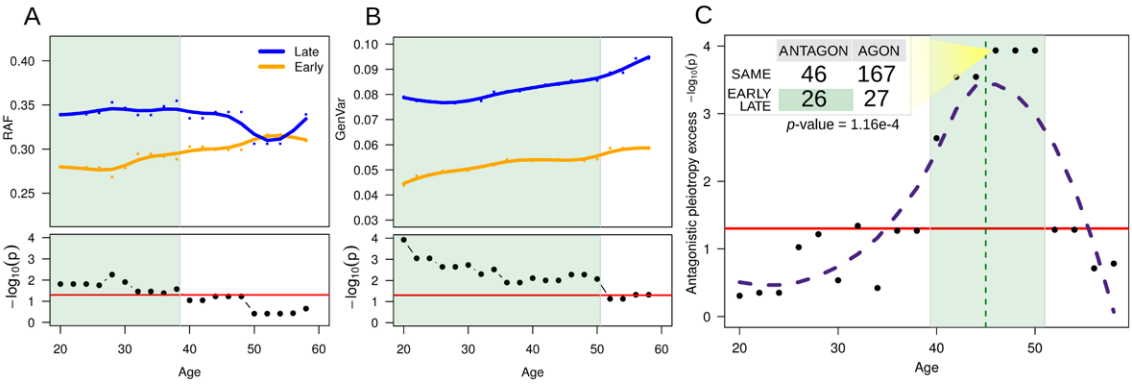


Fig. 1: *Evidence for mutation accumulation and antagonistic pleiotropy from GWAS SNPs characteristics.*

A) Risk Allele Frequencies (RAF) for SNPs associated with early or late onset conditions, as a function of the age threshold used to distinguish early from late. Significant differences are maintained for thresholds from 20 up to 38 years. Black dots represent the -log10 (p-value) at each age threshold (Wilcoxon 1-tail test; early vs. late RAFs for a moving threshold). The red horizontal line represents -log10(0.05) point in all graphs. Only associations with odds ratio ≥ 2 were considered for parts a and b.

B) The same as a, but displaying the average genetic variance explained by each group of SNPs as estimated by the heterozygosity of every SNP times the -log10(Odds Ratio).

C) A significant excess of antagonistic early-late pleiotropies between 40 and 50 years old. The Y-axis indicates -log10 (p-value) of the Chi-Square tests performed for pleiotropies at each age threshold as exemplified for an age-threshold of 46 years in table embedded.

Funded Projects

- **Project Title:** Toward a complete view of adaptation in complete genomes. A bottom-up approach to selection acting upon multiple targets
  Financed by: Ministerio de Economía y Competitividad -MINECO (BFU2012-38236)
  Years: 2013–2015
  PI: Arcadi Navarro

- **Project Title:** Group within the "Red Española de Esclerosis Múltiple" (Spanish Research Network in Multiple Sclerosis)
  Financed by: Within the RETICS (Redes Españolas de Investigación Cooperativa en Salud) on Multiple Sclerosis (RD12/0032/0011)
  Years: 2013–2015
  PI: Arcadi Navarro (Coordinator: Pablo Villoslada)

- **Project Title:** INB GN8
  Financed by: Instituto de Salud Carlos III (Instituto Nacional de Bioinformática)
  Year: 2015
  PI: Arcadi Navarro

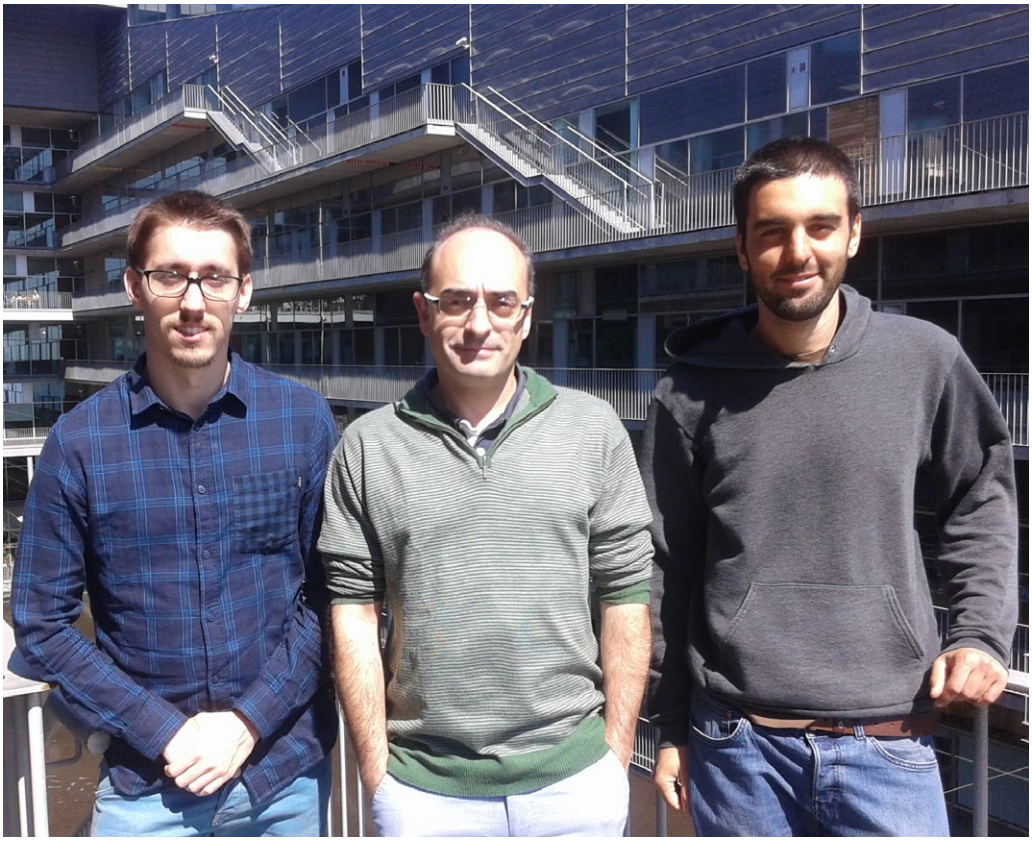
- **Project Title:** Grup de Recerca Consolidat-SGR
  Financed by: Generalitat de Catalunya (2014 SGR 1311)
  Years: 2014–2016
  PI: Arcadi Navarro

- **Project Title:** Developing an European American NGS Network (DEANN)
  Financed by: P7-2013-People-IRSES (International Research Staff Exchange Scheme) Marie-Curie Action (PIRSES-GA-2013-612583)
  Years: 2014–2016
  PI: Arcadi Navarro (Coordinator: Ana Conesa)

- **Project Title:** Fast-track ELIXIR implementation and drive early user exploitation across the life-sciences (Excellerate)
  Financed by: European Commission (INFRADEV-3-2015-676559)
  Years: 2015–2018
  PI: Arcadi Navarro

- **Project Title:** Creating medically-driven integrative bioinformatics applications focused on oncology, CNS disorders and their comorbidities (MedBioinformatics).
  Financed by: European Commission (H2020-PHC-32-2013 Call; Grant # 634143-2))
  Years: 2015–2018
  PI: Arcadi Navarro

group PALEOGENOMICS



From left to right: Íñigo Olalde, Carles Lalueza-Fox, Pere Gelabert Xirinachs

group members

Carles Lalueza-Fox, *Group Leader*
Research Scientist, CSIC

Íñigo Olalde, PhD Student, Basque Country Scholarship
Pere Gelabert Xirinachs, PhD Student

Fig. 1: *Typical Cardial early Neolithic pottery from Cova de la Sarsa in Valencia. The impressed decoration was made with the serrated edge of cockle shells.*

Research Outline

Our research group focuses on paleogenomics -the study of structure, function and organization of ancestral genomes. We are interested in different evolutionary problems that can be answered with ancient DNA data, involving human evolution, population dynamics and diversity, as well as adaptive processes and past migrations. We work with ancient modern humans and also with an extinct hominin species (the Neandertals). In our group we are basically interested in the genomic diversity among Neandertals, and in the individualization of a Neandertal family group from the El Sidrón site (Asturias, Spain). We are also investigating the evolutionary dynamics of the prehistory of Europe through the analysis of Mesolithic, Neolithic and Copper and Bronze Age human genomes.

Research Lines

1. Neandertal genomic diversity

We are analyzing different individuals from the El Sidrón site in Asturias, Spain. This is a family group of at least 13 Neandertal individuals that became accidentally accumulated in a single, synchronic event within a subterranean karstic system. El Sidrón offers the unique opportunity of launching a genomic project for understanding the diversity and kinship relationships within a contemporaneous Neandertal social group. This information will aid a better demographic modelling of the Neandertal extinction process.

2. European prehistory

We are interested in reconstructing the main cultural horizons and evolutionary shifts of European prehistory by analyzing past human genomes from different periods, including the Mesolithic-Neolithic transition and later periods such as the Copper and Bronze Age. We have retrieved the first Mesolithic European genome, that of La Braña-Arintero in León, Spain and the first Cardial agricultural genome. We are also analyzing Bell-Beaker Iberian samples for reconstructing the dynamics and nature of the expansion of the archaeological horizon and its role in the shaping of modern European genetic diversity. In addition, we are analyzing ancient samples from different periods to create an Iberian genomic transect.

Publications 2015

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Ramírez, O.; Rizzi, E.; Vai, S.; Venturo, D.; Piperno, M.; Lalueza-Fox, C.; Barbujani, G.; Caramelli, D. and Manzi, G. (2015). The Neanderthal in the karst: First dating, morphometric, and paleogenetic data on the fossil skeleton from Altamura (Italy). *Journal of Human Evolution* 82(0): 88-94.

Mathieson, I.; Lazaridis, I.; Rohland, N.; Mallick, S.; Patterson, N.; Roodenberg, S.A.; Harney, E.; Stewardson, K.; Fernandes, D.; Novak, M.; Sirak, K.; Gamba, C.; Jones, E.R.; Llamas, B.; Dryomov, S.; Pickrell, J.; Arsuaga, J.L.; de Castro, J.M.B.; Carbonell, E.; Lalueza-Fox, C. and Reich, C. (2015). Genome-wide patterns of selection in 230 ancient Eurasians. *Nature* 528: 499-503.

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Olalde, I.; Schroeder, H.; Sandoval-Velasco, M.; Vinner, L.; Lobón, I.; Ramírez, O.; Civit, S.; García Borja, P.; Salazar-García, D.C.; Talamo, S.; Fullola, J.M.; Oms, F.X.; Pedro, M.; Martínez, P.; Sanz, M.; Daura, J.; Zilhão, J.; Marquès-Bonet, T.; Gilbert, M.T.P.; Lalueza-Fox, C. (2015). A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures. *Molecular Biology and Evolution* 32(12): 3132-3142.

Ramírez, O.; Burgos-Paz, W.; Casas, E.; Ballester, M.; Bianco, E.; Olalde, I.; Santpere, G.; Novella, V.; Gut, M.; Lalueza-Fox, C.; Saña, M. and Pérez-Enciso, M. (2015). Genome data from a 16th century pig illuminate modern breed relationships. *Heredity* 114(2): 175-184.

Sánchez-Quinto, F. and Lalueza-Fox, C. (2015). Almost 20 years of Neanderthal paleogenetics: adaptation, admixture, diversity, demography and extinction. *Philosophical Transactions of the Royal Society B* 370: 20130374.

Vai, S.; Ghirotto, S.; Pilli, E.; Tassi, F.; Lari, M.; Rizzi, E.; Matas-Lalueza, L.; Ramírez, O.; Lalueza-Fox, C.; Achilli, A.; Olivieri, A.; Torroni, A.; Lancioni, H.; Giostra, C.; Bedini, E.; Baricco, L.P.; Di Gaetano, C.; Piazza, A.; Veeramah, K.; Geary, P.; Caramelli, D. and Barbujani, G. (2015). Genealogical Relationships between Early Medieval and Modern Inhabitants of Piedmont. *PLoS ONE* 10(1): e0116801.

Funded Projects

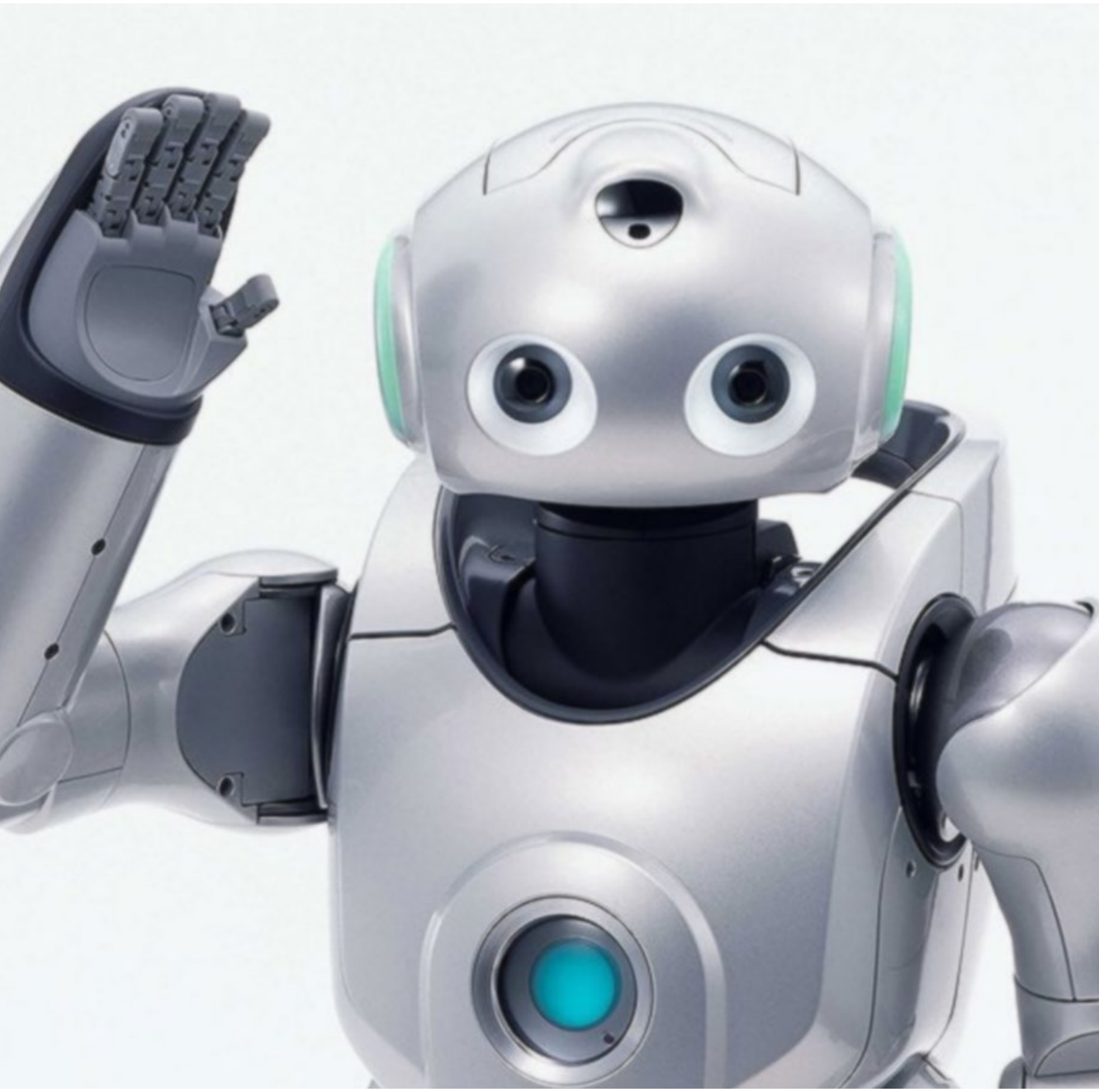
- **Project Title:** Evolutionary inferences from targeted sequence retrieval of Neandertal genomic regions (Ref: BFU2012-34157)
  Financed by: Ministerio de Economía y Competitividad
  Years: 2013–2015
  PI: Carles Lalueza-Fox

- **Project Title:** Grup de Recerca Consolidat en Biologia Evolutiva
  Financed by: Generalitat de Catalunya (2014 SGR 1311)
  Years: 2014–2016
  PI: Arcadi Navarro

Fig. 2: *Inside view of the Cova Bonica site in Vallirana (Barcelona). From this site, the complete genome of a 7,400 year-old Cardial individual was retrieved for first time in the Mediterranean area.*

PROGRAM

COMPLEX SYSTEMS



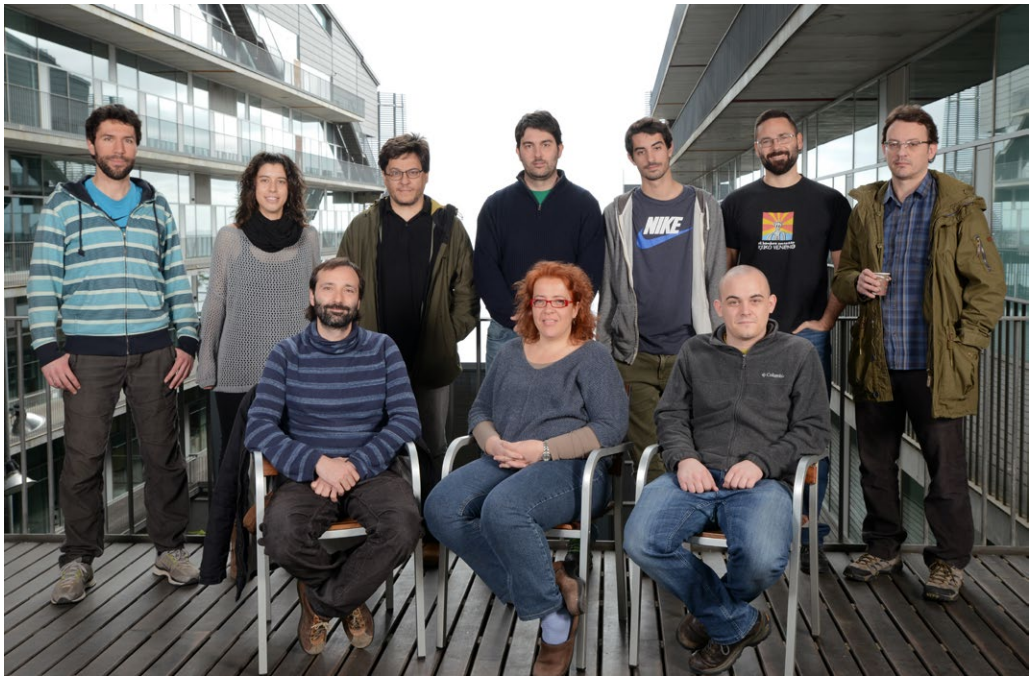
Research Groups

Evolution of Complex Systems
Ricard Solé, *Group Leader*

Language Evolution
Luc Steels, *Group Leader*

This program involves the study of the evolution and organizing principles of both natural and artificial complexity. Using theoretical as well as experimental methods, we study the design principles of natural, technological and synthetic systems and how major transitions can occur. We also explore the possible and the actual in artificially designed systems spanning multiple scales, from engineered bacteria to humanoid robots. Among our major fields of analysis, we study the origins of innovation and universal laws of organization associated to communication, computation, cultural and technological evolution, multicellularity and collective intelligence.

group EVOLUTION OF COMPLEX SYSTEMS



From left to right and top to down: Jordi Piñero, Ricard Solé, Aina Ollé, Josep Sardanyés, Daniel Rodríguez-Amor, Raúl Montañez, Sergi Valverde, Carlos Rodríguez-Caso, Eva García-Ramallo, Salvador Durán

group members

Ricard Solé, *Group Leader*
Professor, UPF and Research Professor, ICREA

Nuria Conde, Postdoctoral Researcher
Javier Macía, Postdoctoral Researcher, Associate Professor UPF
Raúl Montañez, Postdoctoral Researcher, UPF Project Contract
Daniel Rodríguez-Amor, Postdoctoral Researcher, UPF Project Contract
Carlos Rodríguez-Caso, Postdoctoral Researcher, UPF Project Contract
Jordi Sardanyés Cayuela, Postdoctoral Researcher, UPF Project Contract
Sergi Valverde, Postdoctoral Researcher, Visiting Professor UPF
Adriano Bonforti, PhD Student
Max Carbonell, PhD Student
Salvador Durán, PhD Student
Aina Ollé, PhD Student, UPF Project Contract
Jordi Piñero, PhD Student
Luis Seoane, PhD Student
Ben Shirt-Ediss, PhD Student
Eva García-Ramallo, Laboratory Technician

Research Outline

The ICREA-Complex Systems Lab, led by Ricard Solé, is formed by an interdisciplinary team that explores the evolution of complex systems, both natural and artificial, in search of their common laws of organization. We do both theoretical and experimental work, working in close collaboration with the Santa Fe Institute. We study the origins and evolution of complex systems and the boundaries of such complexity (and how to break them) using methods from statistical physics, synthetic/systems biology and network theory.

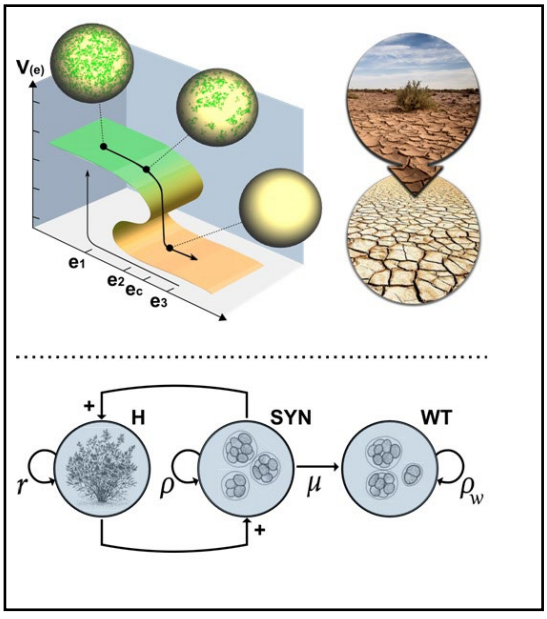
Research Lines

1. Bioengineering the biosphere

We explore (mathematically and experimentally) the potential scenarios that could allow us to redesign our biosphere using synthetic biology as a major engineering approach.

2. Major synthetic transitions

Synthetic biology, evolutionary robotics and artificial life allow us to re-create major innovations of biological evolution while searching for new ones. We want to make a new synthesis of major transitions in human-made, simulated, natural and synthetic systems and look for novel types of artificial transitions.



3. Unstable evolutionary dynamics

Both cancer populations and RNA viruses display high levels of genetic instability. We study how this unstable state contributes to adaptation and, perhaps, to new forms of therapy based on the presence of lethal thresholds.

4. Technological evolution

Both technology and biology share a number of relevant traits. Our lab explores the similarities and differences between them, with special attention to the origins of innovation and the physics of the underlying landscapes.

5. Cognitive networks

We study the architecture and evolution of language and brain networks. Our goal is to develop theoretical models of language emergence and change and explain the origins of their complexity.

6. Theoretical network evolution

We are developing theoretical models of network evolution, with a special interest in the open-ended nature of complexity, its hierarchical organization and the presence of catastrophes and breakpoints in large-scale dynamics

7. Synthetic biology and artificial life

We use approaches from artificial life and synthetic biology to explore questions related to information, multicellularity, collective intelligence and ecology as well as biomedical applications.

8. Biological computation

We explore how to create new forms of multicellular computation and how to build a complex biological computer. By evolving bio-inspired hardware and software, we also search for robust solutions to complex problems http://complex.upf.edu/

Fig. 1: *Biosphere engineering. We have mathematically explored the opportunities to engineer interacting motifs allowing the increase of water retention and therefore helping the manteinance or the rise of the vegatation cover.*

Publications 2015

ISI Articles

Castillo, V.; Lázaro, J.T.; and Sardanyés, J. (2015). Dynamics and bifurcations in a simple quasispecies model of tumorigenesis. *Computational and Applied Mathematics* 1-17.

Duarte, J.; Rodrigues, C.; Januário, C.; Martins, N. and Sardanyés, J. (2015). How complex, probable, and predictable is genetically-driven Red Queen chaos? *Acta Biotheoretica* 63: 341.

Duran-Nebreda, S. and Solé, R. (2015). Emergence of multicellularity in a model of cell growth, death and aggregation under size-dependent selection. *Royal Society Interface* 12: 20140982.

Guillamon, A.; Fontich, E. and Sardanyés, J. (2015). Bifurcations analysis of oscillating hypercycles. *Journal of Theoretical Biology* 387: 23.

Sardanyés, J.; Bonforti, A.; Conde, N.; Solé, R. and Macía, J. (2015). Computational implementation of a tunable multicellular memory circuit for engineered eukaryotic consortia. *Frontiers in Physiology* 6: 281.

Sardanyés, J.; Rodrigues, C.; Januário, C.; Martins, N.; Gil Gómez, G. and Duarte, J. (2015). Activation of effector immune cells promotes tumor stochastic extinction: A homotopy analysis approach. *Applied Mathematics and Computation* 252, 484-495.

Seoane, L. and Solé, R. (2015). Phase transitions in Pareto optimal networks. *Physical Review E* 92: 032807.

Shirt-Ediss, B.; Solé, R. and Ruiz-Mirazo, K. (2015). Emergent Chemical Behavior in Variable-Volume Protocells. *Life* 5(1), 181-211.

Solé, R. 2015. Bioengineering the biosphere? *Ecological Complexity* 22, 40-49.

Solé, R. and Seoane, L.F. 2015. Ambiguity in language networks. *The Linguistic Review* 32, 5-35.

Valverde, S.; Ohse, S.; Turalska, M.; West, B.J. and Garcia-Ojalvo, J. (2015). Structural Determinants of Criticality in Biological Networks. *Frontiers in Physiology* 6: 127.

Valverde, S. and Solé, R. 2015. Punctuated equilibrium in the large scale evolution of programming languages. *Journal of the Royal Society Interface* 12.

Funded Projects

- **Project Title:** SYNCOM
  Financed by: European research Council (ERC)
  Years: 2012–2017
  PI: Ricard Solé and Francesc Posas

- **Project Title:** Física estadística de cánceres inestables genómicamente
  Financed by: Ministerio de Economía y Competitividad (MINECO) (FIS 2012-39288)
  Years: 2013–2015
  PI: Ricard Solé

- **Project Title:** Cellular computation (Convenio de colaboración en materia de apoyo a la transferencia tecnológica en el campo de la biotecnología)
  Financed by: Fundación Marcelino Botín
  Years: 2010–2016
  PI: Ricard Solé

- **Project Title:** Evolució de Sistemes Complexes
  Financed by: Generalitat de Catalunya (SGR 497)
  Years: 2014–2016
  PI: Ricard Solé

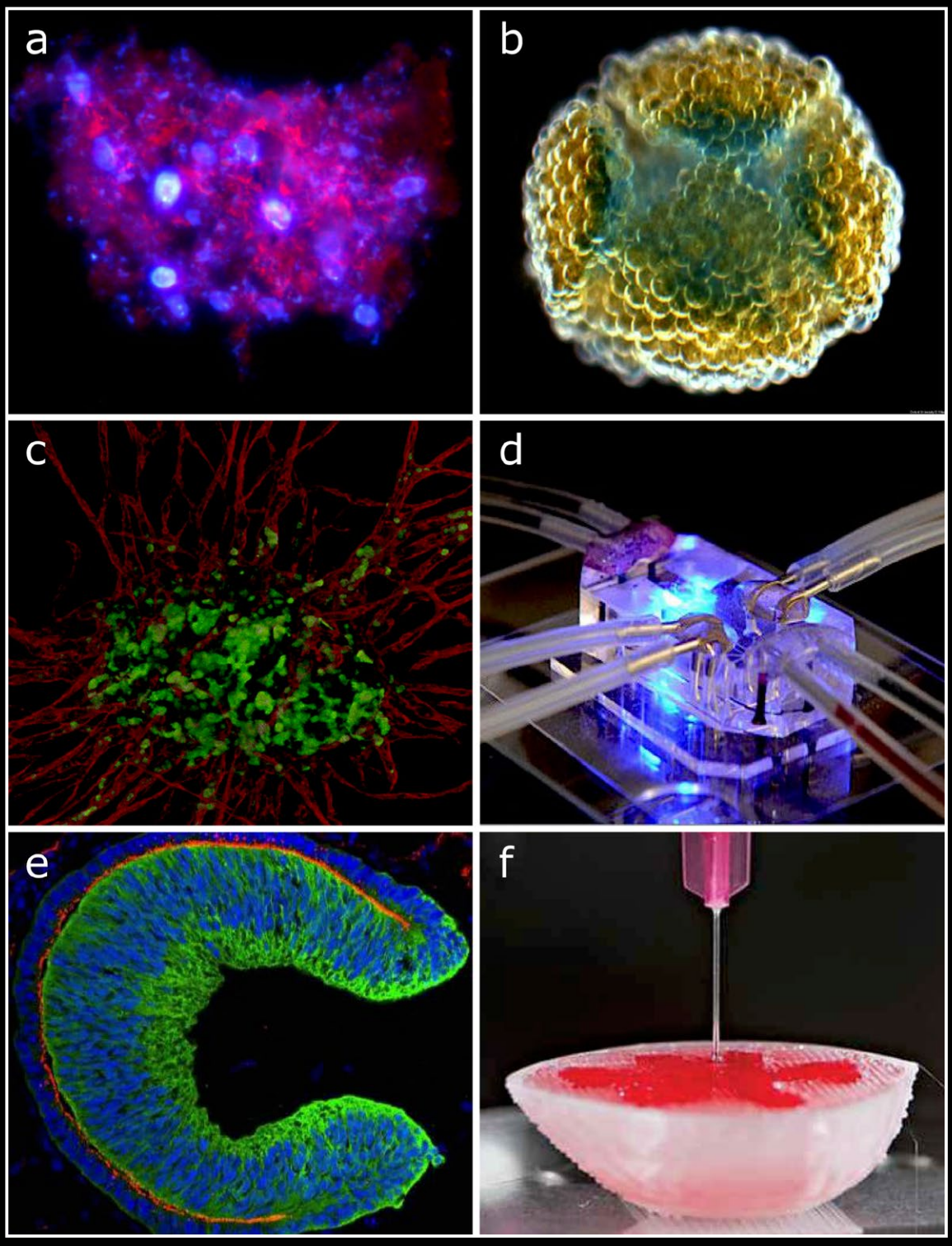
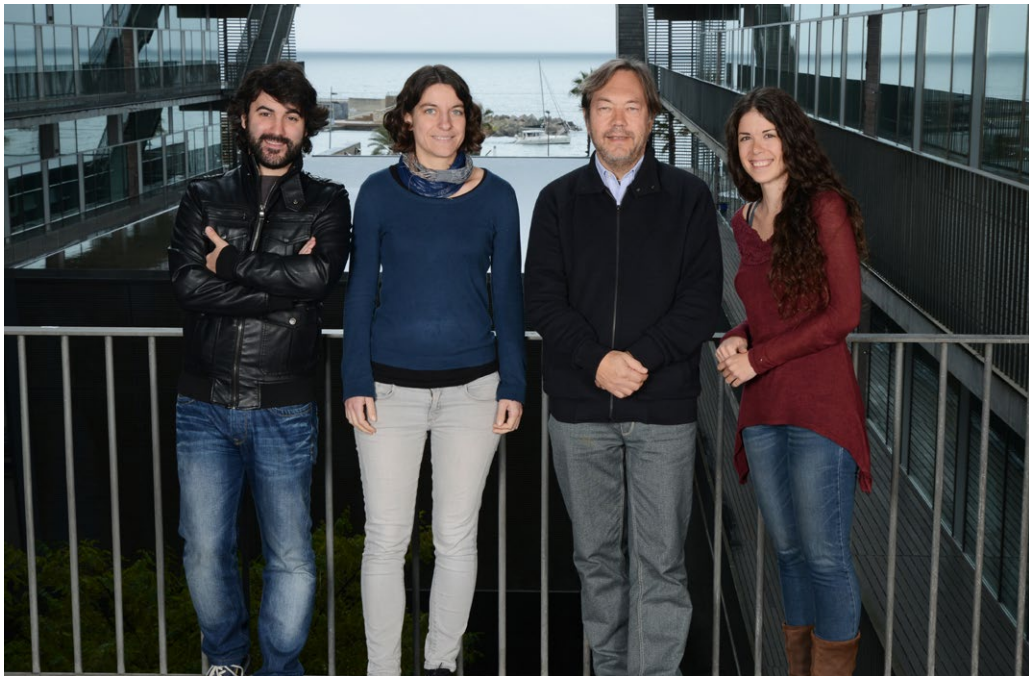


Fig. 2: *Morphospace of organs and organoids. We seek to understand the general rules of the set of structures generated by the evolution.*

group LANGUAGE EVOLUTION



From left to right: Jorge Diz Pico, Emilia García-Casademont, Luc Steels, Maria Ferrer

group members

Luc Steels, *Group Leader*
Research Professor, ICREA

Emília García-Casademont, PhD Student
Maria Ferrer Bonet, Research Assistant
Jorge Diz Pico, Research Assistant

Research Outline

The goal of our research is to develop a theory for the origins and evolution of language. Such a theory necessarily involves three aspects: social, cultural and biological. The social aspect should give us answers to the question "Why did humans start to talk?". The cultural aspect looks to explain how new language forms arise in language and keep on changing over time. The biological aspect addresses how the biological foundations for language may have arisen. We focus mostly on the cultural aspect, developing and testing agent-based models to explain how features of language, such as agreement systems, arise and culturally evolve.

Research Lines

1. Origins and evolution of grammatical structures

Although there is a lot of data about the historical change in language, there is virtually no theory of the fundamental processes underlying this kind of evolution. We try to understand the cognitive mechanisms, interaction patterns, and collective dynamics that could explain how grammatical structures arise in human language by building agent-based models and using the hypothesis that self-organization and (linguistic) selection are the primary driving forces. We analyze the behaviour of our models using the tools of complex systems science, and compare the results with phenomena observed in human languages. At this point we focus in particular on the origins of agreement systems and grammatical patterns (such as noun phrases).

2. Fluid Construction Grammar (FCG)

In order to conduct agent-based experiments in language evolution it is necessary to have a computational formalism that is capable of handling variation, flexibility and change. We are therefore working in collaboration with other research centres on the development of such formalism. The formalism takes a construction grammar viewpoint, which is more appropriate for modelling language evolution. It consists of data structures for representing linguistic knowledge and mechanisms for parsing, production and language learning. FCG has been released as open source and has a growing community of users (http://www.fcg-net.org/).

3. Neural implementations of Fluid Construction Grammar

To bridge the gap between computational models and neurobiology, we are investigating how a replicator dynamics model of the brain could potentially be used to implement the highly complex operations that Fluid Construction Grammar demands.

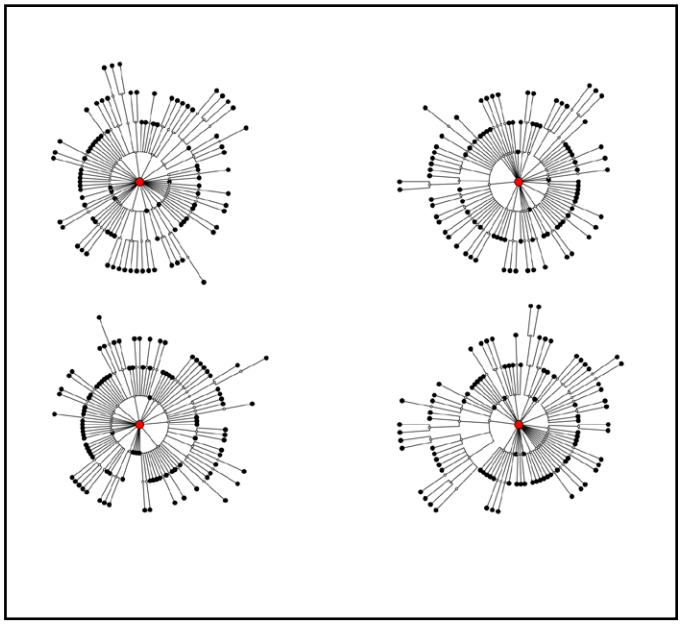


Fig. 1: *Various methods from evolutionary biology have been identified to study the evolutionary dynamics of language: analysis of a linguistic fitness landscape, glossogenetic trees analogous with phylogenetic trees, semiotic webs, and genotype-phenotype mappings. Here we show glossogenetic trees of 4 different agents from of a population jointly constructing a shared phrase structure grammar. Every node in the trees represents a construction, and edges represent its offspring, which are constructions made by reusing material from the parent constructions.*

Publications 2015

Garcia-Casademont, E. and Steels, L. (2015). Usage-based Grammar Learning as Insight Problem Solving. *Proceedings of EAP* CogSci 1419: 258-263.

Spranger, M. and Steels, L. (2015). Co-Acquisition of Syntax and Semantics — An Investigation in Spatial Language. *Proceedings of IJCAI*'15 1909-1915.

Steels, L. and Garcia-Casademont, E. (2015). Ambiguity and the origins of syntax. *The Linguistic Review* 32(1), 37-60.

Steels, L. and Garcia-Casademont, E. (2015). How to Play the Syntax Game. *Proceedings of ECAL* 2015 479-486.

Books

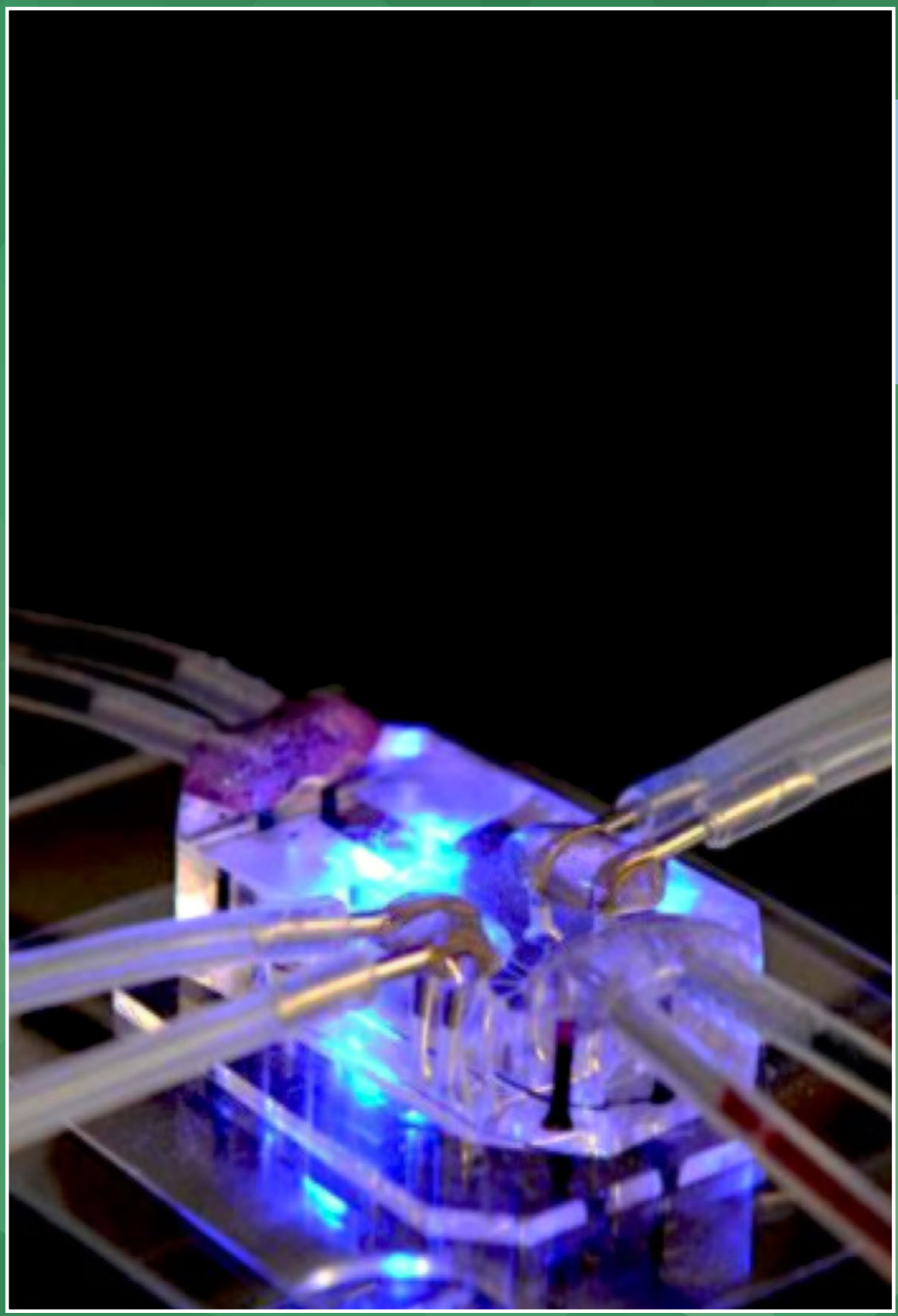
Steels, L. (2015). The Talking Heads Experiment. Berlin: Language Science Press.

Funded Projects

- **Project Title:** LANGEVO
  Financed by: EU Marie Curie Integration Grant
  Years: 2011–2015
  PI: Luc Steels

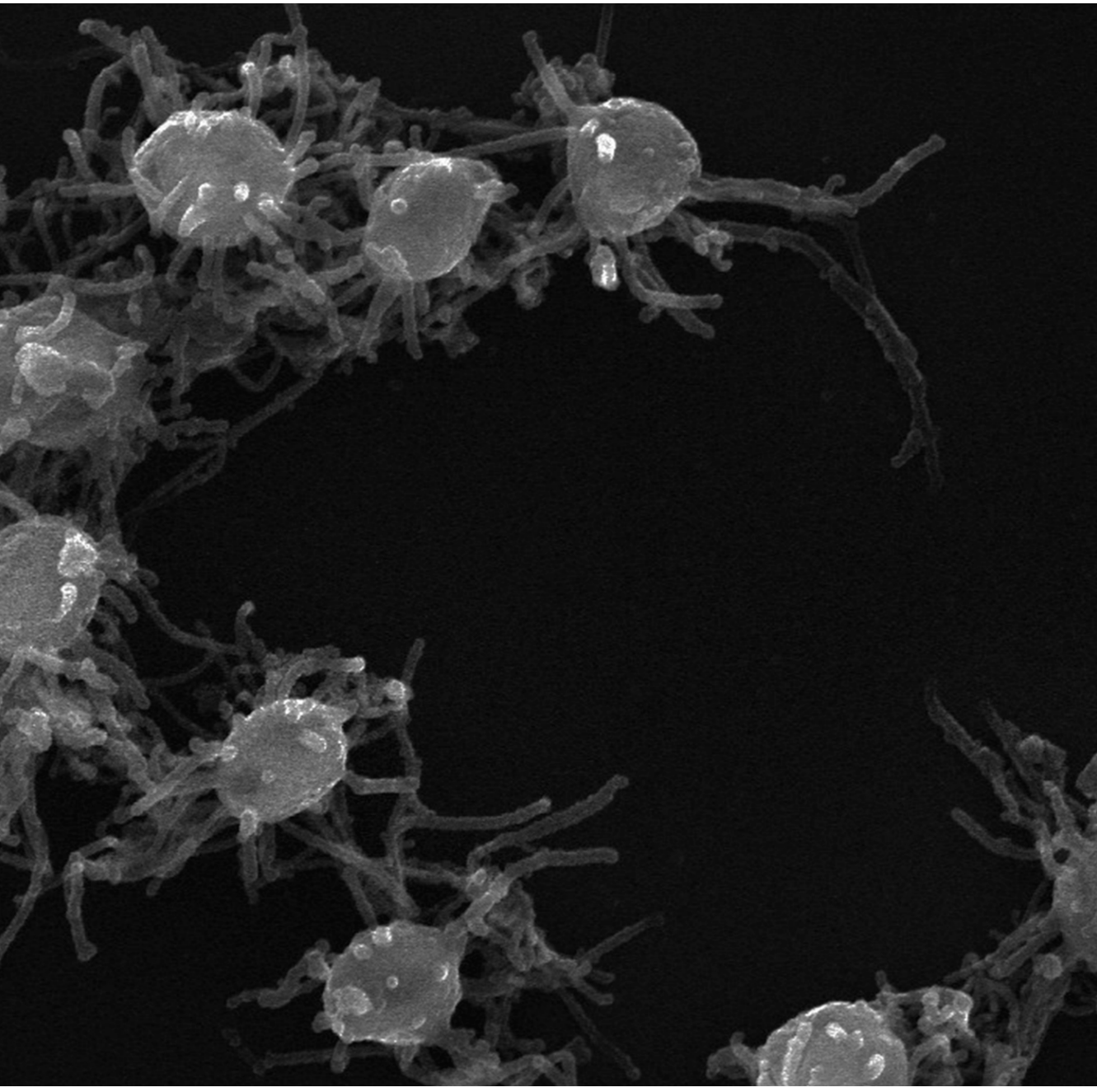
- **Project Title:** INSIGHT - Darwinian Neurodynamics
  Financed by: FP7-EU
  Years: 2013–2016
  PI: Luc Steels

- **Project Title:** ATLANTIS
  Financed by: CHIST-ERA (EU)
  Years: 2015–2018
  PI: Luc Steels



PROGRAM

FUNCTIONAL GENOMICS AND EVOLUTION



Research Groups

Evolution and Developmental Biology
Xavier Franch-Marro, *Group Leader*

Subgroups

Morphology and Signalling
Xavier Franch-Marro, *PI*

Hormonal Control of Insect Development
David Martín, *PI*

Insect Physiology and Molecular Biology
Xavier Bellés, *Group Leader*

Subgroups

Evolution of Insect Metamorphosis
Xavier Bellés, *PI*

Nutritional Signals in Insects
José Luis Maestro, *PI*

Insect Reproduction
Maria-Dolors Piulachs, *Group Leader*

Multicell Genome
Iñaki Ruiz-Trillo, *Group Leader*

The synthesis of evolution, paleontology, genomics and development led to the *new* field of Evolution and Development (so called EvoDevo). The aim of EvoDevo is to approach basic evolutionary questions taking into account the embryological (developmental) data but with a wider, comparative perspective. Our program goes one step forward, by combining evo-devo analyses with functional genomics approaches. The goal is to study fundamental biological questions, such as the evolution of multicellularity, development, growth, metamorphosis and oogenesis.

Most evolutionary research has been restricted to model animal systems, some of which turned out to be rather derived taxa. Our program aims at exploring new horizons by creating new data from yet neglected taxa. Thus, to address our questions, we use both model (*Drosophila melanogaster*) and non-model species (cockroaches, like *Blattella germanica*, beetles, like *Tribolium castaneum*, and unicellular eukaryotes like *Capsaspora owczarzaki* and *Creolimax fragrantissima*). By further developing these new non-model species, we aim to generate data promising to provide new insights into these important evolutionary questions.

In the context of the IBE, this program follows a well differentiated approach since it combines both comparative data generation on a great number of taxa, and at the application of a number of different technical methodologies, such as cell and developmental biology and comparative genomics.

group EVOLUTION AND DEVELOPMENTAL BIOLOGY

Group photo, from left to right: Silvia Chafino, David Martín, Xavier Franch-Barro, Joan Valls, Nicola di Stasi, Adrià Chorro, Elena Casacuberta
Bottom, from left to right: Cristina de Miguel, Mohammed Rahman, Neus Bota

group members

Xavier Franch-Marro, *Group Leader*
Tenured Scientist, CSIC

Subgroups

Morphology and Signalling

Xavier Franch-Marro, Group Leader, Tenured Scientist, CSIC
Mohammed Rahman, Postdoctoral Researcher
Neus Bota Rabassedas, PhD Student, FPI Scholarship, MEC
Cristina Miguel Vijandi, PhD Student, FPI Scholarship, MEC
Joan Valls, Master Student, UB

Hormonal Control of Insect Development

David Martín, Principal Investigator, Tenured Scientist, CSIC
Silvia Chafino, PhD Student, FPI Scholarship, MEC
Adrià Chorro, Master Student UB
Nicola di Stasi, Master Student UB

Research Outline

Throughout the Earth's history, evolution has developed a great number of different organisms with an incredible variety of forms and sizes. These morphologies are tailored during development, by modifying the expression pattern of key genes as well as by the modulation of hormone activation. Thus, our main goal is to understand how changes in gene and hormone regulation affect morphology evolution. We address these questions by using insects as an experimental model, particularly comparing development in *Drosophila melanogaster*, *Tribolium castaneum*, and *Blattella germanica*.

Research Lines

Subgroup: Morphology and Signalling

1. Tracheal System Remodelling and Evolution

The tracheal system is the insect respiratory organ and consists of epithelial tubes, the morphogenesis of which is controlled by distinct sets of signalling pathways and transcription factors. At metamorphosis, the tracheal system undergoes a deep remodelling stage, giving rise to pupae and the tracheal system. This remodelling involves the proliferation of cells that re-enter the cell cycle and regain development potency. Therefore, we aim to discover new genes and signalling pathways involved in such processes.

2. Evolutionary changes in organ morphology allow animals to better exploit diverse habitats

Insects present different morphologies of the tracheal network depending on their habitat. Thus while in Tribolium, tracheal branches are connected to two lateral openings per segment, in Drosophila two thick longitudinal branches extend through the larva from only two posterior openings. We found that changes in the expression pattern of the mutually repressed spalt and cut transcription factors explain the formation of thick tubes and the number of openings respectively. We aim thus to define a molecular mechanism underlying the combined evolution of independent but functionally related structures.

Subgroup: Hormonal Control of Insect Development

1. Genetic and Endocrine basis for the evolution of insect metamorphosis

Holometabolous insects evolved from hemimetabolan ancestors, although the mechanisms underlying this transition are yet to be identified. Our group is characterizing the mechanistic and regulatory changes that underlie the evolution of Holometaboly, focusing, in particular, on the functional characterization of a conserved regulatory metamorphic toolkit formed by three critical genes, E93, Kr-h1 and Br-C.

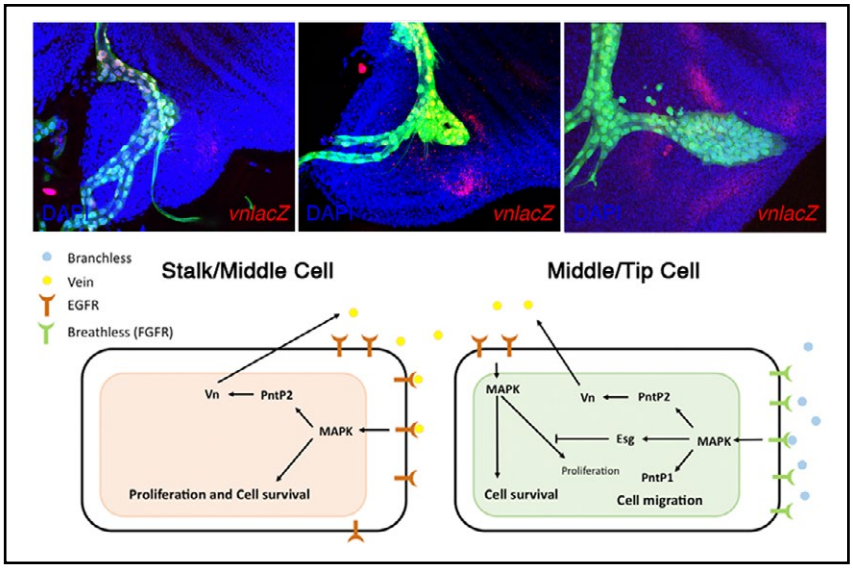


Fig. 1: *Expression of EGF ligand* vein *in the developing Air Sac Primourdium in early, mid and late* Drosophila *L3 instar larva. Diagram depicting the concomitant activation of two RTKs signaling pathways required for outgrowth of the air sac precursors.*

2. Role of E93 in the regulation of insect metamorphosis

Very recently, our group identified E93 as the critical master gene of the metamorphic toolkit that promotes adult differentiation in hemimetabolous and holometabolous insects (Ureña et al., PNAS 2014). Given the metamorphic relevance of E93, our group is currently trying to identify (1) the developmental signals that induce the stage-specific induction of E93 when the appropriate stage of development is attained; and (2) the mechanisms, at the molecular level, of the mode of action of E93 during hemimetabolan and holometabolan metamorphosis.

3. Evolution of SUMO protein functions in insect metamorphosis

Post-translational modification with the small ubiquitin-like modifier, SUMO, is a widespread mechanism for rapid and reversible changes in protein function. In collaboration with the laboratory of Dr. Rosa Barrio (CIC bioGUNE, Vizcaya), we are addressing the functional role of sumoylation in the metamorphosis of hemimetabolous and holometabolous insects.

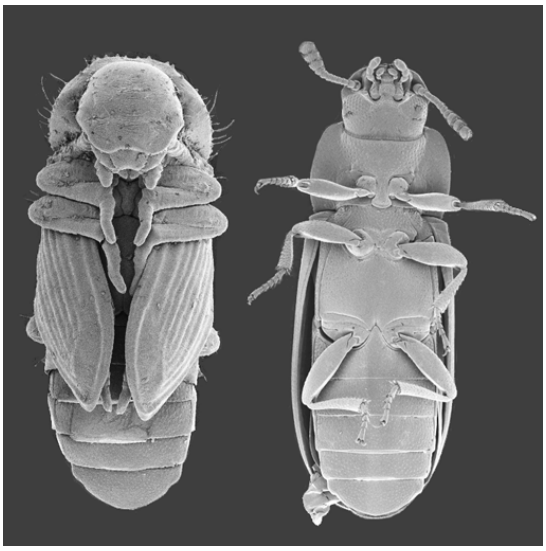


Fig. 2: *Scanning electron microscopy photographs of a pupa (left) and adult (right)* Tribolium castaneum, *an holometabolous insect model used in our laboratory to study the role of the metamorphic toolkit genes, E93, Kr-h1 and Br-C, in the evolution of complete metamorphosis.*

Publications 2015

Cruz, J.; Bota-Rabassedas, N. and Franch-Marro, X. (2015). FGF coordinates air sac development by activation of the EGF ligand Vein through the transcription factor PntP2. *Scientific Reports* 5: 17806.

Herboso, L.; Oliveira, M.M.; Talamillo, A.; Pérez, C.; González, M.; Martín, D.; Sutherland, J.D.; Shingleton, A.W.; Mirth, C.K. and Barrio, R. (2015). Ecdysone promotes growth of imaginal discs through the regulation of Thor in *D. melanogaster*. *Scientific Reports* 5: 12383.

Ureña, E.; Pirone, L.; Chafino, S.; Pérez, C.; Sutherland, J.D.; Lang, V.; Rodriguez, M.S.; Lopitz-Otsoa, F.; Blanco, F.J.; Barrio, R. and Martín, D. (2015). Evolution of SUMO function and chain formation in insects. *Molecular Biology and Evolution* 33(2): 568-84.

Funded Projects

- **Project Title:** Origin of insect metamorphosis: dissection and evolution of the metamorphic gene toolkit
  Financed by: Ministerio de Economía y Competitividad. CGL2014-55786-P.
  Years: 2015–2017
  PI: David Martín and Elena Casacuberta

- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2015 SGR 619)
  Years: 2014–2016
  PI: Xavier Bellés

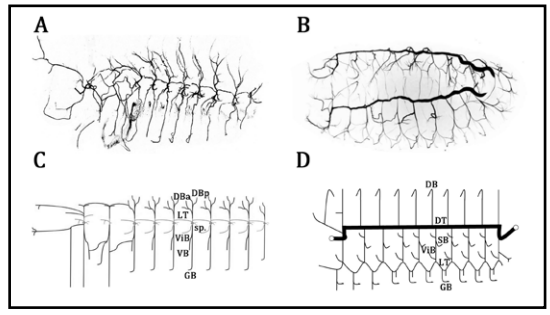


Fig. 3: *Whole-mount* Tribolium *(A) and* Drosophila *(B) embryos immunostained with the 2A12 antibody showing the branches of the fully developed embryonic tracheal system. (B-C) Schematic representation of the* Tribolium *(C) and* Drosophila *(D) embryonic tracheal trees.*

group INSECT PHYSIOLOGY AND MOLECULAR BIOLOGY

Top, from left to right: Judy Wexler, Xavier Bellés, Mahboubeh Naghdi, Ana Fernández Nicolás, Elena Navas, Guillem Ylla
Bottom, from left to right: Marc Castells, José Luis Maestro, Ainoa Marín

group members

Xavier Bellés, *Group Leader*
Research Professor, CSIC

Subgroups

Evolution of Insect Metamorphosis

Xavier Bellés, Research Professor, CSIC
Ana Fernández Nicolás, PhD Student, MICINN Scholarship
Mahboubeh Naghdi, PhD Student, Tehran University Scholarship
Judy Wexler, visiting PhD Student from University of California
Elena Navas, Graduate Student, Project Contract
Guillem Ylla Bou, Bioinformatician, Project Contract
Núria Sanchez, Lab Manager, Project Contract

Nutritional Signals in Insects

José Luis Maestro, Tenured Scientist, CSIC
Ainoa Marín, Undergraduate Student, Universitat de Barcelona
Marc Castells, Undergraduate Student, Universitat de Barcelona

Research Outline

We study the origin and evolution of insect metamorphosis, a line headed by Xavier Bellés, and the physiological and developmental effects of nutritional signals, headed by José Luis Maestro, using the cockroach Blattella germanica as model.

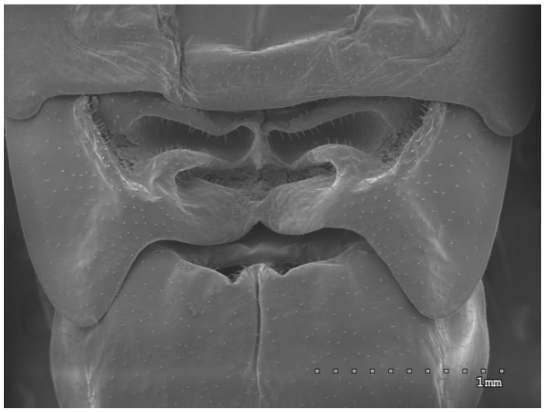


Fig. 1: *The tergal gland of adult male German cockroach, a complex structure formed during adult morphogenesis that can serve as a model of dramatic metamorphosis in a hemimetabolan insect*.

Image: *Guillem Ylla and Xavier Bellés*, 2015

Research Lines

Subgroup: Evolution of Insect Metamorphosis

Our goal is to elucidate the endocrine regulation of metamorphosis in B. germanica and then compare our results with data for holometabolans. The idea is to describe the evolutionary history underlying the transition from hemimetaboly to holometaboly. We work at different levels, from comparative transcriptomics to functional genomics using RNAi, not only on pre-adult nymphal stages, but also on the embryo, where the essential differences between hemimetaboly and holometaboly are to be sought. In postembrionic development, comparisons of tergal gland transcriptomes in metamorphic and non-metamorphic transitions led us to identify important genes involved in metamorphosis, like E93 (a transcription factor that triggers metamorphosis), Nejire (a CREB-binding protein), and Smad factors (from the TGFß signaling pathway). In the last nymphal stage we study the fine regulation of the MEKRE93 pathway: Methoprene-tolerant (Met) and Taiman, the two components of the juvenile hormone (JH) receptor Krüppel homolog 1 (Kr-h1), the main transductor of the repressing signal of JH, and E93, the trigger of metamorphosis. In embryos we are characterizing the regulation of key developmental transitions, looking at hormonal influence and at the transcription factors and microRNAs. We have shown that microRNAs have important functions in metamorphosis, like the role played by miR-2 scavenging the transcripts of Kr-h1 at the beginning of the last instar nymph of B. germanica. This facilitates an increase in E93 expression, which triggers the adult morphogenetic programme and metamorphosis (see IBE highlighted papers in this issue).

Subgroup: Nutritional Signals in Insects

Our research tries to understand how nutritional signalling pathways (insulin receptor and TOR) inform cells and tissues on nutritional status in order to control the hormonal and metabolic processes necessary for reproduction. We perform expression studies under different experimental conditions (RNAi treatments, different reproductive status, feeding-starvation, etc) to detect transcriptional changes derived from these situations. We have demonstrated the involvement of a structurally singular ribosomal S6 kinase, a key factor of TOR pathway, on juvenile hormone and vitellogenin synthesis. Moreover, we are currently working on insulin-like peptides (ILPs) and reproduction, and we have shown that seven discovered B. germanica ILPs are differentially expressed in tissues, respond differently to nutritional conditions and play different roles in reproduction, according to RNAi studies.

Publications 2015

Bellés, X. and Piulachs, M.D. (2015). Ecdysone signalling and ovarian development in insects: from stem cells to ovarian follicle formation. *Biochimica et Biophysica Acta* 1849(2): 181-186.

Dillon, M.B.; Schulten, V.; Oseroff, C.; Paul, S.; Dullanty, L.M.; Frazier, A.; Bellés, X.; Piulachs, M.D.; Visness, C.; Bacharier, L.; Bloomberg, G.R.; Busse, P.; Sidney, J.; Peters, B. and Sette, A. (2015). Different Bla-g T cell antigens dominate responses in asthma versus rhinitis subjects. *Clinical and Experimental Allergy* 45(12): 1856-1867.

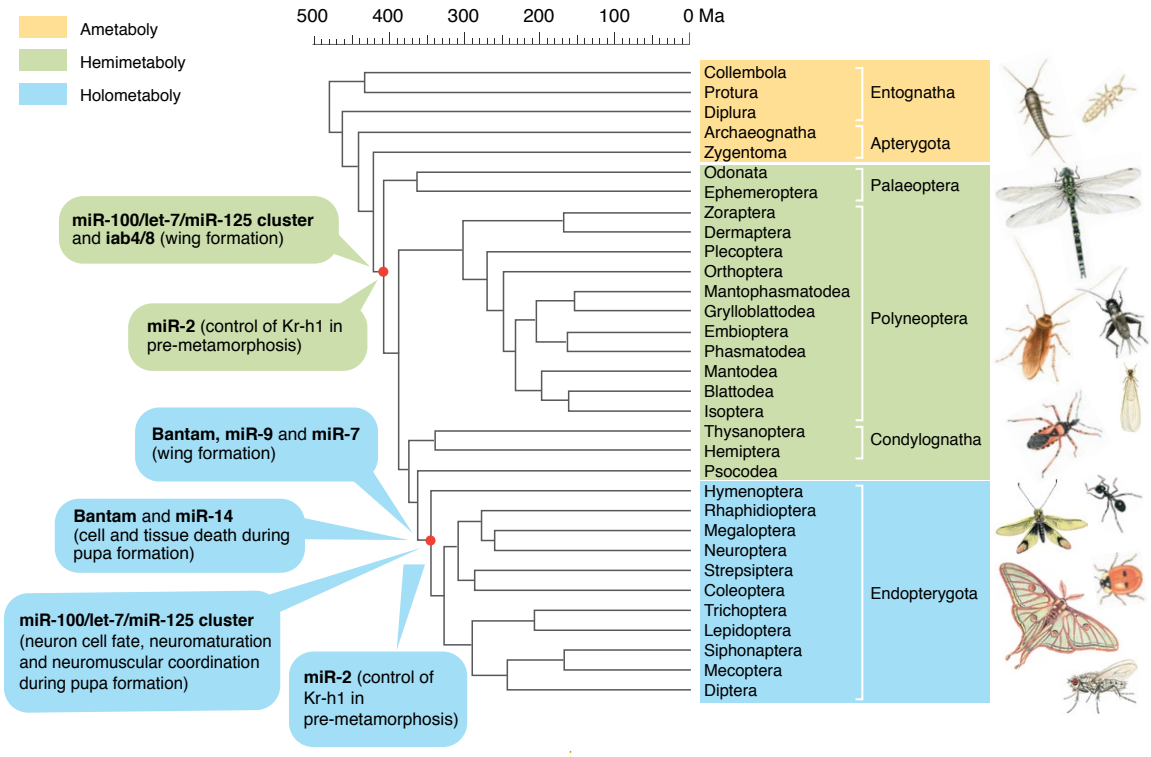


Fig. 2: *MicroRNAs and metamorphosis during insect evolution. MicroRNAs and functions associated to the origin of pterygotes (and the emergence of hemimetaboly), and to the origin of endopterygotes (and the emergence of holometaboly), are indicated. MiR-2 function as Kr-h1 mRNA scavenger appears to have disappeared in endopterygotes.*

Image: *Xavier Bellés*

Finn, R.N.; Chauvigné, F.; Stavang, J.A.; Bellés, X. and Cerdà, J. (2015). Insect glycerol transporters evolved by functional co-option and gene replacement. *Nature Communications* 6: 7814.

Jindra, M.; Bellés, X. and Shinoda, T. (2015). Molecular basis of juvenile hormone signaling. *Current Opinion in Insect Science* 11: 39-46.

Lozano, J.; Montañez, R. and Bellés, X. (2015). MiR-2 family regulates insect metamorphosis by controlling the juvenile hormone signaling pathway. *Proceedings of the National Academy of Sciences USA* 112: 3740-3745.

Ons, S.; Bellés, X. and Maestro, J.L. (2015). Orcokinins contribute to the regulation of vitellogenin transcription in the cockroach *Blattella germanica*. *Journal of Insect Physiology* 82: 129-133.

Ylla, G. and Bellés, X. (2015). Towards understanding the molecular basis of cockroach tergal gland morphogenesis. A transcriptomic approach. *Insect Biochemistry and Molecular Biology* 63: 104-12.

Other Publications

Bellés, X. (2015). Regulación hormonal de la metamorfosis en los insectos. *Investigación y Ciencia* 469: 11-13.

Faille, A.; Bourdeau, C.; Bellés, X. and Fresneda, J. (2015). Allopatric speciation illustrated: The Hypogean genus Geotrechus Jeannel, 1919 (Coleoptera: Carabidae: Trechini), with description of four new species from the Eastern Pyrinees (Spain). *Arthropod Systematics & Phylogeny* 73(3): 439-455.

Funded Projects

- **Project Title:** Regulation of cockroach tergal gland morphogenesis as a minimal model of insect metamorphosis
  Finaced by: MINECO. CGL2012-36251
  Years: 2013–2015
  PI: Xavier Bellés

- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2014 SGR 619)
  Years: 2014–2016
  PI: Xavier Bellés

- **Project Title:** Modifying plants to produce interfering RNA (iPlant)
  Finaced by: COST Program (EU). OC-2015-2-20281
  Years: 2015–2018
  PI: Bruno Mezzetti, main proposer. Xavier Bellés, Spain secondary proposer and Management Committee member.

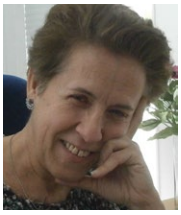
Fig. 3: *Molting defects observed in the adult molt of German cockroach after depleting the expression of CREB-binding protein.*

Image: *Fernández-Nicolas and Xavier Bellés,* 2016

group INSECT REPRODUCTION

From left to right: Carlos Vásquez, Maria-Dolors Piulachs, Elena Navas, Guillem Ylla, Saray Ramos

group members



Maria-Dolors Piulachs, *Group Leader*
Research Scientist, CSIC

Nashwa Elshaer, PhD Student, JAE Pre-CSIC Fellowship
Carlos Vásquez, PhD Student, CONICYT Fellowship Contract
Guillem Ylla, Bioinformatician, Project Contract
Elena Navas, Graduate Student, Universitat de Vic
Saray Ramos, Graduate Student, Universitat de Barcelona

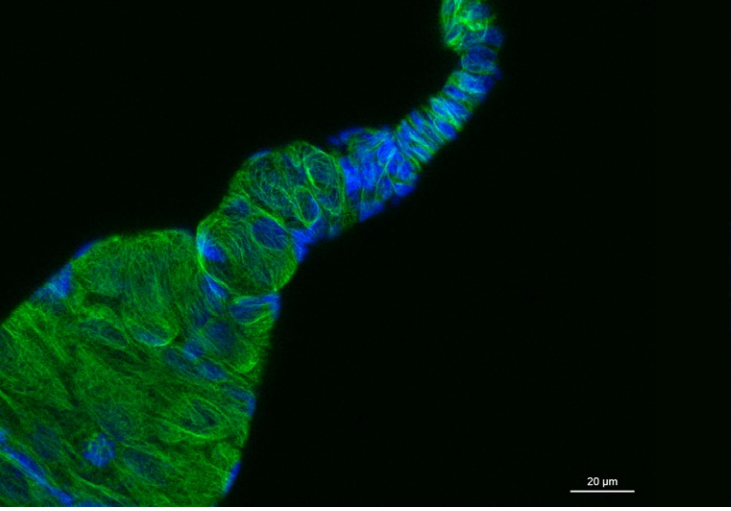


Fig. 1: *Germarium from a* Blattella germanica *6-day-old last instar nymph. Tubulins were revealed using a β-tubulin-anti-mouse (green), and nuclei were stained with DAPI (blue)*

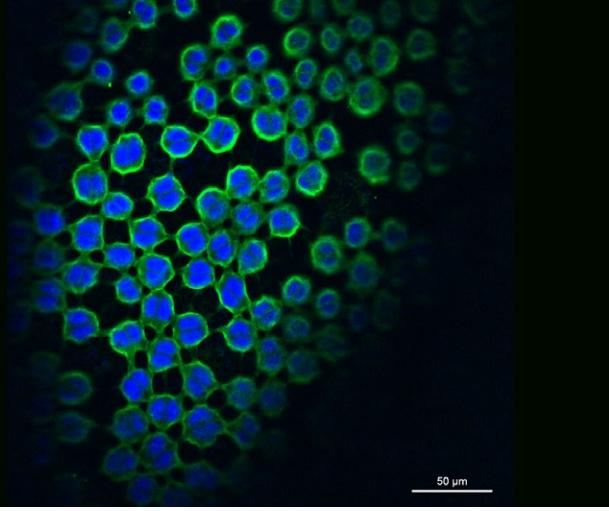


Fig. 2: *Follicular cells in ovarian follicles of* Blattella germanica*. Tubulins were revealed using a β-tubulin-anti-mouse (green), and nuclei were stained with DAPI (blue)*

Research Outline

In our group, our goal is to understand the mechanisms that regulate insect oogenesis. The peculiarity of our research in this field is to use a poorly modified insect like the cockroach *Blattella germanica*, as a model. We are working on the identification of genes responsible for the maturation of the oocyte and the establishment of anterior-posterior and dorsal-ventral axes, using ovary transcriptomes. We have identified genes that are of key importance in the regulation of these processes, and through RNA interference (RNAi) methodologies we are unveiling the function of some of them in the oocyte development of *B. germanica*, an insect with a panoistic ovary type, the most primitive type among insects. The next step in our research will be to study how to regulate the function of these genes and what relationships there are between them that allow the proper development of the oocyte. The comparison of these results with those already described in other, more modified insect species, suggests that some functions are preserved in evolution, although the regulation of these functions could have changed.

Research Lines

Over the last year our research has focused on two main subjects, with *Blattella germanica* used as the experimental subject:

1. Studying the genes that determine oocyte polarization

The establishment of a symmetry axis is crucial for development in many organisms. In animals this occurs in the early stages of embryogenesis by an asymmetric distribution of mRNAs from maternal origin that localize in particular regions of the oocyte, determining its polarization. To study oocyte polarization in our primitive model, we have chosen genes that have been well studied in *Drosophila melanogaster* like *capicua*, EGFR, and Pipe among others, and we are describing their function in a panoistic ovary. Our aim is to understand whether the function and regulation of these genes is preserved or has changed in the transition from the panoistic to the meroistic ovarian type.

2. Studying the regulation of cell proliferation during oogenesis

The rate between cell proliferation and cell death is a critical parameter in determining tissue growth, and the Hippo pathway is crucial to understanding the dynamics of the growth process. Understanding the regulation of the Hippo pathway is important to study not only how cells proliferate, but also how they avoid overproliferation, which could lead to tumorigenesis. Our objective has been to

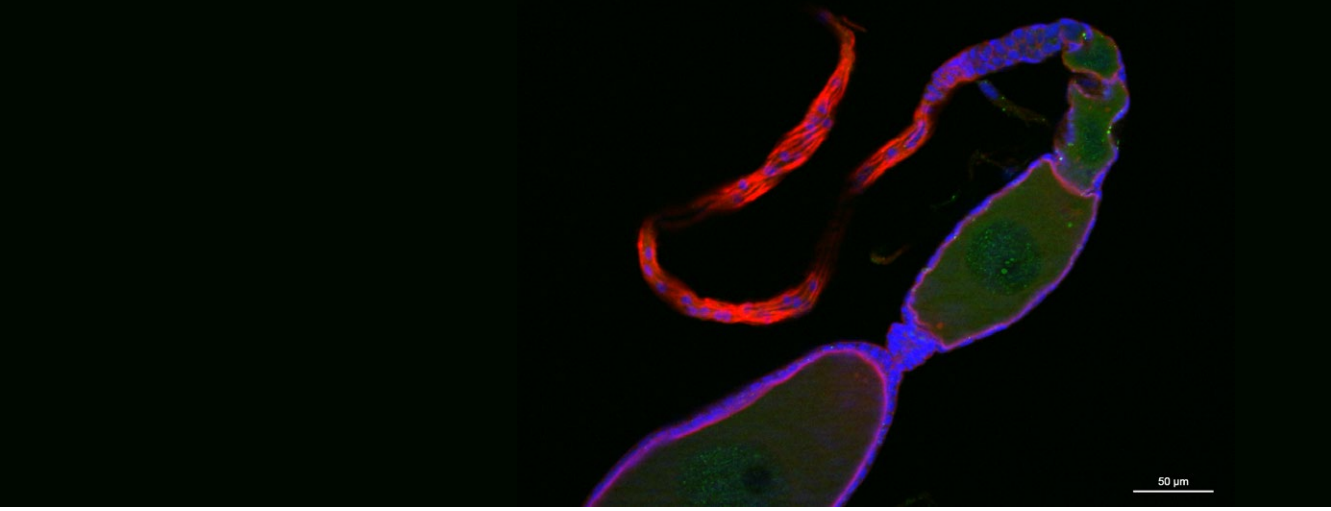


Fig. 3: *Ovariole from a 0-day-old adult* Blattella germanica *female. In red appeared the F-Actins that were stained the with Phalloidin-TRITC, in blue the nuclei stained with DAPI, and in green SPARC labelled with AON antibody.*

study the Hippo pathway and its relationships with EGFR and Notch signalling pathways since all of them participate in maintaining the correct cell number in a given organ and determining the cell fate in the tissues. We identified their components, and described their precise function using RNAi methodologies. Our next step will be to determine the possible regulatory role of miRNAs in the modulation of the different components of these pathways.

Publications 2015

Bellés, X. and Piulachs, M.D. (2015). Ecdysone signalling and ovarian development in insects: from stem cells to ovarian follicle formation. *Biochimica et Biophysica Acta* 1849, 181-186.

Carot-Sans, G.; Muñoz, L.; Piulachs, M.D.; Guerrero, A. and Rosell, G. (2015). Identification and characterization of a fatty acyl reductase from Spodoptera littoralis female gland involved in pheromone biosynthesis. *Insect Molecular Biology* 24(1), 82-92.

Dillon, M.B.; Schulten, V.; Oseroff, C.; Paul, S.; Dullanty, L.M.; Frazier, A.; Bellés, X.; Piulachs, M.D.; Visness, C.; Bacharier, L.; Bloomberg, G.R.; Busse, P.; Sidney, J.; Peters, B. and Sette, A. (2015). Different Bla-g T cell antigens dominate responses in asthma versus rhinitis subjects. *Clinical & Experimental Allergy* 45(12): 1856-67.

Elshaer, N. and Piulachs, M.D. (2015). Crosstalk of EGFR signaling with Notch and Hippo pathways to regulate cell specification, migration and proliferation in cockroach panoistic ovaries. *Biology of the Cell* 107, 1-13.

Funded Projects

- **Project Title:** Global change and physiological diversity
  Financed by: International Laboratory of Global Change (LINCGlobal), CSIC (Spain)-PUC (Chile)
  Years: 2009-
  PIs: Xavier Bellés and Francisco Bozinovic

- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2014 SGR 619)
  Years: 2014-2016
  PI: Xavier Bellés

- **Project Title:** Modifying plants to produce interfering RNA (iPlant)
  Finaced by: COST Program (EU) OC-2015-2-20281
  Years: 2015-2018
  PI: Bruno Mezzetti, main proposer. M.D. Piulachs, Spain Management Committee member

group MULTICELL GENOME

Top from left to right and top to bottom: Maria Rubio, Xavier Florenza, Alberto Pérez, Helena Parra, Matija Harcet, Alicia S. Arroyo, David López-Escardó, Xavier Grau-Bové, Edu Ocaña, Takaaki Kai, Sebastián Najle, Gema Blasco, Iñaki Ruiz-Trillo, Meritxell Antó, Maria Ferrer, Núria Ros, Cristina Aresté

group members

Iñaki Ruiz-Trillo, *Group Leader*
Research Professor, ICREA

Matija Harcet, Postdoctoral Researcher, Marie Curie Fellowship
Sebastián Najle, Postdoctoral Researcher, Project Contract
Cristina Aresté, Postdoctoral Researcher, Moore Foundation
Arnau Sebé-Pedrós, Postdoctoral Researcher, Project Contract
Xavier Grau-Bové, PhD Student, FPI Scholarship
David López-Escardó, PhD Student, Project Contract
Eduard Ocaña, PhD Student, FPI Scholarship
Helena Parra, PhD Student, Project Contract
Núria Ros, PhD Student, FPU Scholarship
Alicia Sánchez, PhD Student, Project Contract
Xavier Florenza, Master Student
Alberto Pérez, Master Student
Meritxell Antó, Research Technician
Gemma Blasco, Research Technician
Maria Ferrer, Research Technician
Maria Rubio, Research Technician, Moore Foundation

Research Outline

We want to understand how unicellular organisms became multicellular. Specifically, we focus on the origin of multicellular animals or metazoans. To this end, we compare the genomes of animals with the genomes of their closest unicellular relatives.

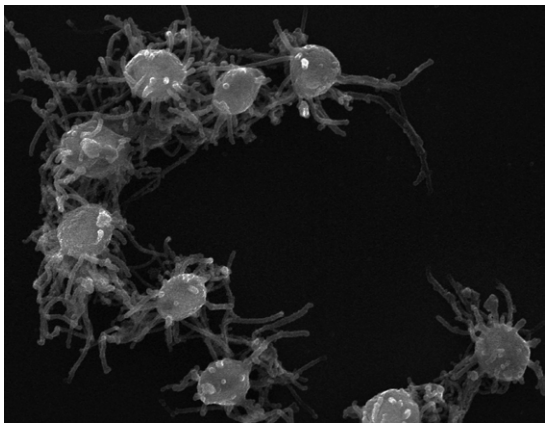


Fig. 1: *Capsaspora owczarzaki (Filasterea) cells, SEM microscopy.*
Image: *Arnau Sebé-Pedrós*

Research Lines

1. Biodiversity and Molecular Ecology of Opisthokonts

The real diversity of opisthokonts remains unknown. To address this we analysed environmental data and identified several novel opisthokont clades. To increase our understanding, we are currently analyzing molecular data from the Biomarks project to have a better idea of the real diversity of the different opisthokont lineages.

2. Comparative genomics to unravel the metazoan "genetic starter kit"

Our goal is to elucidate the evolutionary history of genes that are key for animal development and multicellularity. To this end, we are part of the UNICORN (UNICellular Opisthokonts Research iNitiative) initiative: an international and multi-taxon genome project recently funded by NHGRI (National Institute for Human Genome Research), which aims to gain insights into how multicellularity first evolved in both animals and fungi. UNICORN, through the Broad Institute, is obtaining the genome sequence from several of the closest unicellular relatives of both animals and fungi (see the Multicellularity Project at the Broad Institute). By performing comparative genomic analyses we will unravel the genome structure and gene composition of the last common unicellular ancestor that gave rise to Metazoa.

For example, we have recently analyzed the genome sequence of the filasterean amoeboid *Capsaspora owczarzaki*, a close unicellular relative of Metazoa. We identified in the *Capsaspora* genome several genes that are required for metazoan development, such as the protein tyrosine kinases, integrins and several transcription factors. This implies that the unicellular ancestor of animals was much more complex than previously thought.

Currently we are obtaining the genome sequence of several ichthyosporean taxa.

3. Unravelling the ancestral function of genes relevant to animal multicellularity

We want to know what roles the genes involved in multicellularity are playing in the unicellular *Capsaspora*, and how these genes were later on co-opted to the new functions in metazoans. Thus, by elucidating the "ancestral function" of those genes, we will provide significant insights into the role that cell-signalling and cell-adhesion genes played in the origin of Metazoa.

To this end we are currently working on developing transgenesis protocols in the filasterean *Capsaspora owczarzaki* and the ichthyosporean *Creolimax fragrantissima*.

4. Phylogenomics

If we want to approach the evolution of multicellular animals, we need a robust phylogenetic framework for the opisthokonts (i.e., the clade that comprises Metazoa, Fungi and their closest unicellular lineages). Thus, among our goals is to obtain new molecular data in order to perform phylogenetic and phylogenomic analyses to further improve the opisthokont (or the eukaryote) tree of life. We are currently working on having a highly taxon-rich phylogenomic analysis of the opisthokonts.

Publications 2015

ISI Articles

Alzayady, K.J.; Sebé-Pedrós, A.; Chandrasekhar, R.; Wang, L.; Ruiz-Trillo, I. and Yule, D.I. (2015). Tracing the Evolutionary History of Inositol, 1, 4, 5-trisphosphate receptor: Insights from Analyses of Capsaspora owczarzaki Ca2+ Release Channel Orthologs. *Molecular Biology and Evolution* 32(9): 2236-53.

de Mendoza, A.; Suga, H.; Permanyer, J.; Irimia, M. and Ruiz-Trillo, I. (2015). Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. *eLife* 4: e08904.

del Campo, J.; Mallo, D.; Massana, R.; de Vargas, C.; Richards, T.A. and Ruiz-Trillo, I. (2015). Diversity and distribution of unicellular opisthokonts along the European coast analyzed using high-throughput sequencing. *Environmental Microbiology* 17(9): 3195-207.

Grau-Bové, X.; Sebé-Pedrós, A. and Ruiz-Trillo, I. (2015). The eukaryotic ancestor had a complex ubiquitin signalling system of archaeal origin. *Molecular Biology and Evolution* 32(3): 726-39.

Grau-Bové, X.; Ruiz-Trillo, I. and Rodríguez-Pascual, F. (2015). Origin and evolution of lysyl oxidases. *Scientific Reports* 5: 10568.

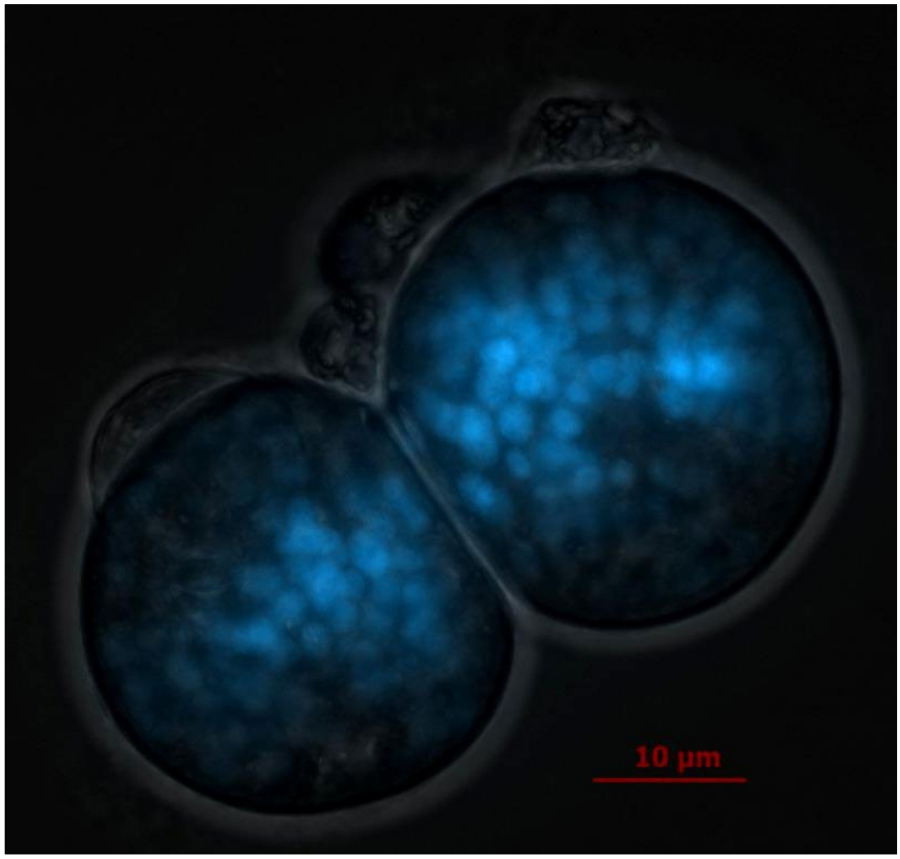


Fig. 2: *Pirum gemmata (Ichthyosporea), nuclei stained in blue with DAPI.*
Image: *Maria Rubio and Cristina Aresté*

Torruella, G.; de Mendoza, A.; Grau-Bové, X.; Antó, M.; Chaplin, M.A.; del Campo, J.; Eme, L.; Pérez-Cordón, G.; Whipps, C.M.; Nichols, K.M.; Paley, R.; Roger, A.J.; Sitjà-Bobadilla, A.; Donachie, S. and Ruiz-Trillo, I. (2015). Phylogenomics reveals convergent evolution of lifestyles in close relatives of animals and fungi. *Current Biology* 25(18): 2404-10.

Books / Book Chapters / Other Publications

Ruiz-Trillo, I. and Nedelcu, A. (editors). *Evolutionary transitions to multicellular life: principles and mechanisms.* Advances in Marine Genomics Series. Springer.

Suga, H. and Ruiz-Trillo, I. *Unraveling the origin of animal multicellularity. Jikken Igaku (Experimental Medicine)* vol. 33, nº.6, pp. 968-973.

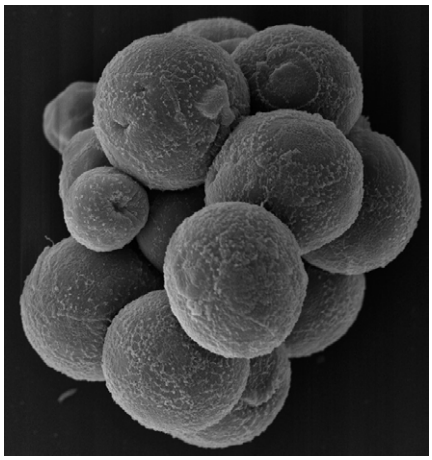


Fig. 3: *Sphaeroforma arctica 8 Colony of Sphaeroforma arctica (Ichthyosporea); SEM microscopy.*
Image: *Arnau Sebé-Pedrós*

Funded Projects

- **Project Title:** Unravelling the unicellular prehistory of metazoans by functional analyses and single-cell genomics
  Financed by: European Research Council (ERCCo-PREMETAZOANEVOLUTION-616960)
  Years: 2014–2019
  PI: Iñaki Ruiz-Trillo

- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2014 SGR 619)
  Years: 2014–2016
  PI: Xavier Bellés

- **Project Title:** Origen, diversificación y diversidad de metazoos, hongos y sus parientes unicelulares; una aproximación ecológica y evolutiva
  Financed by: Ministerio de Ciencia e Innovación
  Years: 2015–2017
  PI: Iñaki Ruiz-Trillo and Josefa González

- **Project Title:** Screening marine holozoans, the closest unicellular relatives of animals
  Financed by: Gordon and Betty Moore Foundation
  Years: 2015–2016
  PI: Iñaki Ruiz-Trillo and Elena Casacuberta

PROGRAM

POPULATION GENETICS

Research Groups

Evolutionary Population Genetics
Elena Bosch, *Group Leader*

Evolutionary Systems Biology
Jaume Bertranpetit, *Group Leader*

Genomics of Individuallity
Francesc Calafell, *Group Leader*

Human Genome: Diversity and Adaptation
David Comas, *Group Leader*

Subgroups

Human Genome Diversity
David Comas, *PI*

microRNAs in Human Adaptation and Disease
Yolanda Espinosa-Parrilla, *PI*

In the population genetics line, intraspecific diversity patterns within populations and comparative data are explored with the general aim of reconstructing the processes that have created such diversity. Genetic diversity is the result of the intricate interaction of different processes: some are embedded in the genome, such as mutation and recombination; others are absolutely independent from the genome and affect its entirety, such as demographic events; and finally, other processes result from the exposure of the genetic diversity to the environment, such as natural selection. Within this line, we are interested in all three types of processes mainly in humans. Namely, we investigate how recombination can be affected by genetic differences between populations; the demographic histories of particular populations or population groups; and the extent of the adaptation of humans to their pathogen exposure or to nutrient availability in their diets through the detection of selection footprints in the genome. In addition, the functional consequences of these processes in the human non-coding genome are also evaluated. Finally, the integration of the different levels of functional variation on genes related to particular human traits is used to understand human adaptation as a system network phenomenon.

group EVOLUTIONARY POPULATION GENETICS

From left to right: Juan Antonio-Rodriguez, Elena Bosch, Nino Spataro, Ana Roca-Umbert

group members

Elena Bosch, *Group Leader*
Associate Professor, UPF

Juan Antonio-Rodríguez, PhD Student, UPF Scholarship
Nino Spataro, PhD Student, UPF Scholarship
Ana Roca-Umbert, Master Student

Research Outline

Our research focuses on investigating different aspects of human genetic diversity. In particular, we are interested in: (i) human adaptation, that is, in identifying traits that have undergone positive selection during human evolution in order to understand the adaptive events that have shaped our genomes; and (ii) the architecture of the genetic predisposition to complex disease. The search for genetic signatures of selection is pursued at different levels using comparative data and exploring intraspecific diversity patterns mainly within human populations but also in chimpanzees. In those cases where the imprint of selection is confirmed, we aim to determine the molecular bases of the functional adaptation. As for complex disease, we believe that the application of population-genetic models can help in unravelling the genetic contribution to them.

Research Lines

1. Recent human adaptation and nutrition

Micronutrients play an important role in human health and their physiological and cellular concentrations are kept in homeostasis by a number of membrane transport proteins and metal-binding proteins. Our goal is to describe the interplay between genetic variation, mRNA and protein expression, together with the trace element content in different human tissue samples in order to learn about possible adaptive responses to nutrient availability and diet changes that occurred in our past.

2. Role of selection in coding and noncoding regions of the genome

We are analyzing sequence data at both intraspecific and interspecific levels in order to investigate the role of natural selection in all coding and regulatory elements of particular gene pathways. This project is carried out in collaboration with Hernán Dopazo (Universidad de Buenos Aires, Argentina).

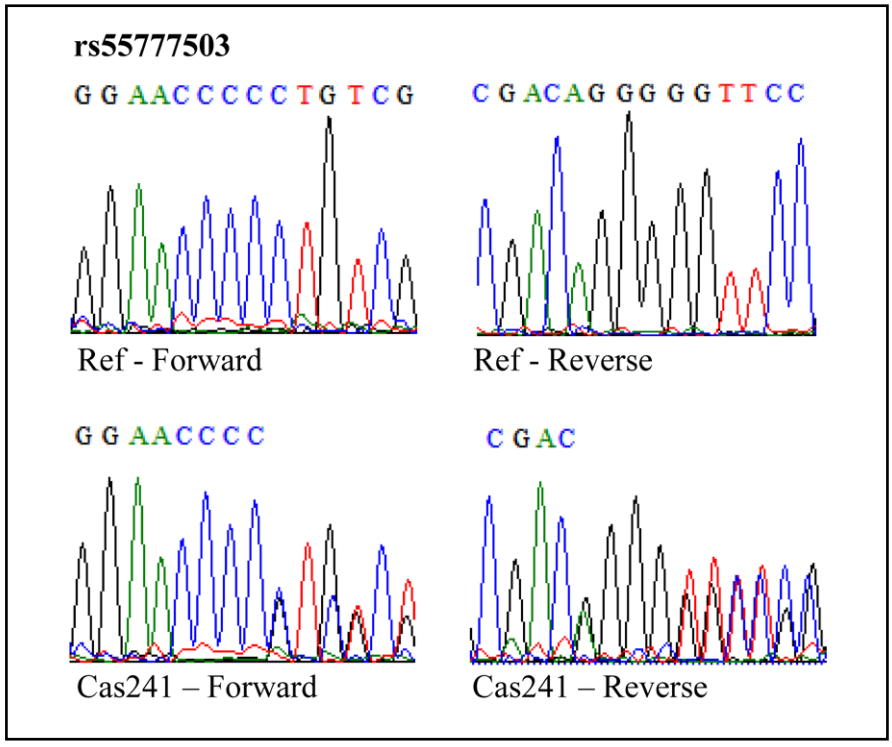


Fig. 1: *Sequencing chromatograms showing the location of the p.Gln34Argfs frameshift (rs55777503) on the PARK2 gene in a Parkinson disease case.*

3. Role of natural selection in human disease genes

By analyzing human sequence data from the 1000 Genomes Project, divergence data and network properties, we hope to characterize the selective pressures acting on genes associated to Mendelian and complex diseases in order to understand differences in penetrance, age of onset, and risk allele frequencies between genetic disorders.

Fig. 2: *Labeling of boxes for storage of DNA, RNA and protein extractions from human liver and kidney samples.*

In collaboration with Arcadi Navarro (Evolutionary Genomics Lab) and by identifying antagonistically pleiotropic variants and signatures of natural selection in genes associated to age-related disease in humans we hope to provide insights into the evolutionary theories of senescence.

4. Rare variants in Parkinson's disease (PD)

Our working hypothesis is that an excess of rare variants may indicate the involvement of a gene in a complex disease such as PD. Using resequencing data and adapting classical evolutionary tests we evaluate the possible deviations of the spectrum of allele frequencies between cases and controls in individual genes, gene pathways and, in particular, regulatory regions. We are also detecting and characterizing structural variants in different Mendelian and susceptibility genes for PD from targeted sequencing data in multiple individuals.

Publications 2015

Santpere, G.; Carnero-Montoro, E.; Petit, N.; Serra, F.; Hvilsom, C.; Rambla, J.; Heredia-Genestar, J.M.; Halligan, D.L.; Dopazo, H.; Navarro, A. and Bosch, E. (2015). Analysis of five gene sets in chimpanzees suggests decoupling between the action of selection on protein-coding and on noncoding elements. *Genome Biology and Evolution 7*(6): 1490-1505.

Spataro, N.; Calafell, F.; Cervera-Carles, L.; Casals, F.; Pagonabarraga, J.; Pascual-Sedano, B.; Campolongo, A.; Kulisevsky, J.; Lleó, A.; Navarro, A.; Clarimón, J. and Bosch, E. (2015). Mendelian genes for Parkinson's disease contribute to the sporadic forms of the disease. *Human Molecular Genetics* 24(7): 2023-2034.

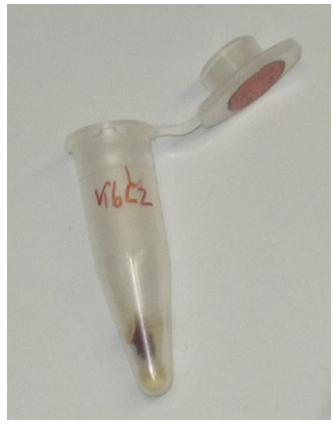


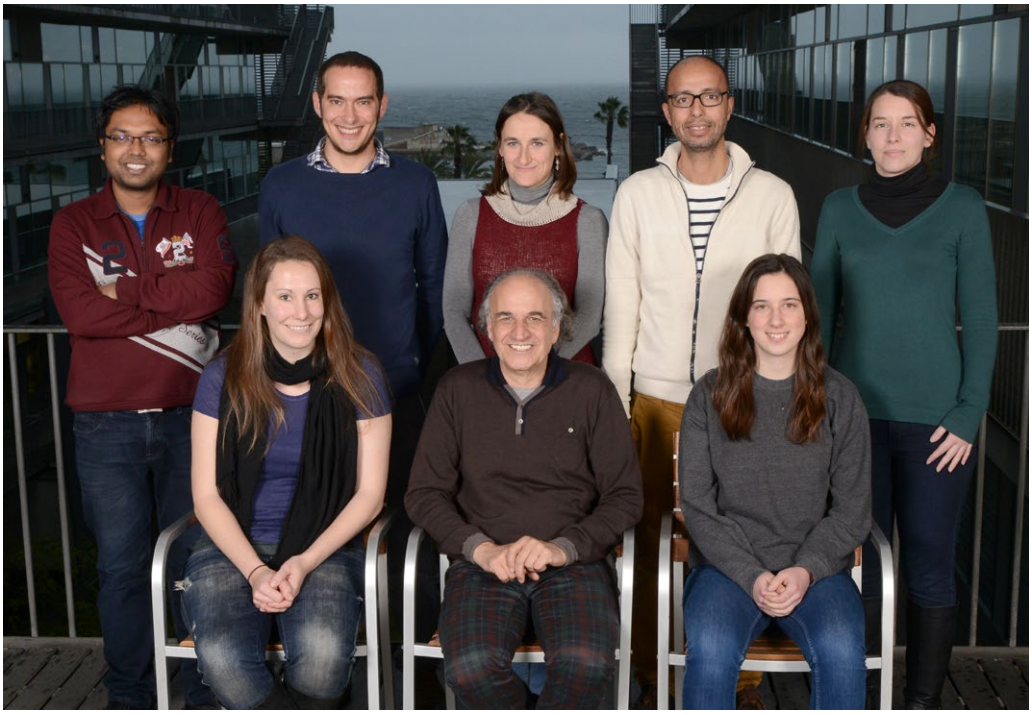
Fig. 3: *Processing of a kidney sample for mass spectrometry detection of micronutrients.*

Funded Projects

- **Project Title:** Genètica de les Poblacions Humanes
  Financed by: Generalitat de Catalunya (2014 SGR-866)
  Years: 2014–2016
  PI: Jaume Bertranpetit

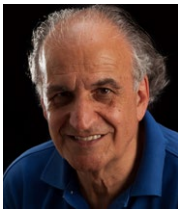
- **Project Title:** AdaptNET. Genomics of adaptation network (CGL2015-71726-REDT).
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2015–2017
  PI: Julio Rozas

group EVOLUTIONARY SYSTEMS BIOLOGY



From left to right and top to bottom: Mayukh Mondal, Marc Pybus, Ludovica Montanucci, Hafid Laayouni, Begoña Dobón, Jessica Nye, Jaume Bertranpetit (GL), Sandra Walsh Capdevila

group members



Jaume Bertranpetit, *Group Leader*
Professor, UPF

Hafid Laayouni, Senior Scientist, UPF Contract
Ludovica Montanucci, Postdoctoral Researcher, Juan de la Cierva Fellowship
Mayukh Mondal, PhD Student, FI Scholarship, Generalitat de Catalunya
Jessica Nye, PhD Student, FI Scholarship, Generalitat de Catalunya
Marc Pybus, PhD Student, FPI Scholarship, MICINN
Sandra Walsh, PhD Student, FPI Scholarship, MINECO
Begoña Dobón, Master Student

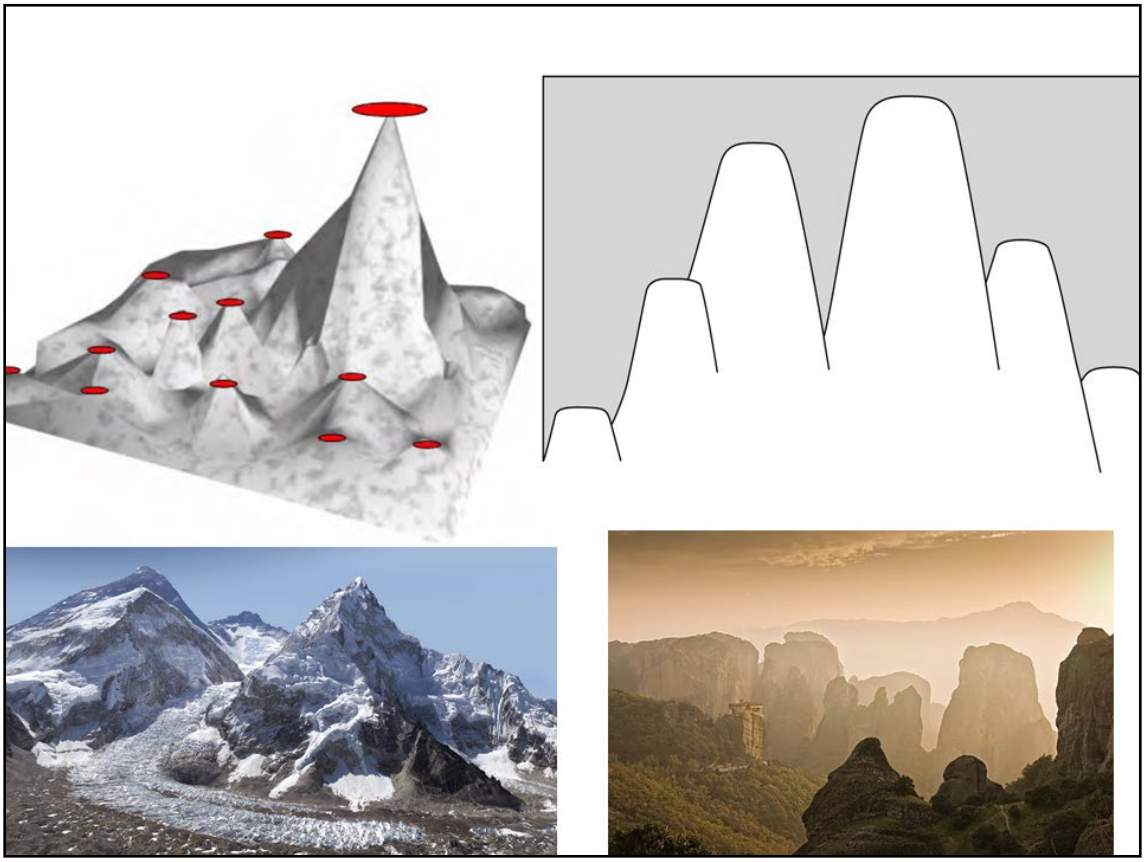


Fig. 1: **A new shape for adaptive landscapes**
In the paper by Luisi et al., results support a new view on the shape of adaptive landscapes, traditionally seen as sharp mountains (left) while the results of this paper suggest a more vertical slope produced by selected mutations that have a strong phenotypic effect.

Research Outline

Presently, our main research focuses on the understanding of natural selection and adaptation in humans and primates through the comparative analysis of genomes. Our goal is to understand complex adaptations through genome-wide analyses of the footprints that natural selection leaves in genomes after their action, and not only by detecting single signals (in one specific gene or genome region) but trying to place selection in a functional molecular framework of molecular pathways.

The different forms of selection (purifying, balancing and positive) are analyzed at two levels: among human populations in order to detect population-specific adaptations, and among primates in order both to recognize species-specific adaptive selection and to measure the relative strength of purifying selection.

We also have an ongoing project reconstructing population history by studying human genetic diversity.

Research Lines

1. Footprints of adaptation in humans and purifying selection in higher primates

The action of natural selection is at the base of different amounts of gene dispensability or relative importance (in cases of negative or purifying selection) or of adaptation (in cases of positive selection and in the special case of balancing

selection). The final goal is, on the one hand, to understand in specific pathways how evolution has taken place, where positive selection (and balancing selection) has taken place and where purifying selection has been shaping the genome, and on the other, to obtain possible general patterns of evolution in molecular pathways and networks. The study of the whole metabolome is of special interest.

Some special cases are being studied. For humans, Indian (including Andaman) and African populations are being studied, with a particular focus on the existence of admixture in these populations. Moreover, the study of apes, and especially chimpanzees, will shed light on their specific adaptations.

2. Human genetic diversity and population history

Thanks to a collaborative project with NIBMG, India (Prof. Partha Majumder) and with Ferran Casals (Genomic Service, UPF) we have undertaken a major study of population genetics of several Indian populations, including the analysis of whole human sequences. The specific study of the population of Andaman has helped to propose the existence in present SE Asian and Pacific human populations of remnants of an extinct hominin genome.

In collaboration with Mihai Netea (Nijmegen Medical Center) we are analyzing data from Roma people.

Publications 2015

Alonso, A.; [22 authors]; Bertranpetit, J.; Absher, D.; Myers, R.; Marsal, S. and Gisbert, J.P. (2015). Identification of Risk Loci for Crohn's Disease Phenotypes Using a Genome-wide Association Study. *Gastroenterology* 148: 794-8052014.

Dall'Olio, G.M.; Vahdati, A.R.; Bertranpetit, J.; Wagner, A. and Laayouni, H. (2015). VCF2Networks: applying Genotype Networks to Single Nucleotide Variants data. *Bioinformatics* 2015 31(3): 438-9.

Dobon, B.; Hassan, H.Y.; Laayouni, H.; Luisi, P.; Ricano-Ponce, I.; Zhernakova, A.; Wijmenga, C.; Tahir, H.; Comas, D.; Netea, M.G. and Bertranpetit, J. (2015). The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. *Scientific Reports* 5: 9996.

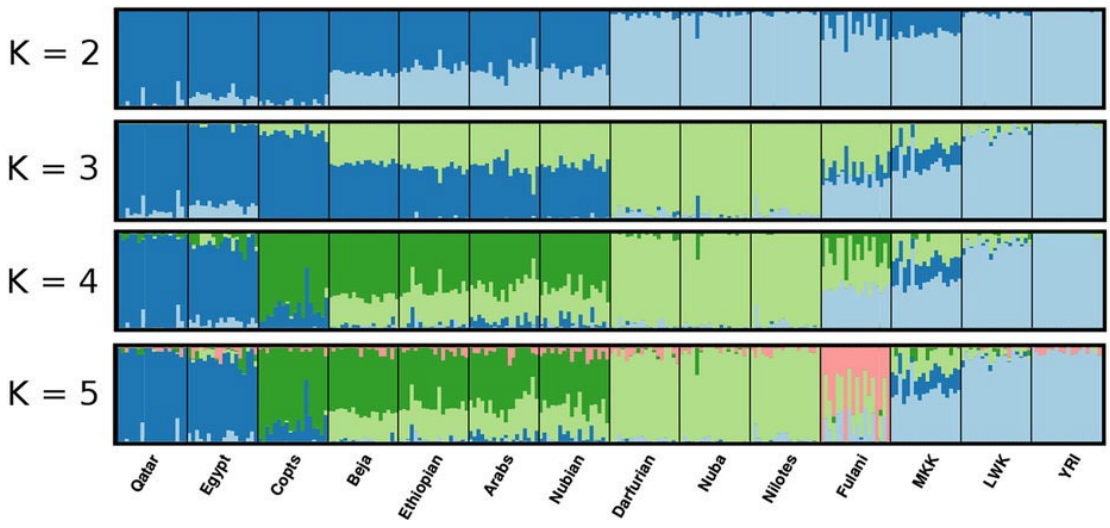


Fig. 2: **Analysis Of Human Populations In Sudan**

Columns represent individuals, where the size of each colour segment represents the proportion of ancestry from each cluster. Although k = 3 is the statistically supported model, here we show the results from k = 2 through k = 5 as they explain several ancestral components: North African/Middle Eastern (dark blue), Sub-Saharan (light blue), Coptic (dark green), Nilo-Saharan (light green) and Fulani (pink). MKK = Maasai from Kinyawa, Kenya; LWK = Luhya from Webuye, Kenya; YRI = Yoruba from Ibadan, Nigeria.

Invergo, B.M.; Montanucci, L. and Bertranpetit, J. (2015). A dynamic model of mammalian phototransduction reveals insights into the molecular evolution of systems. *Proceedings of the Royal Society B* 282(1820).

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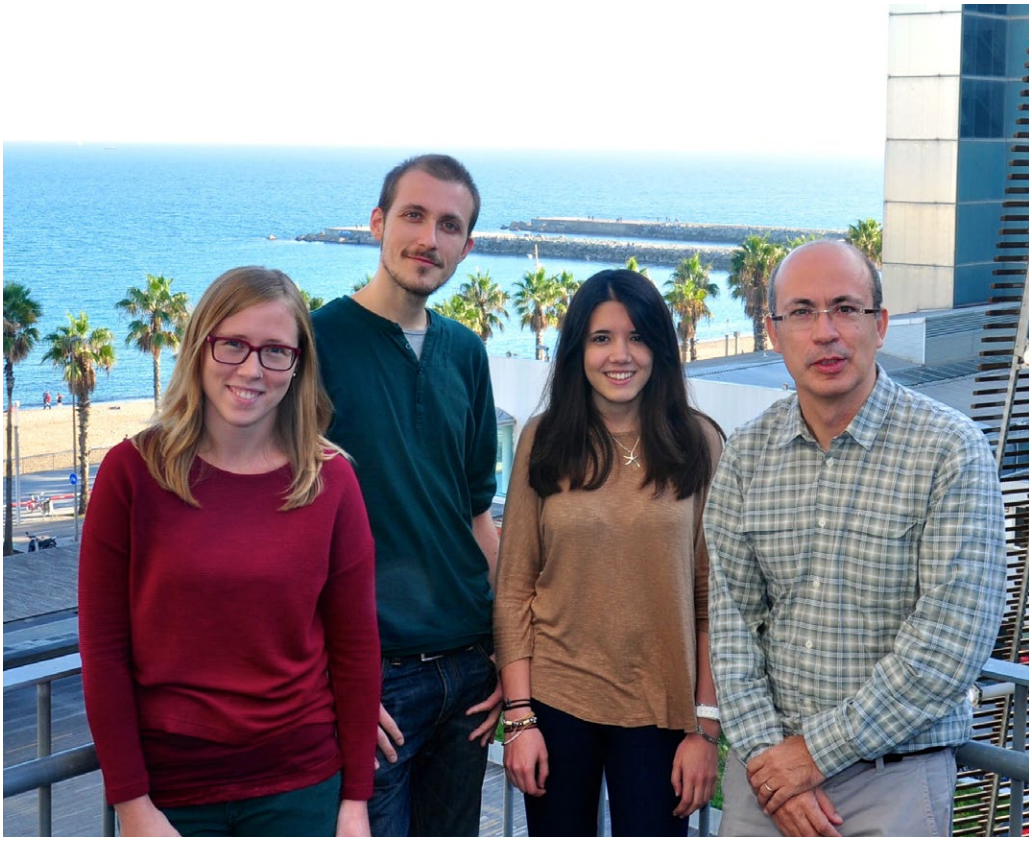
Solé-Morata, N.; Bertranpetit, J.; Comas, D. and Calafell, F. (2015). Y chromosome diversity in Catalan surname samples: Insights into surname origin and frequency. *European Journal of Human Genetics* 23(11): 1549-57.

Funded Projects

- **Project Title:** Deteccion y comprension de las huellas de seleccion natural en el genoma de humanos y simios
  Financed by: Ministerio de Ciencia y Tecnología (BFU2013-43726-P)
  Years: 2014–2016
  PI: Jaume Bertranpetit

- **Project Title:** Genètica de les Poblacions Humanes
  Financed by: Generalitat de Catalunya (2014 SGR 866)
  Years: 2014–2016
  PI: Jaume Bertranpetit

group GENOMICS OF INDIVIDUALITY



From left to right: Neus Solé, Simone Biagini, Neus Font, Francesc Calafell

group members

Francesc Calafell, *Group Leader*
Associate Professor, UPF

Simone Andrea Biagini, PhD Student, FPI Scholarship
Neus Solé Morata, PhD Student, FI Scholarship

Research Outline

The general topics that interest us revolve around the genomics of individuality: what is there in our genomes that makes us the way we are? What does it tell us about our ancestry? How does it affect our susceptibility to diseases? How can this be applied in practical settings (i.e., in forensic genetics)? We have recently applied this frame to a wider scope that views the individual as part of a genealogy, sharing lineages with individuals that are related to them. In particular, we focus on both sides of the Western Mediterranean, their genetic structure and their contacts.

Research Lines

1. The geography of genetic diversity at a local scale

Major geographical and linguistic barriers are often major drivers of genetic differentiation among human populations. We want to investigate the role of a third factor, isolation by distance, in a geographically and linguistically homogenous territory. To that effect, we have sampled individuals with all four grandparents born <30 Km away from each other, in Catalonia, Valencia, and the Balearic Islands, and have genotyped >600,000 SNPs in them. We will correlate genetic with geographic distance, and find whether genetic relatedness is linked to geographic distance. Two factors can be considered: the Balearics are islands (and some results show Ibiza as divergent), and varying amounts of ancestral N. African admixture.

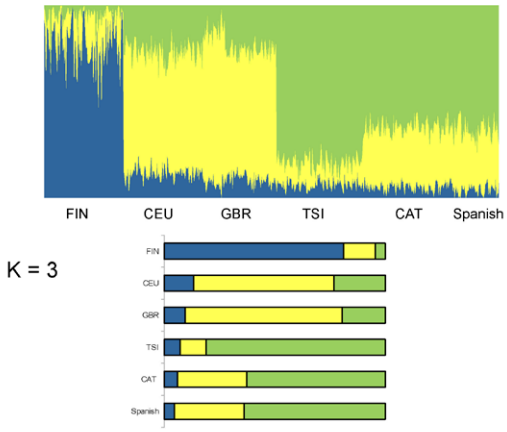


Fig. 1: *Admixture plot showing the estimated proportions of three different ancestries (represented in color) for individuals (vertical lines) in several European populations.*

Author: *Simone Biagini*

2. The Western Mediterranean genetic landscape

Most human population genetic studies take either continents or countries (or even smaller sampling units) as reference frames. Whole continents may comprise separate, even independent histories, but national boundaries are exceedingly recent. We are investigating one such subcontinental area, the Western Mediterranean. Beyond the pure description of the genetic differentiation among populations, we aim to measure and date gene flow among them and with external populations such as the Middle East and Sub-saharan Africa.

3. Phylogeography of the Y chromosome in the Western Mediterranean

The genetic diversity available in the Y chromosome can be arranged easily into a phylogenetic tree, with different branches found with different frequencies and diversities in different populations. This pattern, phylogeography, can be used to make inferences about the origin and dispersal of Y-chromosome tree branches, and, more importantly, about the history of the populations carrying them. We are analyzing two such branches, E-M81 and DF-27. The E-M81 branch is found at frequencies of 50-70% in NW Africa, while in Europe it is found only in Iberia and Sicily. We are sequencing whole E-M81 chromosomes in order to discern their internal phylogenetic structure. In collaboration with Marian Martínez de Pancorbo (Basque Country University, Vitoria), we are studying the R1b-DF27 branch of the Y-chromosome phylogeny in Western European populations where, particularly in Iberia, it accounts for >40% of all Y chromosomes.

Publications 2015

Bekada, A.; Arauna, L.R.; Deba, T.; Calafell, F.; Benhamamouch, S. and Comas, D. (2015). Genetic heterogeneity in Algerian human populations. *PLoS ONE* 10(9): e0138453.

Garcia-Etxebarria, K.; Bracho, M.A.; Galán, J.C.; Pumarola, T.; Castilla, J.; Ortiz de Lejarazu, R.; Rodríguez-Dominguez, M.; Quintela, I.; Bonet, N.; Garcia-Garcerà, M.; Domínguez, A.; González-Candelas, F. and Calafell, F. on behalf of the CIBERESP Cases and Controls in Pandemic Influenza Working Group. (2015). No Major Host Genetic Risk Factor Contributed to A(H1N1)2009 Influenza Severity. *PLoS ONE* 10(9): e0135983.

Riyahi, S.; Sánchez-Delgado, M.; Calafell, F.; Monk, D. and Senar, J.C. (2015). Combined epigenetic and intraspecific variation of the *DRD4* and *SERT* genes influence novelty seeking behavior in great tit *Parus major*. *Epigenetics* 10: 516-25.

Solé-Morata, N.; Bertranpetit, J.; Comas, D. and Calafell, F. (2015). Y chromosome diversity in Catalan surname samples: Insights into surname origin and frequency. *European Journal of Human Genetics* 23(11): 1549-57.

Spataro, N.; Calafell, F.; Cervera-Carles, L.; Casals, F.; Pagonabarraga, J.; Pascual-Sedano, B.; Campolongo, A.; Kulisevsky, J.; Lleó, A.; Navarro, A.; Clarimón, J. and Bosch, E. (2015). Mendelian genes for Parkinson's disease contribute to the sporadic forms of the disease. *Human Molecular Genetics* 24(7): 2023-2034.

Other Publications

Calafell, F. and Comas, D. (2015). Genetics and the reconstruction of African population history. In "Population in the Human Sciences. Concepts, Models, Evidence". Edited by Philip Kreager, Bruce Winney, Stanley Ulijaszek, and Cristian Capelli. Oxford, Oxford University Press, pp. 379-400. ISBN 978-0-19-968820-3.

Funded Projects

- **Project Title:** Genètica de les Poblacions Humanes
  Financed by: Generalitat de Catalunya (2014 SGR 866)
  Years: 2014–2018
  PI: Jaume Bertranpetit

- **Project Title:** Análisis genómico de la biodiversidad humana en el Mediterráneo: en la encrucijada entre tres continentes
  Financed by: Ministerio de Economía y Competitividad
  Years: 2014–2016
  PI: David Comas - Francesc Calafell

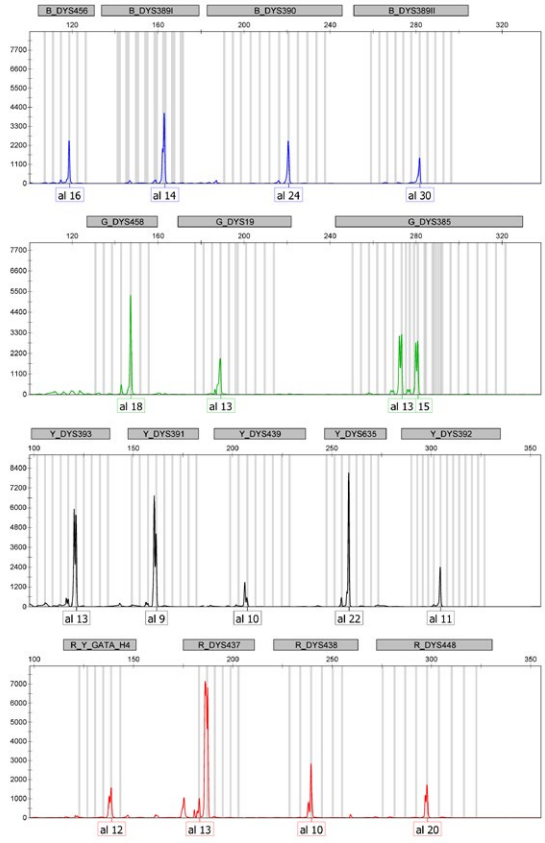
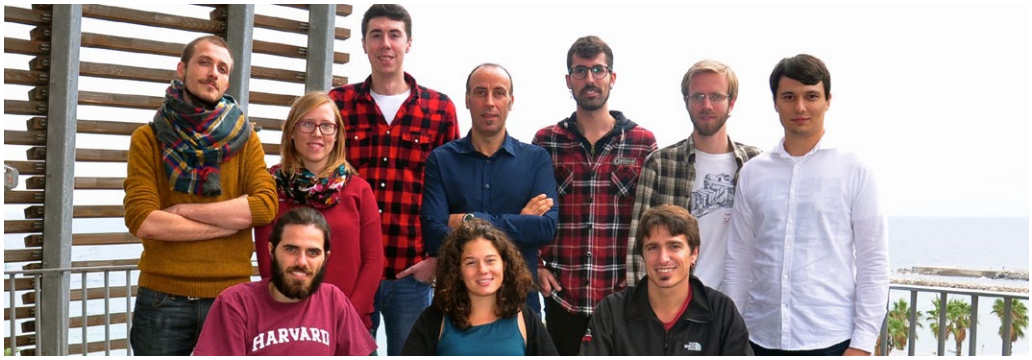


Fig. 2: *Electropherogram showing the genotypes for 17 Y-chromosome STRs in one individual.*
Author: *Neus Solé*

group HUMAN GENOME: DIVERSITY AND ADAPTATION



Top, from left to right and top to bottom: Simone Biagini, Neus Solé-Morata, Carles Llorca, David Comas, André Flores, Gerard Serra, Joao Pimenta, David Mas, Lara Rubio Araúna, Àlex Mas
Bottom, from left to right: Ignasi Torruella, Yolanda Espinosa, Alicia Gallego, David María López

group members

David Comas, *Group Leader*
Associate Professor, UPF

Subgroups

Human Genome Diversity

David Comas, Associate Professor, UPF
Simone Biagini, PhD Student, FPI Scholarship
Àlex Mas, PhD Student, UFRGS Scholarship
Joao Pimenta, PhD Student, FCT Scholarship
Lara Rubio Araúna, PhD Student, UPF Scholarship
Gerard Serra, PhD Student, FI Scholarship
Neus Solé-Morata, PhD Student, FI Scholarship
André Flores, Masters Student, UB
Carles Llorca, Master Student, UPF
David Mas, Master Student, UPFF

microRNAs in Human Adaptation and Disease

Yolanda Espinosa-Parrilla, Visitor Professor, UPF
Alicia Gallego, PhD Student, FPU-MEC Scholarship
Maria López-Valenzuela, PhD Student, FI-AGAUR Scholarship
Ignasi Torruella, PhD Student, FPI-MINECO Scholarship

Research Outline

Our group is focused on the analysis of the human genome and that of our closest related species in order to understand the processes that have modelled the extant genetic diversity of humans. We are interested in unravelling the demographic and adaptative processes that have given rise to the genetic composition of human populations and their consequences in health and disease, taking into consideration both the protein-coding and non-protein coding portions of the genome.

Research Lines

Subgroup: Human Genome Diversity

1. Demographic history of European populations: differential migrations and genetic composition of some European minorities

2. Migrations and adaptations in North African populations

3. Genomic composition of African populations: demography and adaptation using complete genomes

Subgroup: microRNAs in Human Adaptation and Disease

1. Involvement of microRNA related mechanisms in human disease susceptibility

2. Molecular evolution of microRNAs in primates

Publications 2015

Alves, J.M.; Lima, A.; Pais, I.; Amir, N.; Celestino, R.; Comas, D.; Heutink, P.; Chikhi, L.; Amorim, A. and Lopes, A.M. (2015). Reassessing the evolutionary history of the 17q21 inversion polymorphism *Genome Biology Evolution* 7: 3239-3248.

Bekada, A.; Araúna, L.R.; Deba, T.; Calafell, F.; Benhamamouch, S. and Comas, D. (2015). Genetic heterogeneity in Algerian human populations. *PLoS ONE* 10(9): e0138453.

Bilgin Sonay, T.; Carvalho, T.; Robinson, M.; Greminger, M.; Krutzen, M.; Comas, D.; Highnam, G.; Mittelman, D.A.; Sharp, A.J.; Marquès-Bonet, T. and Wagner, A. (2015). Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. *Genome Research* 25(11): 1591-1599.

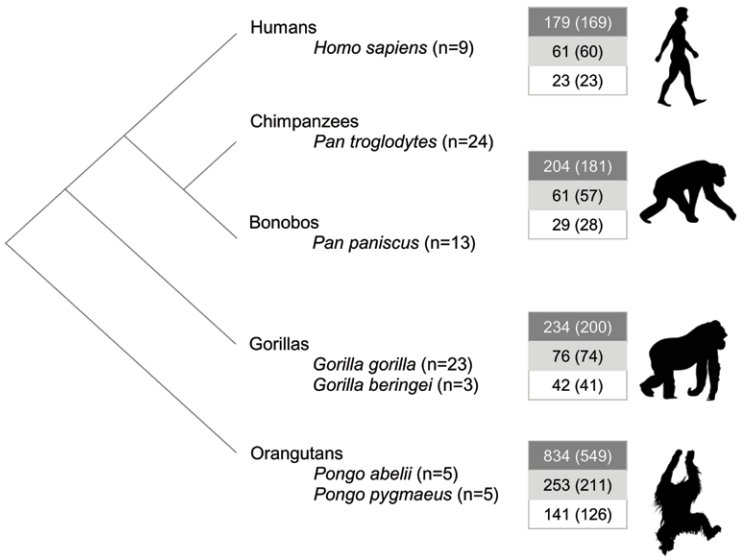


Fig. 1: *Great ape phylogeny showing the number of specific fixed changes in each population since the split with humans (or with chimpanzees in the case of humans), in the precursor (dark grey), mature (light grey) and seed (white) microRNA regions. Total number of microRNAs in which these changes occur is shown in brackets.*

Figure: © *Alicia Gallego*

Dobon, B.; Hassan, H.Y.; Laayouni, H.; Luisi, P.; Ricaño-Ponce, I.; Zhernakova, A.; Wijmenga, C.; Tahir, H.; Comas, D.; Netea, M.G. and Bertranpetit, J. (2015). The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. *Scientific Reports* 5: 9996.

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Vargas-Pinilla, P.; Paixão-Côrtes, V.R.; Paré, P.; Tovo-Rodrigues, L.; Vieira, C.M.; Xavier, A.; Comas, D.; Pissinatti, A.; Sinigaglia, M.; Rigo, M.M.; Vieira, G.F.; Lucion, A.B.; Salzano, F.M. and Bortolini, M.C. (2015). Evolutionary pattern in the OXT-OXTR system in primates: coevolution and positive selection footprints. *Proceedings of the National Academy of Sciences USA* 112: 88-93.

Books / Book Chapters

Calafell, F. and Comas, D. (2015). Genetics and the reconstruction of African population history. In Population in the Human Sciences. Kreager, Winney, Ulijaszek and Capelli Eds. Oxford University Press, pp. 379-400.

Funded Projects

- **Project Title:** Análisis genómico de la biodiversidad humana en el Mediterráneo: en la encrucijada entre tres continentes (CGL2013-44351-P)
  Financed by: Ministerio de Economía
  Years: 2014–2016
  PI: Francesc Calafell and David Comas

- **Project Title:** Práticas culturais e seu papel na saúde e na doença de populaçoes nativas americanas e de seus descendentes (405996/2013-6)
  Financed by: National Council for Scientific and Technological Development of the Ministry of Science, Technology and Innovation (CNPq/MCTI) of Brazil
  Years: 2014–2016
  PI: Maria Cátira Bortolini and David Comas

- **Project Title:** Genètica de les Poblacions Humanes
  Financed by: Generalitat de Catalunya (2014 SGR 866)
  Years: 2014–2018
  PI: Jaume Bertranpetit


PRH
ASC
AGC Group
PVC RESIN
ASNYL
FJ - 65
Net Weight : 25 kg
PT. Asahimas Chemical
Banten - Indonesia

SCIENTIFIC PUBLICATIONS

ISI Publications

Abellán, P. and Sánchez-Fernández, D. (2015). A gap analysis comparing the effectiveness of Natura 2000 and national protected area networks in representing European amphibians and reptiles. *Biodiversity and Consevation* 24: 1377-1390.

Alonso, A.; [22 authors]; Bertranpetit, J.; Absher, D.; Myers, R.; Marsal, S. and Gisbert, J.P. (2015). Identification of Risk Loci for Crohn's Disease Phenotypes Using a Genome-wide Association Study. *Gastroenterology* 148: 794-8052014.

Alves, J.M.; Lima, A.; Pais, I.; Amir, N.; Celestino, R.; Comas, D.; Heutink, P.; Chikhi, L.; Amorim, A. and Lopes, A.M. (2015). Reassessing the evolutionary history of the 17q21 inversion polymorphism. *Genome Biology Evolution* 7: 3239-3248.

Alzayady, K.J.; Sebé-Pedrós, A.; Chandrasekhar, R.; Wang, L.; Ruiz-Trillo, I. and Yule, D.I. (2015). Tracing the Evolutionary History of Inositol, 1, 4, 5-trisphosphate receptor: Insights from Analyses of Capsaspora owczarzaki Ca2+ Release Channel Orthologs. *Molecular Biology and Evolution* 32(9): 2236-53.

Amat, F.; Oromí, N.; Sanuy, D. and Carranza, S. (2015). Sexual dimorphism and age structure of the Montseny newt (*Calotriton arnoldi*). *Amphibia-Reptilia* 36: 245-252.

Aragón, P.; Sánchez-Fernández, D.; Abellán, P. and Varela, S. (2015). Effects of temporal bias on the assessment of an ecological perturbation: a case study of the Prestige oil spill. *Environmental Research Letters* 10: 094006.

Avena-Koenigsberger, A.; Goñi., J.; Solé, R. and Sporns, O. (2015). Network morphospace. *Journal of the Royal Society Interface* 12(103): 20140881.

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Bergland, A.O.; Tobler, R.; González, J.; Schmidt, P. and Petrov, D. (2015). Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in Drosophila melanogaster. *Molecular Ecology* 25(5): 1157-74.

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Bustamante, M.F.; [22 authors]; Navarro, A.; Montalban, X. and Comabella, M. (2015). Pharmacogenomic study in multiple sclerosis patients responders and non-responders to IFNb. *Neurology: Neuroimmunology & Neuroinflammation* 2(5): e154.

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Carot-Sans, G.; Muñoz, L.; Piulachs, M.D.; Guerrero, A. and Rosell, G. (2015). Identification and characterization of a fatty acyl reductase from Spodoptera littoralis female gland involved in pheromone biosynthesis *Insect Molecular Biology* 24(1), 82-92.

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Cruz, J.; Bota-Rabassedas, N. and Franch-Marro, X. (2015). FGF coordinates air sac development by activation of the EGF ligand Vein through the transcription factor PntP2. *Scientific Reports* 5: 17806.

Dall'Olio, G.M.; Vahdati, A.R.; Bertranpetit, J.; Wagner, A. and Laayouni, H. (2015). VCF2Networks: applying Genotype Networks to Single Nucleotide Variants data. *Bioinformatics* 2015 31(3): 438-9.

De Freina J.J.; Monasterio-León, Y.; Antonietty, C.A. and Vila, R. (2015). Notes on the biology, distribution and taxonomy of Chondrostega LEDERER, 1857 in the Iberian Peninsula with a description of the southern Spanish *Chondrostega escobesae sp. nov.* (Lepidoptera: Lasiocampidae, Chondrosteginae). *Deutsche Entomologische Zeitschrift* 125(4): 195-207.

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IBE HIGHLIGHTED PAPERS

The opisthokonts and convergent evolution in unicellular relatives of animals and fungi

The opisthokonts is an ideal eukaryotic clade to analyze transitions to multicellularity, since it comprises Metazoa, Fungi and a series of unicellular lineages that all shared a common ancestor. However, there is still a lack of knowledge on the phylogenetic relationships of some poorly-known opisthokont taxa, as well as in the biology of those. Two manuscripts shed addtional light on the evolution of opisthokonts. First, we provide the most complete (taxon rich) multigene phylogenetic analysis of the opisthokonts. This allow us to suggest that the last common ancestor of the opisthokonts (LOCA) was amoeboid, with flagellum and bacteriovor. We also observe that there was convergent evolution of lifestyles in opisthokonts. For example, osmotrophy was independently acquired by fungi and by some animal relatives (the Terestosporea). We the analyze how *Creolimax fragrantissima*, a close relative of animals, regulate transitions between different life stages. To this end we obtained the genome sequence of Creolimax and performed RNAseq on both the amoeba and the multinucleate stages and analyzed gene expression and alternative splicing. We found that Creolimax differentially expresses thousands of genes in one cell stage or the other, dynamically regulating alternative splicing, long intergenic non-coding RNAs, as well as co-regulating gene modules associated with animal multicellularity in a cell-type specific manner. We compared it to what was found in choanoflagellates and filastereans (the other unicellular lineages closely related to animals) and found that the cell types from all those taxa are the product of lineage-specific innovations. Finally, we performed a proteomic survey of the secretome of Creolimax, which revealed secondary adaptations to a fungal-like lifestyle (i.e., a specialized osmotrophic feeding mode) through both lateral gene transfer from prokaryotes (such as the CotH family) and lineage-specific expansions (such as trypsins).

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Ubiquitin system in the last common eukaryotic ancestor

It is known that the last eukaryotic common ancestor (LECA) was quite complex at the cellular level. It was unclear, however, whether LECA also had a complex regulatory toolkit. To address this question, we here performed genome-wide evolutionary analyses to unravel the origin and evolution of one of the most important regulatory layers in eukaryotes, the ubiquitin signaling. We found that the basic components of the ubiquitin system had a pre-eukaryotic (archaeal) origin and that the LECA already had a complex ubiquitin signaling. Moreover, by phylogenetic analyses we show that the evolution of the ubiquitin system in eukaryotes was characterized by lineage-specific gene family expansions and by massive domain architecture reorganization (especially in multicellular lineages). Thus, this study shows that LECA was not only complex at a cellular level, but also had a complex ubiquitin regulatory toolkit.

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Hormonal and miRNA regulation of insect metamorphosis

MicroRNAs (miRNAs) are single-stranded RNAs that bind target mRNAs and block their translation. In 2009, Xavier Belles group reported that depletion of dicer-1, the enzyme that catalyzes miRNA maturation, prevents metamorphosis in *Blattella germanica*. However, the precise regulatory miRNA roles remained elusive. The results reported this year by the same group show that the miRNA involved is miR-2 whereas the target is the transcription factor Krüppel homolog 1 (Kr-h1), a master repressor of metamorphosis. Experiments showed that dicer-1 depletion increases mRNA levels of Kr-h1 and depletion of Kr-h1 in dicer-1 knockdowns rescues metamorphosis. Moreover, the Kr-h1 mRNA contains a binding site for miR-2.

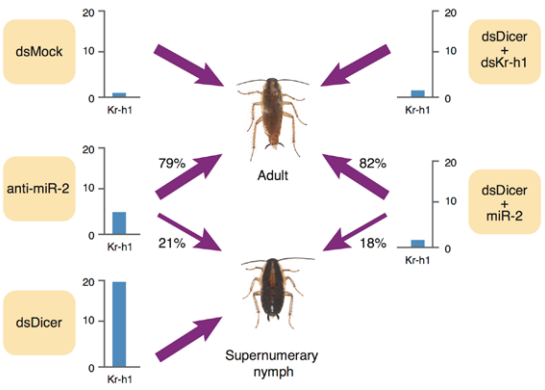

Fig. 1: *Experiments showing that miR-2 scavenges Kr-h1 in the last nymphal instar and controls metamorphosis in* Blattella germanica. *Depletion of dicer-1 (dsDicer-1 treatment) in last nymphal instar inhibits metamorphosis, triggering the formation of a supernumerary nymph; the treatment impairs the decrease of Kr-h1 transcripts observed in controls (dsMock treatment). Depletion of Kr-h1 (dsKr-h1 treatment) in dsDicer-1-treated animals rescues metamorphosis. Administration of a miR-2 inhibitor (anti-miR-2 treatment) impairs metamorphosis. Administration of a miR-2 mimic (miR-2 treatment) in dsDicer-1-treated animals rescues metamorphosis. Levels of Kr-h1 mRNA are also indicated.*

This suggested that metamorphosis impairment is caused by dicer-1 depletion is caused by a deregulation of Kr-h1 expression that derives from a miR-2 deficiency. This was corroborated by treating the last nymphal instar of *B. germanica* with a miR-2 inhibitor, impairing metamorphosis, and treating dicer- 1-depleted specimens with a miR-2 mimic, restoring metamorphosis (Fig. 1). The conclusion is that miR-2 rapidly clears Kr-h1 transcripts in the last nymphal instar, which is crucial for proper metamorphosis. An elegant mechanism by which a single miRNA leads metamorphosis to its correct conclusion.

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Genomic structure and regulation

In 2015, two papers from "Comparative Genomics Lab" provided a better understanding of how gene regulation has contributed to recent human and non-human primate evolution. One manuscript (Hernando-Herraez et al. NAR 2015) described a global comparative analysis of CpG methylation patterns between humans and great apes (chimpanzee, gorilla and orangutan) using whole genome bisulfite sequencing and its comparison to patterns of SNP diversity in these species. We identified hundreds of novel regions showing an exclusive pattern of DNA methylation in blood from humans compared to great apes and estimated that ~25% of these regions were still detectable throughout several human tissues, highlighting that they most likely fixed. Moreover, these regions were enriched for specific histone modifications and, contrary to expectations, they were located distal to transcription start sites. We also reported, for the first time, a close interplay between inter-species genetic and epigenetic variation which offers a

novel perspective to decipher the mechanistic basis of human-specific DNA methylation patterns and the interpretation of inter-species non-coding variation.

The second manuscript (Bilkin et al. Genome Research 2015) described for the first time VNTR (tandem repeat) diversity on the genome-wide level in human and non-human great ape populations. We demonstrated the role of VNTRs as a source for expression divergence between humans and their closest primate relatives. The presence of tandem repeats in genes, even controlling for polymorphisms, was associated with higher levels of expression divergence between human and these primates, and this association holds for genes with repeats in their 3' untranslated region, in introns, and in exons. We believe that our work supports the notion that non-coding variation has a prominent role in genome regulation.

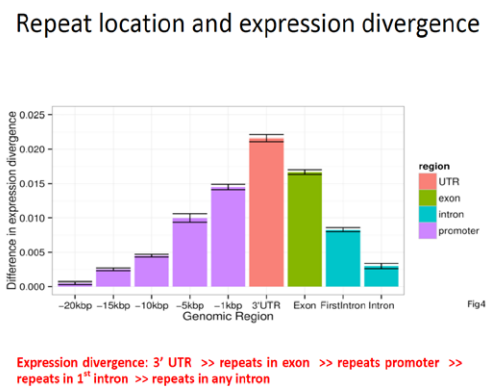

Fig. 1: *Gene expression divergence between human and chimpanzee according to the genomic position of VNTR differences. Several patterns can be noticed: VNTR variation in 3'UTR regions seems to have a higher influence in gene expression divergence than other genic regions. Also, there is a decreasing effect of gene expression in relation to the distance of VNTR to the transcription start site.*

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Identification and functional validation of candidate adaptive transposable element insertions

In 2015, "The Evolutionary and Functional Genomics lab" has further contributed to the analysis of transposable element insertions in genome sequences. We have spearheaded the development of *T-lex2* in collaboration with Prof. Dmitri Petrov at Sanford University (USA), and with Dr. Anna-Sophie Fiston-Lavier at ISEM (France). *T-lex2* software allows to genotype and estimate TE population frequencies using single or pooled next-generation sequencing data. Additionally, a new module of T-lex2, TE-TSD detection, allows re-annotating TE insertions by automatically detecting Target Site Duplications (TSDs) in an unbiased and accurate way. The flexible and customizable design of T-lex2 allows running it in any genome and we showed that it does provide accurate frequency estimates in the fruitfly and the human genomes. (Fiston-Lavier et al 2015).

We have run T-lex2 for all TEs annotated in the *Drosophila melanogaster* genome using next-generation sequencing data from four natural populations. These data allowed us not only to study which factors govern the dynamics of TEs in populations but also to generate a catalogue of putatively adaptive TEs. One of the TEs included in this catalogue is *FBti0019386*. This insertion was first hypothesized to be under spatially varying selection because it was present at higher frequency in temperate compared with tropical North American and Australian populations. In our recent publication in Molecular Biology and Evolution, we showed that the functional effects of this mutation are not consistent with a role in temperate adaptation: flies with *FBti0019386* insertion do not show differences in fecundity and are more sensitive to cold stress. On the other hand, flies with this insertion show a faster development time. Quick development is an

adaptive trait in organisms that fed on ephemeral food sources, as is the case for *D. melanogaster*. In the light of these results, we reassessed the clinality of this mutation and found that no clinal patterns are present in European populations. This is consistent with the evidence for African admixture in North American and Australian populations reported recently. Our results highlight the necessity to perform functional assays to confirm the adaptive effect of mutations that show clinal patterns. (Ullastres et al 2015).

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Mountain Gorillas genomics and diversity

A general dogma in conservation genetics suggests that genetic depression might be the beginning of an extinction vortex. In this manuscript, we provide evidence that there might be some exceptions. Mountain gorillas are the most intensively great ape studied in the wild after they were made famous by late primatologist Dian Fossey. There are just a few hundreds of individuals living in Rwanda, Uganda and the Democratic Republic of Congo. We sequenced the complete genome of 7 Mountain gorillas (>1% of the total population) and we compare it to a newly sequence population of 6 Eastern lowland gorilla. The comparison revealed that the Mountain gorillas contained the lowest diversity of all great apes sequenced so far. Despite of containing up to 20% of their genomes in regions of complete homozygosis, these high levels of inbreeding have been genetically beneficial by removing a substantial part of harmful loss-of-function variants.

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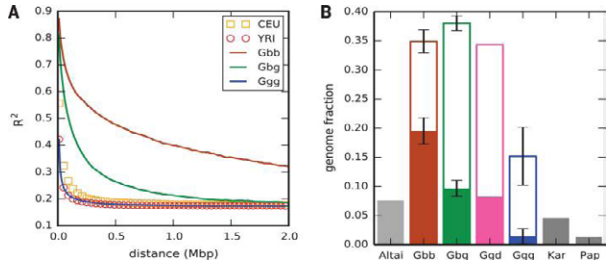

Fig. 1: *Linkage disequilibrium and homozygosity in Mountain gorillas (Gbb) compared to other gorillas and two human populations (Utah residents with European ancestry (CEU) or Yoruba in Ibadan, Nigeria (YRI)). Notice that Mountain gorillas has the higher genome fractions found in homozygous tracts, even compared to an Altai Neandertal and two human individuals [Karitiana (Kar) and Papuan (Pap)].*

Genomics of Recent European Prehistory

The retrieval and analysis of ancient genomes, triggered by the development of second generation sequencing technologies, is revolutionazying the study of the past, allowing now the testing of genomic affinities of past cultural horizonts in European prehistory as well as the detecting of selective events in space and time. In a collaborative study published at Nature, we have revealed twelve genes upon which natural selection acted, notably during the transition from hunting and gathering to farming. These genes are associated to pigmentation, metabolism and immunity and show the adaptive challenges that shaped modern European genomes.

In a second study directed but the Paleogenomics group, the first complete ancient genome from

the Mediterranean area was retrieved; it consisted in a 6,400 years-old Cardial individual from Cova Bonica in Vallirana (Barcelona). The spreading of farming into Europe took place following two distinct colonization routes. The oldest migration, represented by the Cardial ware (named for the impressed decorations made on the pottery with the serrated edge of cardium shells) followed the North Western Mediterranean coast; a subsequent migration followed the Danube river into Central Europe, leading to the emergence of the LBK tradition. Cova Bonica genome clusters with other Early Neolithic farmers as well as modern Sardinians (the latter is a European population that have preserved the original farming component due to isolation). Our analyses support that Cardial and LBK people derive from a common ancient population that originated most likely in or near Anatolia, the point of entrance of the Neolithic farmers from the Near East.

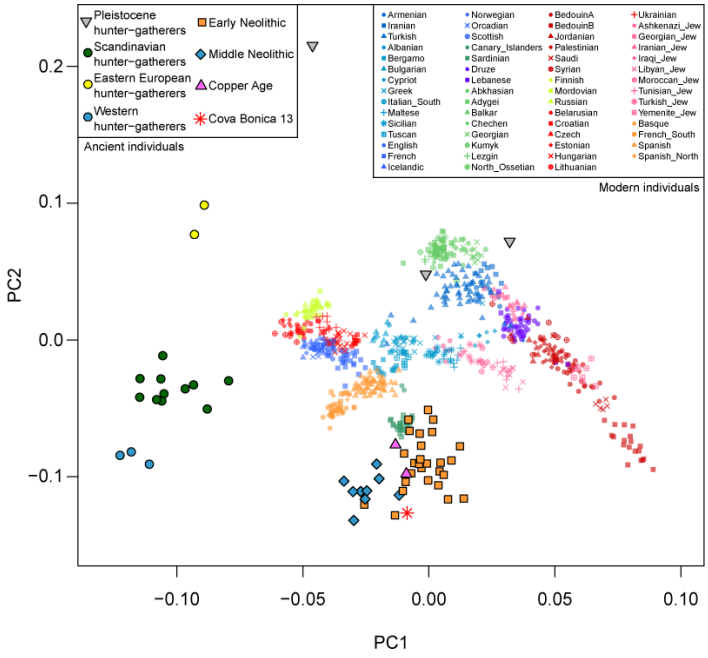

Fig. 1: *Procrustes Principal Component Analysis (PCA) of Mesolithic hunter-gatherers, Early Neolithic, Middle Neolithic and Copper Age farmers from ancient Europe, along with modern human populations. The PCA analysis was performed using only transversions (to avoid confounding effects related to* post-mortem *damage).*

IBE COLLECTIONS

The IBE collections have continued growing during 2015 thanks to the research effort of our scientists. Currently, the bulk of the collection is formed by insects (more than 120,000 specimens of Coleoptera and near 50,000 Lepidoptera, plus a smaller representation of Himenoptera and other orders) and reptiles (more than 11,000 tissue samples). Besides, there is a significant representation of Amphibians (ca. 2,500 tissue samples) and small mammals (ca. 1,500 DNA samples). In terms of species, this represents ca. 5,000 species of Coleoptera, 930 of Lepidoptera, 668 of reptiles and 117 of amphibians. We also keep type material of many of the new species that we have described, either in the form of DNA aliquotes, tissue samples or whole specimens.

The huge amount of samples and specimens stored in the IBE collections has been achieved by several donations from researchers and, above all, by the numerous national and international field expeditions carried out by our research groups. On account of this, over the years, our collections have acquired a totally global nature, with specimens and samples from a lot of countries from almost all continents – except Antarctica (Fig. 1).

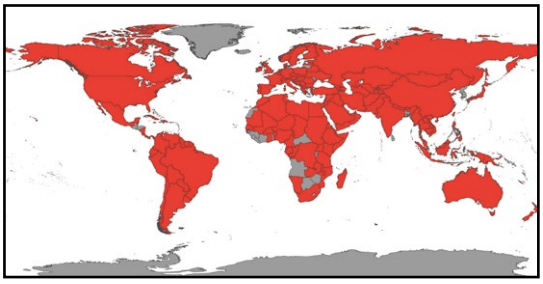

Fig. 1: *Truly global collections: in red, countries that are represented by samples at the IBE collections.*

The IBE collections are not only a storage of biological samples, but also a repository of vouchers used in published research and a dynamic resource for ongoing and future studies. Due to the constant increase of its volume and importance, a new IBE member will start on January 2016 that will be exclusively devoted to the management of the IBE collections.

Among other aspects, we expect to improve our collections databases and to make them more accessible to the scientific and educational community. We are planning to create a biological collections website with a public database and easy procedures to check the information of our samples and request loans or transfers of them. We also expect to establish new protocols and methodologies to fit into the increasing demands of the new international agreements about the use of genetic resources, especially the Nagoya Protocol. In this regard, we will work in the design of a Biological Collections Policy and in different models of Material Transfer Agreements (MTAs).

Developments and discoveries of 2015

The Institute of Evolutionary Biology has carried out several collecting campaigns in almost all continents of the world during 2015.

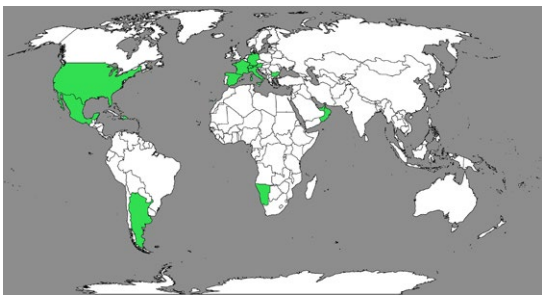

Fig. 2: *Sampling locations for the new collection specimens obtained by IBE members during 2015.*

Here is a brief description of some of our 2015 international expeditions.

Argentina
Our butterfly researchers visited Argentina to study the genus *Aricoris*, a butterfly group that shows many extreme adaptations, such as living in inhospitable environments like the South American Chaco thanks to mutual association with ants.

Namibia, Republica Dominicana, Mexico and the USA
Vila and colleagues organized expeditions in these countries within the framework of the "*Vanessa cardui* Project" in order to study *V. cardui*, a migratory butterfly that is capable of travelling from northern latitudes to the equator every year, surviving to adverse climatological conditions and the intense effort that these moves involve.

Northern Morocco
Our coleopteran researchers studied the adaptations of water coleopterans to saline environments, taking advantage of the huge quantity of coastal lagoons and marshes found in Moroccan coasts.

New York State (USA)
This region of the US is very rich in species of the coleopteran genus *Calligrapha*. There, our butterfly researchers conducted research on these beetles and the role of their mitochondrial endosymbionts in determining their sex.

Oman and UAE
Thanks to the financial aids of MINECO and the Mohamed Bin Zayed Species Conservation fund, our reptile researchers can continue studying the reptile diversity of south-eastern Arabia year-by-year. As a result, 3 reptile species from the genus *Hemidactylus* have been described during this year.

Europe
Different teams performed multiple collecting trips to localities in the Iberian Peninsula, the Mediterranean basin, Central and Eastern Europe.

The IBE researchers perform a strong effort in taxonomic research. This is reflected in the discovery of 7 new animal species during 2015, including:

3 beetles (*Coleoptera*)
Troglochinarus pallisei (Rizzo & Comas, 2015)

Calligrapha catarinae (Gómez-Zurita et al., 2015)

Calligrapha anabelae (Gómez-Zurita et al., 2015)

1 ant (*Hymenoptera*)
Lasius balearicus (Talavera et al., 2014)

3 reptiles (*Reptilia*)
Hemidactylus adensis (Smid et al., 2015)
Hemidactylus awashensis (Smid et al., 2015)

Hemidactylus mandebensis (Smid et al., 2015)

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De Freina, J.J.; Monasterio-León, Y.; Antonietty, C.A. and Vila, R. (2015). Notes on the biology, distribution and taxonomy of Chondrostega LEDERER, 1857 in the Iberian Peninsula with a description of the southern Spanish *Chondrostega escobesae* sp. nov. (Lepidoptera: Lasiocampidae, Chondrosteginae). *Deutsche Entomologische Zeitschrift* 125(4): 195-207.

Smid, J.; Moravec, J.; Kratochvil, L.; Nasher, A.K.; Mazuch, T.; Gvozdik, V. and Carranza, S. (2015). Multilocus phylogeny and taxonomic revision of the *Hemidactylus robustus* species group (Reptilia, Gekkonidae) with descriptions of three new species from Yemen and Ethiopia. *Systematics and Biodiversity* 13: 346-368.

Gómez-Zurita, J. (2015). Systematic revision of the genus Calligrapha Chevrolat (Coleoptera: Chrysomelidae, Chrysomelinae) in Central America: the group of Calligrapha argus Stål. *Zootaxa (Monograph)* 3922: 1-71.

Besides the discovery of animal species, the IBE researchers propose new taxonomic combinations and status in basis of their intense collecting campaigns and taxonomic studies each year. Among all of the findings from 2015, we would want to highlight an important record from our reptile researchers:

The rediscovery of a lost species: *Rhynchocalamus arabicus* (Schmidt, 1933)

On 2015, the researchers of the Systematics, Biogeography and Evolution of Reptiles and Amphibians Group, leaded by Dr. Salvador Carranza, have rediscovered one of the strangest snakes in the world. This is *Rhynchocalamus arabicus*, commonly known as the Aden Black-headed Snake. Before the finding of their group, this species had only been registered once – in 1932 – at Aden, Yemen. The confirmation of this second register has been possible thanks to morphological studies based on the species holotype – and sole representative of the species until now – and genetic sequencing.

After 80 years with no news from this species, the discovery of his group not only marks the current existence of this species. This time *R. arabicus* was found at Dhofar, Oman - more than 1,000 km far from the location of the first register. This finding suggests that the distribution area of this species could be really wide and continuous between Oman and Yemen. In an interview to the Omani Newspaper *Muscat Daily*, Dr. Carranza stated: "Nothing is known about the distribution, population, status, natural history or threats of *R. arabicus*. Additional fieldwork in the Dhofar region will be needed to collect more data on this species."

Discoveries like this show the importance of field surveys even in well-studied areas such as Dhofar, and they encourage the Institute of Evolutionary Biology to carry on with the numerous expeditions every year.

Reference Article

Smid, J.; Martinez, G.; Gebhart, J.; Aznar, J.; Gallego, J.; Göçmen, B.; de Pous, P.; Tamar, K. and Carranza, S. (2015). Phylogeny of the genus *Rhynchocalamus* (Reptilia; Colubridae) with a first record from the Sultanate of Oman. *Zootaxa* 4033: 380-392.

THESES, COURSES AND SEMINARS

Doctoral Thesis presented during 2015

- **PhD Student:** Maria López Valenzuela
  Title: Funtional and evolutionary implications of single nucleotide substitutions in human microRNAs across primates
  Thesis Director: Yolanda Espinosa
  Institution & Date: Universitat Pompeu Fabra, 15 January 2015
- **PhD Student:** Valeria Rizzo
  Title: Evolution, diversification and ecology of a clade of strictly subterranean beetles (Troglocharinus, Family Leiodidae)
  Thesis Director: Ignacio Ribera
  Institution & Date: Universitat de Barcelona , 8 October 2015
- **PhD Student:** Karim Tamar
  Title: Phylogeny and phylogeography of the Lacertid genera *Acanthodaxtylus* Fitzinger, 1834 and *Phoenicolarcerta* Arnold, Arribas & Carranza 2007 (reptilia: Lacertidae)
  Thesis Director: Shai Meiri/Salvador Carranza
  Institution & Date: University of Tel-Aviv 10 June 2015
- **PhD Student:** Cristina de Miguel Vijandi
  Title: Morfogénesis y evolución del sistema traqueal de los insectos
  Thesis Director: Xavier Franch-Marro/ Jordi Casanova Roca
  Institution & Date: Universitat de Barcelona 10 July 2015
- **PhD Student:** Philiphe de Pous
  Title: Integrating geospatial methods into evolutionary biology and conservation: case studieson selected Western Paleartic hepertofauna
  Thesis Director: Salvador Carranza
  Institution & Date: 6 July 2015
- **PhD Student:** Neus Bota Rabassedas
  Title: Funció de la vía de senyalització de wingless en la morfogènesi del disc d'ala de Drosophila
  Thesis Director: Xavier Franch-Marro
  Institution & Date: Universitat de Barcelona 26 June 2015
- **PhD Student:** Irene Hernando Herraez
  Title: Evolutionary insights into human DNA methylation
  Thesis Director: Tomàs Marquès-Bonet
  Institution & Date: Universitat Pompeu Fabra, 24 July 2015
- **PhD Student:** Nashwa Ahmed Ali Mohammed Elshaer
  Title: Molecular keys in structural evolution of insec ovaries
  Thesis Director: Maria-Dolors Piulachs
  Institution & Date: Universitat Pompeu Fabra 16 March 2015
- **PhD Student:** Emilio Valbuena Ureña
  Title: Conservation genetics of the critically endangered Montseny brook newt *(Caloriton arnoldi)*
  Thesis Director: Salvador Carranza
  Institution & Date: Universitat Autònoma de Barcelona 24th Juliol 2015
- **PhD Student:** Raluca Vodă
  Title: Biodiversity and comparative phylogeography of western Mediterranean butterflies.
  Thesis Director: Roger Vila/Leonardo Dapporto
  Institution & Date: Universitat Autònoma de Barcelona 11th December 2015

Teaching

IBE Scientists belonging to the Universitat Pompeu Fabra are in charge of the coordination and main teaching of several academic subjects in undergraduate degrees and master programs, as follows.

GRADUATE STUDIES

Bachelor's Degree in Human Biology

- **Human Evolution and Health (4 ECTS)**
  Coordinators: Elena Bosch and David Comas
- **Zoology (4 ECTS) Coordinator:** Ferran Casals
- **Ecology (4 ECTS)**
  Coordinator: Francesc Calafell
- **Integrated Biomedicine I (4 ECTS)**
  Coordinator: David Comas.
- **Basic Sciences 1. (7 ECTS)**
  Coordinator: Ricard Solé
- **Genomics (4 ECTS)**
  Coordinator: Jaume Bertranpetit
- **Human Biology Seminars (English) (4 ECTS)**
  Coordinator: Jaume Bertranpetit

Bachelor's Degree in Medicine

- **Human Evolution and Health (4 ECTS)**
  Coordinators: Elena Bosch and David Comas

Bachelor's Degree in Biomedical Engineering

- **Molecular Biology of the Cell II (BMCII) (4 ECTS)**
  Coordinator: Yolanda Espinosa Parrilla
- **Cells and Tissues Engineering (5 ECTS)**
  Coordinator: Ricard Solé

MASTER STUDIES

Master in Biomedical Research (BIOMED)

- **Genomes and Systems (5 ECTS)**
  Coordinator: Tomàs Marquès-Bonet
- **Introduction to Biomedicine (5ECTS)**
  Coordinator: David Comas

Master in Bioinformatics for Health Sciences (BIOINFO). Joint master of the Universitat Pompeu Fabra (coordination) and Universitat de Barcelona, in cooperation with the Università di Bologna.

- **Analisis of Biomedical Data (5 ECTS)**
  Coordinator: Arcadi Navarro
- **Biomedical Informatics (5 ECTS)**
  Coordinator: Arcadi Navarro
- **Introduction to Biomedicine (5ECTS)**
  Coordinator: David Comas

Furthermore, most IBE scientists actively participate in several international master programs and specialized courses in different universities:

- **Master:** Biodiversity; Universitat de Barcelona (UB)
  Teachers: J. González, S. Carranza, I. Ruiz-Trillo
- **Postgraduate Course:** Filogenias y Genealogías de DNA: Reconstrucción y Aplicaciones; Universitat de Barcelona (UB)
  Teachers: J. Castresana, S. Carranza, I. Ruiz-Trillo
- **Master:** Human Biology; Universitat de Barscelona (UB) / Universitat Autònoma de Barcelona (UAB)
  Teacher: Francesc Calafell
- **Master:** Genetic Counselling; IDEC/UPF
  Teacher: Francesc Calafell
- **Master:** Genetics and Genomics, Universitat de Barcelona (UB)
  Teacher: Iñaki Ruiz-Trillo

Last but not least, every year IBE hosts several undergraduate and master students through his/her scientific projects coming from most of Catalan Universities.
Along 2015 IBE has hosted a total of 37 students. In particular:

- 7 High school juniors from "Programa Joves i Ciència" (5)- *financed by Fundació La Caixa-la Pedrera*-, Institut la Guineueta (1), Col.legi Jesus Mª José (1)
- **21 undergraduate students (practicums) from:** Universitat de Barcelona (10), Universitat Pompeu Fabra (3), Universitat Autònoma de Barcelona (4), Universitat de Girona (2), Universitat de València (1), University of Hiroshima (1)
- **6 master students from:** Universitat Pompeu Fabra (1), Universitat de Barcelona (3), Universidad de Sevilla (1), Universidad de Murcia (1)
- **3 ERASMUS students from:** Universidad de Szent Istvan (1), University of Upsala (1), Universidade do Porto (1).

Seminars

Speaker	Title	Institution	Date
Urko Martínez Marigorta	Gene-by-environment interactions in disease: hidden effects in GWAS results?	Georgia Institute of Technology	9/1/2015
Isabel Mendizábal	Experimentally defined hypomethylated CpG islands mark hotspots of tissue-specific regulation	Georgia Institute of Technology and University of the Basque Country UPV/EHU	9/1/2015
Casper J. Breuker	Oogenesis and early embryogenesis in Speckled Wood butterflies	Oxford Brookes University	28/1/2015
Diego Ayala	Decrypting aridity adaptation in the malaria mosquito *Anopheles gambiae*	IRD Montpelier	5/3/2015
David M. Alba	Fossil primates from Abocador de Can Mata: Implications for hominoid evolution	Institut Crusafont	18/3/2015
Isaac Salazar	Understanding the genotype-phenotype of development and its evolutionary consequences	Helsinki University	26/3/2015
Frederic Bartumeus	The movement ecology revolution: standing on the shoulders of bioinformatics?	CEAB, CSIC	20/5/2015
Nick Brown	Dialogue between cell adhesion receptors and the cytoskeleton during morphogenesis	Cambridge University	3/6/2015
Javier Etxabe	Protección de Resultados de Investigación y creación de spin-offs en el CSIC. Formas de transferencia y colaboración con empresas	Unidad de Protección de Resultados y Promoción de Empresas de Base Tecnológica (CSIC)	10/6/2015
Fran Supek	Mutational processes in human cancer: the what, where and why of somatic mutation	CRG	29/10/2015
Elena Gómez-Díaz	Epigenetic regulation of Plasmodium falciparum clonally variant gene expression in the mosquito	Department of Biology, Emory University, Atlanta. Estación Biológica de Doñana (EBD-CSIC)	26/11/2015
Lluís Ribas de Pouplana	The emergence of eukaryotes and the evolution of the genetic code	ICREA, IRB	10/12/2015

IBE RETREAT CHRONICLE

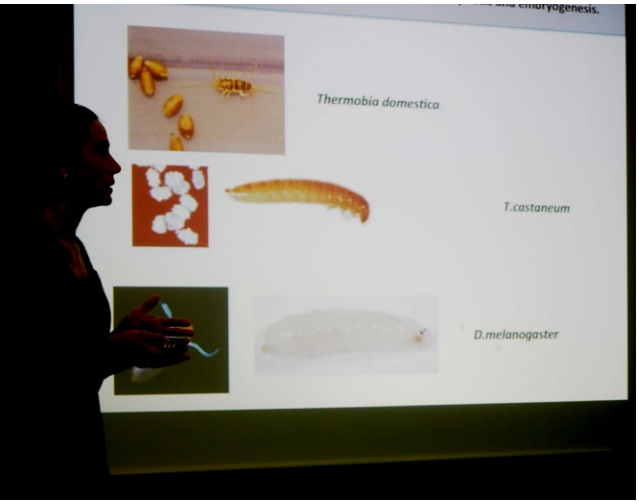
The 5th IBE Retreat took place on the 1st and 2nd of October at Ametlla de Mar (Tarragona). As well as providing an opportunity for around 100 members of the Institute to interact and learn more about the research taking place at IBE, this year the meeting, co-organized by Josefa González, Jordi Lanuza and Iñaki Ruiz, incorporated a series of technical and informative speeches, as well as several social activities.

The Retreat was opened by the traditional welcome address of the Director, Xavier Belles, who presented an overview of the developments occurring in the institute since last general meeting.

Important highlights of the Retreat were the research talks from some of our senior scientists, which showed both the breadth and depth of evolutionary biology research taking place throughout the IBE. In this edition, the speakers were José Luis Maestro (Nutritional Signals in Insects), Josep Sardanyés (Complex Systems), Luc Steels (Language Evolution), Leonardo Dapporto (Butterfly Diversity & Evolution), Elena Casacuberta (Evolution and Development), and José Castresana (Phylogeny and Phylogeography of Mammals). In keeping with our aims, many collaborative links between members were clearly apparent, with the talks stimulating a lot of debate.

In a slight change from previous years, the 2015 IBE Retreat also included a series of presentations from junior researchers, including post-doctoral fellows and PhD students. Lara Rubio (Human Diversity), Iñigo Olalde (Paleogenomics), and Daniel Rodríguez (Complex Systems) shared their most recent results.

On a different note, this year brought the novelty of the PowerPoint Karaoke, which is an improvisational activity in which a participant must deliver a presentation based on a set of slides that they had never seen before. Another member of the Institute prepared those slides based on his or her project and at the end of the karaoke presentation he/she



told what they were exactly about. The brave ones to volunteer were Guillem Ylla (Insect Reproduction and Evolution of Insect Metamorphosis), David López (Multicellgenome), Marc de Manuel (Primate Genomics) and Nino Spataro (Evolutionary Population Genetics). They all did a very good effort to guess what were the graphics about and drew laughter from the crowd.

All this scientific talks were supported by a series of technical speeches. Núria Bonet, from the UPF Genomics Unit, explained the news of the platform; Elena Casacuberta told us about unconscious bias and the Diversity Committee; Elena Bosch and José Luis Maestro discussed about Good Laboratory Practices; Anna Pérez introduced the news at the Administrative Unit; and Josefa González and Jordi Lanuza introduced the BCNBioPro Science Meeting and the recently established Communications Unit respectively.

Another highlight of the meeting were the social activities. On Thursday afternoon, attendees split in teams to play football, Ping-Pong or hiked to the Cap de Santes Creus through the Camí de Ronda. After dinner, IBE members were divided into 20 mixed groups, who battled for a prize in a four-part general culture quiz organized by Francesc Calafell. The winners were the *Jynx* team, formed by Leonardo Dapporto, Jesús Gómez-Zurita, Matija Harcet, and David Mas. Once the quiz was finished, the youngest (and some of the elder) IBE members stayed a little bit longer for additional social networking and some dancing.

The retreat finished with a stimulating session called "Making the IBE stronger". All the attendees were divided in groups of eight and agreed on three different topics that should be considered to improve the Institute. At the end, the proposals were discussed among all IBE members including the IBE Executive Board.


مجلس تنوف العام

TRAINING AND OUTREACH UNIT (TAO)

The Training and Outreach Unit was created in May 2012 with two main objectives: to establish a post-graduate training program in Evolutionary Biology, and to inform and educate the general public about the research that is carried out at the Institute of Evolutionary Biology (IBE). The IBE Executive Board appointed David Comas and Josefa González, as joint coordinators of the Training and Outreach Unit.

TRAINING ACTIVITES

The IBE develops a training program for PhD and Postdoctoral students. The main goals of the program are:

- to establish a deep knowledge in Evolutionary Biology including theoretical, analytical and experimental tools.
- to reinforce oral and writing abilities.
- to develop leadership and management qualities.
- to promote the abilities to evaluate the bioethical implications of a research project.

PhD students and Postdoctoral fellows carry out their PhD theses and projects in outstanding research laboratories and facilities working on a diverse range of topics in the evolutionary biology field. Researchers have access to high-quality seminars and conferences, as well as to a range of services and networks.

Furthermore, in the context of PRBB centres, IBE members have access to the Intervals Programme, an interdisciplinary education programme for professionals working in the Barcelona Biomedical Research Park (PRBB). The activities of the Intervals programme currently focus on:

A: Leadership, Management, and Career Development
B: Communication
C: Good Science, Honest Science

OUTREACH ACTIVITIES

The Institute of Evolutionary Biology is committed to informing and educating the general public about the research being carried out at the Institute. During 2015, IBE organized and participated in several outreach activities.

La Ciència Al Teu Món

Several PIs and students at the IBE are collaborating with *La Ciència Al Teu Món (LCATM)* outreach project lead by Josefa González. Besides raising awareness of the importance and the implications of Science in everyday life, *LCATM* also aims at conveying the value of a scientific way of thinking and a rational attitude towards problems.

Some examples of posts written by members of IBE:
http://lacienciaalteumon.cat/compartir-confiar-salud-y-privacidad/
http://lacienciaalteumon.cat/alzheimer-e-identidad/
http://lacienciaalteumon.cat/aventura-cientifica-per-lantartida/
http://lacienciaalteumon.cat/pluto-el-petit-planeta-que-ho-canvia-tot/

BioScience Pro Meeting

23rd November 2015
This conference fro 250 students aged between 12 and 18, consisted in five talks by researchers on evolutionary biology, genetics, biomedicine and

biotechnology. Additionally, selected high school students had the chance to present their project in a talk or a poster session. The highlight of the day was the seminar of Michael Levitt, 2013 Nobel Prize laureate in Chemistry. The event was organized by Josefa Gonzalez in collaboration with LCATM.

+Humans Exhibition and CCCB Debats
From October 2015 to April 2016

These two activities that took place in the Centre de Cultura Contemporània of Barcelona were participated by IBE scientists, especially by Ricard Solé. Artists and scientists explored uncharted territory that relates to the present by, more importantly potential futures. They exhibit and the debates sought to share with citizens the state of the art but also what scientists do best: asking all those open questions that will affect our near and far-distant future.

Bee Devices and other curious observations
May 2015

The research group led by Luc Steels at IBE co-organized an exhibition about bees, art and technology. Given the situation of bees and the catastrophic environmental consequences if they become extinct, this exhibition, which will travelled around the world during 2015, aimed to show not only the result of years of research with bees, but also to raise awareness about this problem both within the general population and the scientific community.

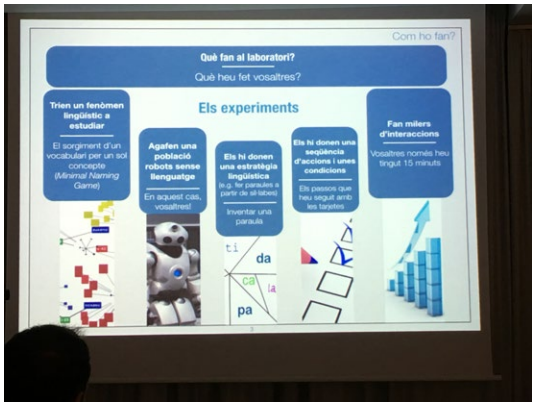
Saló de l'Ensenyament (teaching fair)
18th to 22nd March 2015.
Organized by: Generalitat de Catalunya

IBE collaborated with the stand of the Catalan Delegation of CSIC (Consejo Superior de Investigaciones Científicas), at the 'Space Science', which aims to bring the centres' research to young

people who visit the show. The 'Space Science' is organized by the Catalan Foundation for Research and Innovation (FCRI). The objective of the Education Fair is to inform children and young people between 12 and 18 years about the training at all levels in Catalonia.

Programa Professors i Ciència
(Science and Professors programme). 2nd and 9th December 2015. Funded by: Fundació Catalunya-La Pedrera.

IBE participated in the Professores i Ciència program in collaboration with LCATM by offering a course to high-school teachers:
Playing with robots: evolutionary theory and language evolution



PRBB Open Day
October 3rd, 2015. Organized by: Parc de Recerca Biomèdica de Barcelona (PRBB)

The IBE participated with several activities, including the scientific conferences "The mystery of metamorphosis: from the egg to the buttefly" by David Martín and "Origin, diversity and evolution of hominid", by Tomàs Marquès. This year IBE also did the photography exhibition named "Butteflies in a click", where Vlad Dincă, Raluca Vodă and Roger Vila shared some of their favourite close-ups of European butterflies.

(Re)volució: Conquereix amb nosaltres les noves fronteres del coneixement
The main event took place on 2013, when researchers at the IBE discussed diverse topics such as predicting the behaviour of biological systems, butterfly diversity and the information the give us about climate change, the origin of multicellularity, the role of genes in our decisions, and the past of the human species through the genome. On 2015, videos and educational material were created in collaboration with LCATM and disseminated in face-to-face and online events.

Joves i Ciència

This is a program of short-term (1-2 months) internships for pre-selected secondary school students interested in science, organized and supported by Fundació Catalunya-La Pedrera. The students engage directly in scientific research guided by and collaborating with senior researchers who are at least at the PhD student level. In 2015, seven students spend the summer at the IBE labs.

Activities for students in collaboration with the PRBB

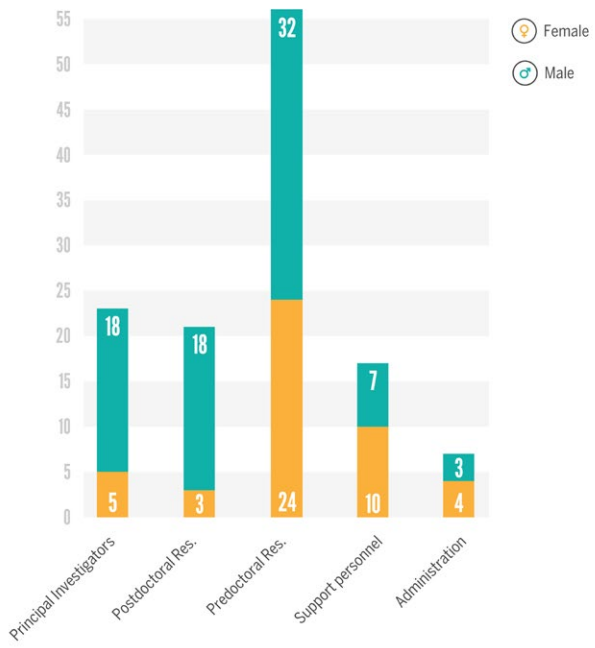
The PRBB provides a programme of activities for high school students. As part of the initiative Escolab, IBE offered high school students the chance to get to know the PRBB and some of its facilities and lines of research. The programme consists of a brief presentation of the park, a visit to one of the scientific-technical services and a talk by a researcher who explains their work.

PlayDecide is a discussion game for high school students to debate socio-scientific issues. It was developed as part of a project involving different EU countries to encourage public participation in such debates. Currently, there are more than 30 PlayDecide kits in different languages dealing with topics as diverse as climate change, pre-natal selection, animal testing, and nanotechnology. The PlayDecide workshops that the IBE offered were about genomics and evolution.

IBE researchers also gave scientific talks that took place in the PRBB conference hall, which can hold up to 250 people.

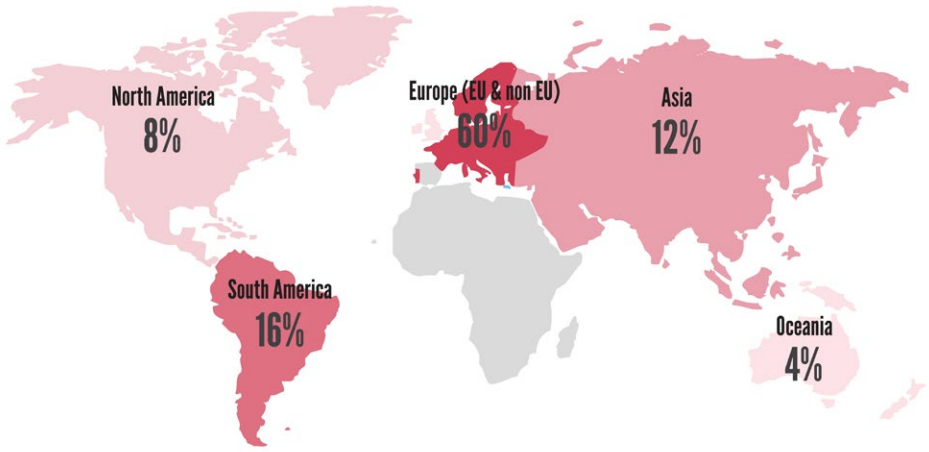
IBE IN NUMBERS

DISTRIBUTION OF 2015 PERSONNEL BY CATEGORIES AND GENDER



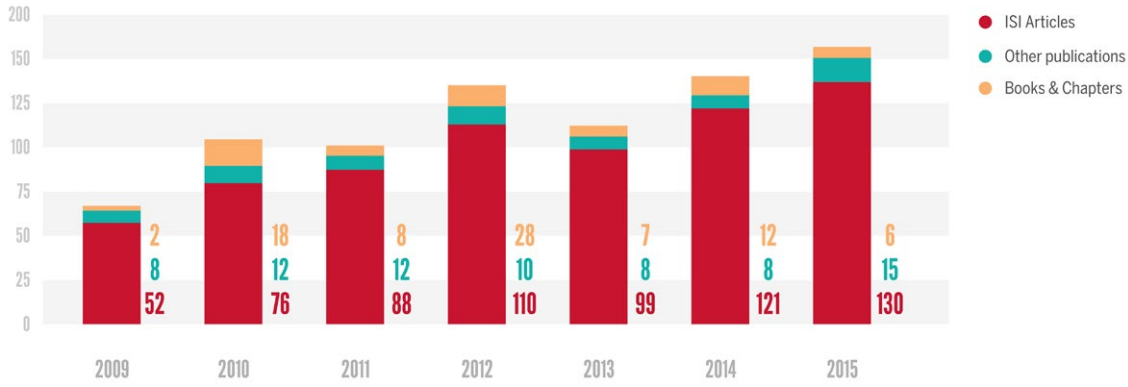
2015 INTERNATIONALISATION

FOREIGN PERSONNEL REPRESENTS A 20% OF THE TOTAL OF IBE MEMBERS (VISITORS NOT INCLUDED).
WE HAVE RESEARCHERS FROM 23 DIFERENTS COUNTRIES.

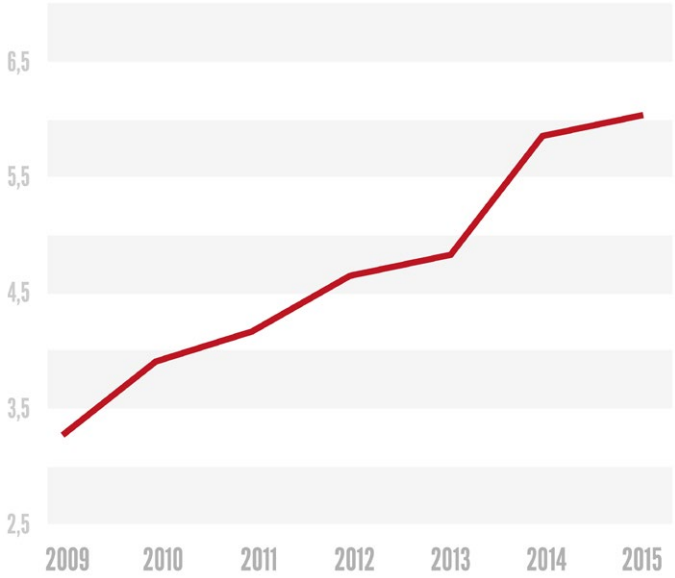


EVOLUTION IN NUMBER OF THESES DEFENDED EACH YEAR

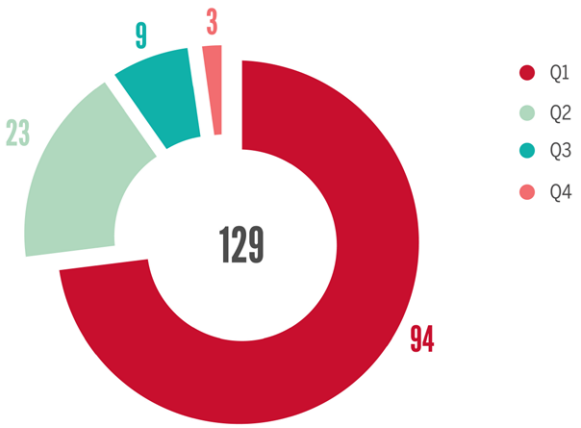
EVOLUTION OF PUBLICATIONS DISTRIBUTION PER KIND OF PUBLICATION



EVOLUTION OF MEAN IMPACT FACTOR FOR ISI PUBLICATIONS

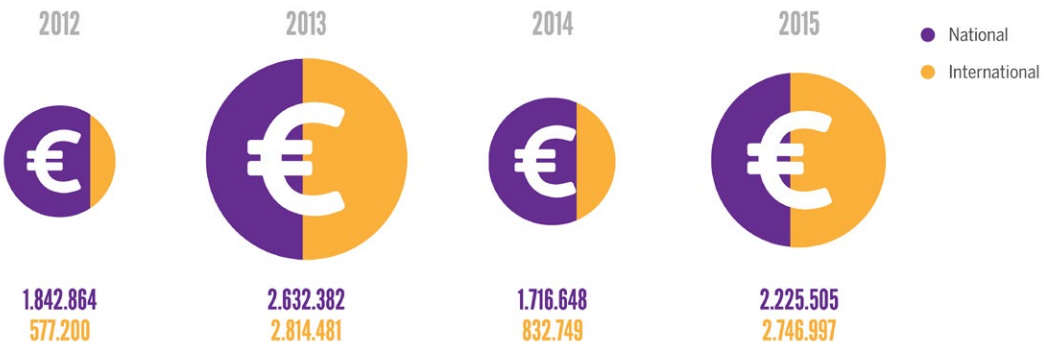


DISTRIBUTION OF 2015 ISI ARTICLES ACORDING TO THEIR QUARTILE



DISTRIBUTION OF ANNUAL COMPETITIVE FUNDS OF ONGOING PROJECTS IN 2015 ACORDING TO THE ORIGIN OF FUNDS (FELLOWSHIPS NOT INCLUDED)

NEW COMPETITIVE FUNDS RAISED (IN M€) CLASSIFIED BY SOURCE

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