ANNUAL REPORT

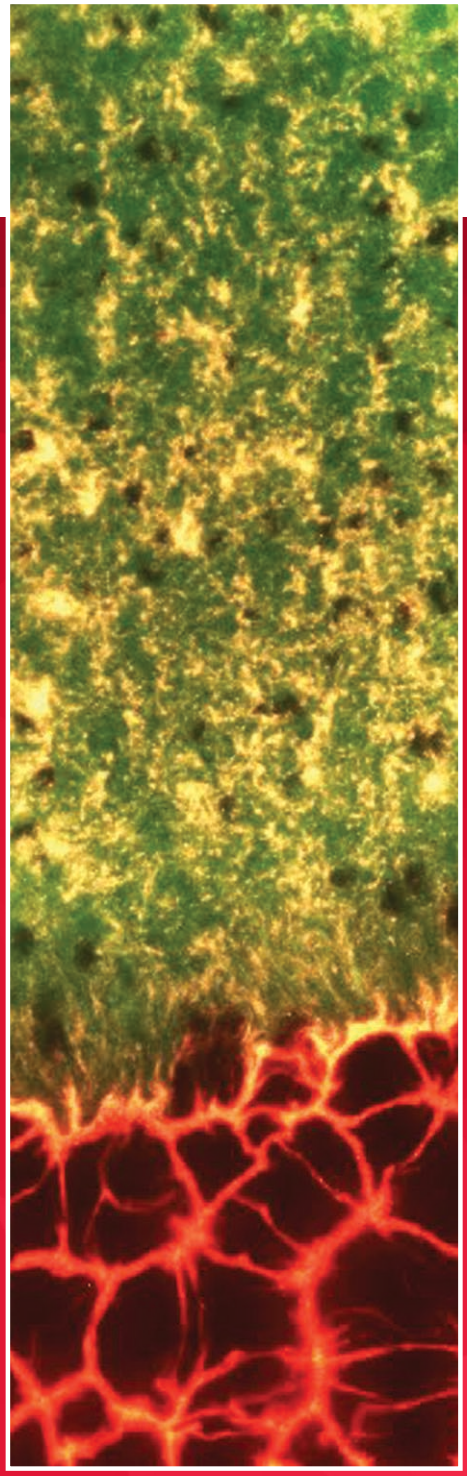
2014

INSTITUT de BIOLOGIA EVOLUTIVA

CSIC UPF

ANNUAL REPORT

2014



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prbb Barcelona Biomedical Research Park

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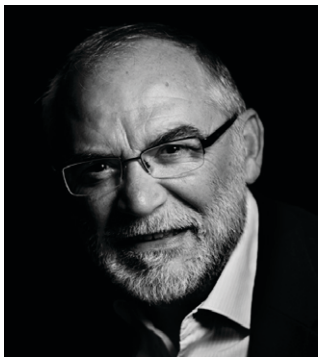
FOREWORD

By Xavier Bellés, Director of the IBE



The samples were incubated at ambient temperature in a remote border customs office for five months.

Record from an anonymous graduate student notebook (*#overyhonestmethods*)

A number of significant events punctuate the activities of the IBE in 2015, but in this occasion I will highlight two of them that are not strictly scientific achievements. The first one is the adherence of our institute to the new edition of the Code of Good Scientific Practice of the Barcelona Biomedical Research Park (PRBB). The directors of the PRBB centres, including that of the IBE, publicly signed the formal adherence to this Code in Barcelona on October 15, 2014. The Code represents a set of recommendations and commitments governing scientific activities. The aim is to create an environment conducive to high-quality research and prevent problems from arising in relation to the integrity of scientists in their work.

The general public, who, by the way, pays for publicly-funded research and is ultimately affected by its outcomes, entrusts us with the responsibility for undertaking high quality scientific research. But besides this responsibility, the public expects as well that this research is conducted with honesty and integrity. In order to do so, professional and personal values of scientists should also agree with these premises. The IBE is in full agreement with these principles, which care not only about serious misconducts, but also about "minor" aspects, like recording the results accurately in laboratory notebooks of the graduate students or the honest description of the results (that is, exactly as they were) in internal reports and public papers. It is fundamental that the students that we train internalize these concepts and the sense of social responsibility, in addition to the tools to do an excellent research along their careers.

The second significant event was the signature of an agreement of cooperation between the IBE and CERCA, which took place on June 19, 2014. CERCA was founded by the Government of Catalonia in 2010 as a service for supervising, supporting and facilitating the activities of the Catalan research centres in the CERCA system. The model for these centres is characterized by

fluid and self-governed management structures, the attraction of talent, and efficiency in obtaining competitive funding founded on scientific activity of the highest degree. The agreement establishes the collaboration between the two institutions to develop activities in research, development, innovation and science dissemination. Although our Institute fulfils the standards of governance and scientific organization that characterize CERCA institutes, the IBE cannot formally belong to this Institution because particular administrative and legal constraints. However, the IBE, besides a clear and internally fostered vocation for internationalization, which is consubstantial with doing good science, aims also at being well integrated into the Catalan system of research, not only to take advantage of collaborations and synergies with the physically closest institutions and colleagues, but also to contribute to promote social good and prevent or mitigate social harms through research in our Country.

In relation with the integration of the IBE in the Catalan system of research, there are also good news about the output of the last funding call, in 2014, of the Government program of Consolidated Research Groups. For the first time we proposed that our five Scientific Programs, on which the scientific organization of the IBE is based, were considered as five respective Consolidated Research groups. Our proposal was submitted as so, and was successful. Thus, the five IBE Scientific Programs are now considered as formal Consolidated Research Groups, and financed accordingly, by the Government of Catalonia.

One of the greatest news of 2014 was that Iñaki Ruiz-Trillo signed the agreement of his Consolidator Grant with the European Research Council (ERC), for the project entitled "Unravelling the unicellular prehistory of metazoans with functional analyses and single-cell genomics". The grant is worth almost two million euros for a 5-year project, starting 2014. Ruiz-Trillo leads the Multicellgenome lab at IBE and is one of the 20 researchers awarded with this grant in Spain and of the 312 selected throughout Europe. Also in 2014, Tomàs Marquès and Javier Prado were among the eight final candidates to the "IV Premi Vanguardia de la Ciència" award. The competition was organized by the Godó Group and the Catalunya-La Pedrera Foundation to recognise research excellence and achievements carried out in Spain. In the end, Tomas and Javier were not the winners, who were decided by a Scientific Assessment Committee and public polling, but it is already an honour for these IBE researchers to be among the nominees.

Financial support from grants and projects followed the usual oscillations determined by the schedules of the national and international calls. This year, in contrast with 2013, has relied mostly on Spanish rather than international funds. As far as scientific production is concerned, the number of publications of IBE researchers has substantially increased with respect to that of 2013, but, much better, quality has also increased in parallel. Taking as a reference the impact factor of the journals where we publish our papers (it is not the most suitable, I know, but it serves as a practical and most used reference), it has constantly increased since the foundation of the IBE in 2008. In 2014 the average impact factor has been 6.04, which approaches the highest standards of our most praised neighbouring research centres. Let us to continue in this direction.

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 18 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 2013:

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 5 people and covers at a micro scale level all basic institute running processes (accounting, human resources, purchasing, logistics and safety, and support to projects).

From left to right:
Emiliano González, Anna Pérez-Lezaun, Rita Arias, Judit Sainz, Blanca Álvarez

group members

General Manager:

Anna Pérez-Lezaun (UPF)

Vice Manager and Accountant:

Rita Arias (CSIC)

Administrative Support:

Emiliano González (CSIC)

Blanca Álvarez (CSIC)

Judit Sainz (UPF)

Experimental Techniques Unit

This unit coordinates the maintenance and use of the insect colonies and of the specialized technical instrumentation and facilities mainly related to the activities of those groups belonging to the Functional Genomics and Evolution program. Right now, it relies on a staff technician from the CSIC. 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.

Technical support:
Cristina Olivella, Technical staff (CSIC)

Program Research Assistants

Apart from the mentioned formal units, there are some long-term laboratory technicians that give key scientific support to different IBE programs:

From left to right:
Mònica Vallés, Cristina Olivella

Mònica Vallés, Technical staff (UPF), Supporting the Population Genetics Program and the Comparative and Computational Genetics Program
Eva García-Ramallo, UPF Contract, Supporting the Complex Systems Program

Personnel

At the end of 2014, the IBE had 123 members (research visitors not included; Table 1) with a ratio of men to women around 1.5, and an internationalization level of close to 25% of foreign members (in postdoctoral researchers this percentage increases up to 45 %).

Table 1. IBE personnel categories and gender distribution. December 2014.

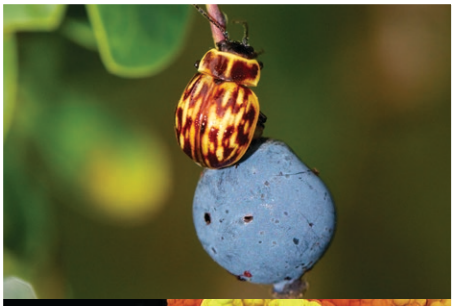
		2014		
		Males	Females	Totals
PIs	Faculty and long term senior researchers*	18	5	23
Postdoctorals	Postdoctoral researchers	19	5	24
PhD Students	Predoctoral researchers	26	22	48
Support Staff	Support personnel (Lab techn., bioinformaticians,)	10	13	23
Administration	Administrative staff	1	4	5
TOTAL		74	49	123

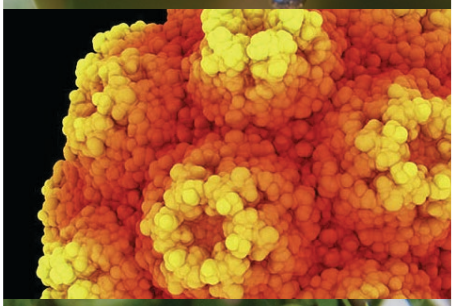
* ICREA researchers

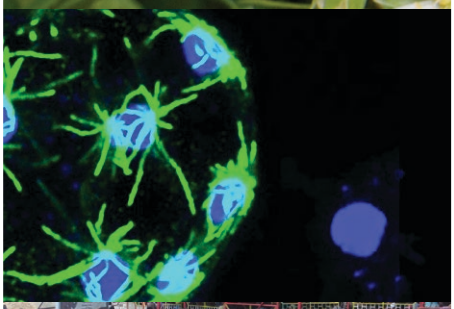
Localisation

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:
Lucas Kaminski, Gerard Talavera, Marga Marín, Roger Vila, Raluca Vodă, Vlad Dincă, Leonardo Dapporto

group members

Roger Vila, *Group Leader*
Tenured Scientist, CSIC

Gerard Talavera, Postdoctoral Researcher, Marie Curie Fellowship
Lucas Kaminski, Postdoctoral Researcher, CAPES Fellowship
Vlad Dincă, Postdoctoral Researcher, Marie Curie Fellowship
Leonardo Dapporto, Visiting Postdoctoral Researcher, Santander Research Scholarship
Raluca Vodă, PhD Student, FPU Scholarship, MEC
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 chromosomal evolution, the limits between species, and the link between phylogeography and ecology. When and following what route did a group of tiny butterflies colonize the New World, how did parasitism evolve from a friendly association between species, or if a given population constitutes a new species worth protecting 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 the DNA barcoding of Romania (which has been the first country with all butterfly species barcoded), 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 at large scale, and to develop tools based on barcoding technology in order to characterize diversity and phylogeography.

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., nuclear and mitochondrial markers, geometric and linear morphometry, analysis of karyotype, and ecological niche modelling) to deeply analyse each case, and to shed light on the origin and status of highly diverged taxa.

Fig. 1: *Thanks to a National Geographic Society Exploration Grant, Gerard Talavera and Roger Vila have been in multiple African countries, including Ethiopia, Chad, Benin and Senegal, in search of the migratory butterflies* Vanessa cardui *that disappear at the end of summer from Europe to an unknown destination.*

Photo: *Gerard Talavera*

Fig. 2: *The relationship between* Aricoris *riodinid butterflies and ants is a new line of research in our lab developed by Lucas Kaminski. In the picture,* Aricoris notialis *meets an ant in Rio Grande do Sul, Brasil.*
Photo: *Lucas Kaminski*

3. Ecological factors determining butterfly biogeography

We aim at unravelling 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. This year we started a project about 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 focusing our studies on understanding the origin and evolutionary consequences of karyotype instability in *Polyommatus* and *Leptidea*.

Fig. 3: *The Balkans have been the main target to complete the sampling for the European butterfly DNA barcoding project funded by the EU. Vlad Dincă, Raluca Vodă and our collaborator Sylvain Cuvelier, extensively explored Greece, Serbia, Bulgaria, Macedonia and Romania.* Tarucus balkanicus *is a beautiful and emblematic species of this region.*

Photo: *Raluca Vodă*

Publications 2014

ISI Articles

Cavalleri, A., and Kaminski, L.A. 2014. Two new ectoparasitic species of Aulacothrips Hood, 1952 (Thysanoptera: Heterothripidae) associated with ant-tended treehoppers (Hemiptera). *Systematic Parasitology* 89: 271-278.

Dapporto, L., Fattorini, S., Vodă, R., Dincă, V., and Vila, R. 2014. Biogeography of western Mediterranean butterflies: combining turnover and nestedness components of faunal dissimilarity. *Journal of Biogeography* 41: 1639-1650.

Dapporto, L., Vodă, R., Dincă, V., and Vila, R. 2014. Comparing population patterns for genetic and morphological markers with uneven sample sizes. An example for the butterfly *Maniola jurtina*. *Methods in Ecology and Evolution* 5: 834-843.

Hernández-Roldán, J.L., Bofill, R., Dapporto, L., Munguira, M.L., and Vila, R. 2014. Morphological and chemical analysis of male scent organs in the butterfly genus *Pyrgus* (Lepidoptera: Hesperiidae). *Organisms Diversity and Evolution* 14: 269-278.

Marín, M.A., Álvarez, C.F., Giraldo, C.E., Pyrcz, T., Uribe, S.I., and Vila, R. 2014. Mariposas en un bosque de niebla andino periurbano en el valle de Aburrá, Colombia. *Revista Mexicana de Biodiversidad* 85: 200-208.

Non ISI Publications

Monasterio León, Y., Vicente Arranz, J.C., Moreno Iriondo, O., Escobés Jiménez, R., Parra Arjona, B., Dincă, V., and Vila R. 2014. Tres nuevas especies de mariposas diurnas (Lepidoptera, Papilionoidea) para la comunidad autónoma de La Rioja y confirmación de la presencia de *Heteropterus morpheus* (Hesperiidae). *Zubía* 32: 73-83.

Book Chapters

Vila, R. 2014. *Lepidopterans. Butterflies and Moths*. In: Vargas, P. and Zardoya, R. (Eds.) *The tree of life: evolution and classification of living organisms*, Sunderland, Massachusetts, U.S.A., Sinauer Associates, Inc. Publishers.

Fig. 4: *Gerard detected a southwards migration of* Vanessa cardui *butterflies in Chad. The males of this species gather at hilltops in the afternoon, like the one in the picture.*

Photo: *Albert Marsiñach*

Fig. 5: *In Romania, home of Vlad and Raluca, still exist a high number of well-preserved habitats which host species of high conservation value, including many species of butterflies. Here, Raluca is photographing a* Phengaris alcon *in a meadow from SW Romania.*

Photo: *Vlad Dincă*

Funded Projects

- **Project Title:** Dynamics of Mediterranean butterflies in a phylogeographic framework: mapping genetic diversity across time and space (DynaGen)
  Financed by: Spanish 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

Fig. 6: Apatura metis *is a species with restricted distribution and local populations in Europe. The adults are shy, usually resting high in the canopy of their host plant* Salix sp. *This courageous male, photographed in Northern Greece, came down to appease its thirst.*

Photo: *Raluca Vodă*

- **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
  Coordinator: Roger Vila. Research Fellow: Vlad Dincă

- **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: 2014-2017
  Coordinator: 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

Fig. 7: Hypolimnas misippus, *a spectacular species photographed in Benin in November that exemplifies the high biodiversity of this African country.*
Photo: *Roger Vila*

- **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: Suport als Grups de Recerca de Catalunya, Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014-2016
  PI: Salvador Carranza

group HERBIVORE BEETLE EVOLUTION

From left to right:
Nguyen Thi Dhin, Helena Vizán, Anabela Cardoso, Gissela De la Cadena, Jesús Gómez-Zurita

group members

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

Gissela De la Cadena, PhD Student, SENESCYT Scholarship
Helena Vizán, PhD Student, MICINN Scholarship
Nguyen Thi Dinh, PhD Student, CSIC Scholarship (International Cooperation)
Anabela Cardoso, Lab manager and PhD Student, MICINN Contract

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 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. Hybridization and the evolution of unisexuality
2. Evolution of male-specific genes in thelytokous species
3. Origin and diversification of New Caledonian leaf beetles
4. Systematics and evolution of American Chrysomelinae
5. Characterization of insect-plant associations in tropical dry forests
6. DNA-based species delimitation

Fig. 1: Strichosa eburata *Blanchard resting on a fruit of its host-plant* Berberis microphylla *G. Forst. in the reserve of Huinay (Los Lagos, Chile). This spiny plant, the box-leaved barberry (or* calafate*, in Spanish), is the emblem of Patagonia, and it is believed that one who eats these purple fruits will return to this place. This would provide a poetic if unscientific explanation for the distribution of this species of beetle, endemic to southern Chile and Argentina.*

Photo: *Roger Vila*

Fig. 2: *A couple of a male (on top) and a female* Calligrapha philadelphica *(L.) contributing to the perpetuation of the species. This conventional amorous behaviour is nonetheless one of two reproductive alternatives in these beetles. Other species of* Calligrapha *in North America have given up males and the energy expenditure related to sex, leaving the fate of the species in the reproductive potential of parthenogenetic females alone.*

Photo: *Tinguaro Montelongo*

Publications 2014

ISI Articles

Andújar, C., Arribas, P., Ruíz, C., Serrano, J., and Gómez-Zurita, J. 2014. Integration of conflict into Integrative Taxonomy: Fitting hybridization in the delimitation of species in *Mesocarabus* (Coleoptera: Carabidae). *Molecular Ecology* 23: 4344-4361.

Andújar, C., Soria-Carrasco, V., Serrano, J., and Gómez-Zurita, J. 2014. Congruence test of molecular clock calibration hypotheses based on Bayes factor comparisons. *Methods in Ecology and Evolution* 5: 226-242.

Chaboo, C.S., Frieiro-Costa, F.A., Gómez-Zurita, J., and Westerduijn, R. 2014. Origins and diversification of subsociality in leaf beetles (Coleoptera: Chrysomelidae: Cassidinae, Chrysomelinae). *Journal of Natural History* 48: 2325-2367.

Gómez-Zurita, J., and Cardoso, A. 2014. Systematics of the New Caledonian endemic genus *Taophila* Heller (Coleoptera: Chrysomelidae, Eumolpinae) combining morphological, molecular and ecological data, with description of two new species. *Systematic Entomology* 39: 111-126.

Montelongo, T., and Gómez-Zurita, J. 2014. Multilocus molecular systematics and evolution in time and space of *Calligrapha* (Coleoptera: Chrysomelidae, Chrysomelinae). *Zoologica Scripta* 43: 605-628.

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
  Years: 2012-2014
  PI: Jesús Gómez-Zurita

- **Project Title:** El código de barras genético como aproximación a la biodiversidad de insectos de Huinay
  Financed by: ENDESA / CSIC.
  Years: 2014
  PI: Roger Vila

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

Fig. 3: *Carefully checking riverine growth of alder (*Alnus incana *var.) and dogwood (*Cornus *sp.) in Mount Whiteface (New York, US). These plants and several others that typically grow in humid places host a large number of species of* Calligrapha *in North America. Entomology and botany usually go hand in hand.*

Photo: *Tinguaro Montelongo*

group PHYLOGENY AND PHYLOGEOGRAPHY OF MAMMALS

Top, from left to right:
Karla García, José Castresana

Bottom, from left to right:
Marina Querejeta, Lídia Escoda

group members

José Castresana, *Group Leader*
Research Scientist, CSIC

Marina Querejeta, PhD Student, FPI Fellowship, MINECO
Lídia Escoda Assens, Master Student, Universitat de Barcelona
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. Using multiple markers as well as next-generation sequencing techniques, we are studying the phylogeographic patterns and the population history of several species of small mammals, some of them of great conservation importance. We are also analyzing the speciation process in different groups of closely related lineages using multilocus species tree approaches. Finally, since phylogenies are one of the main tools of our work, we are always trying to improve phylogenetic analyses by introducing new methodologies and programs.

Research Lines

1. Phylogeny and speciation of mammals

The reconstruction of species trees of closely related species based on multiple genomic markers can help to estimate accurate speciation times, to study patterns of genetic diversity and gene flow, to delimit species and, in general, to 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 generate a large numbers of genomic markers. We are sequencing these markers in several groups of small mammals such as water shrews of the genus *Neomys*, shrews of the genus *Sorex*, and Mediterranean voles of the genus *Microtus*. To obtain material for these studies we are making extensive use of noninvasive samples such as skulls obtained from owl pellets.

2. Conservation genomics of the Pyrenean desman (*Galemys pyrenaicus*)

The Pyrenean desman 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 genomics of this unique species using mitochondrial and nuclear data as well as next-generation sequencing techniques. Much of the material that we use for genetic studies comes from the droppings that desmans deposit on emerged rocks of the rivers. To get additional samples and to carry out this research we are collaborating with scientists from different institutions. 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 analyses. 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. One of the aspects in which we have recently been working is related to the methodological issues that arise in the analysis of diversification patterns extracted from phylogenetic trees. Furthermore, we are interested in methodologies at the interphase between phylogenetics and coalescence, in the reconstruction of species trees, and in the estimation of accurate speciation times. The software that we develop is made freely available online.

Publications 2014

ISI Articles

Rodríguez-Prieto, A., Igea, J., and Castresana, J. 2014. Development of rapidly evolving intron markers to estimate multilocus species trees of rodents. *PLOS ONE* 9, e96032.

Book/Book Chapters

Castresana, J. 2014. Deuterostomes: the ancestry of the vertebrates. In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates, Sunderland, MA, pp. 440-447.

Funded Projects

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

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

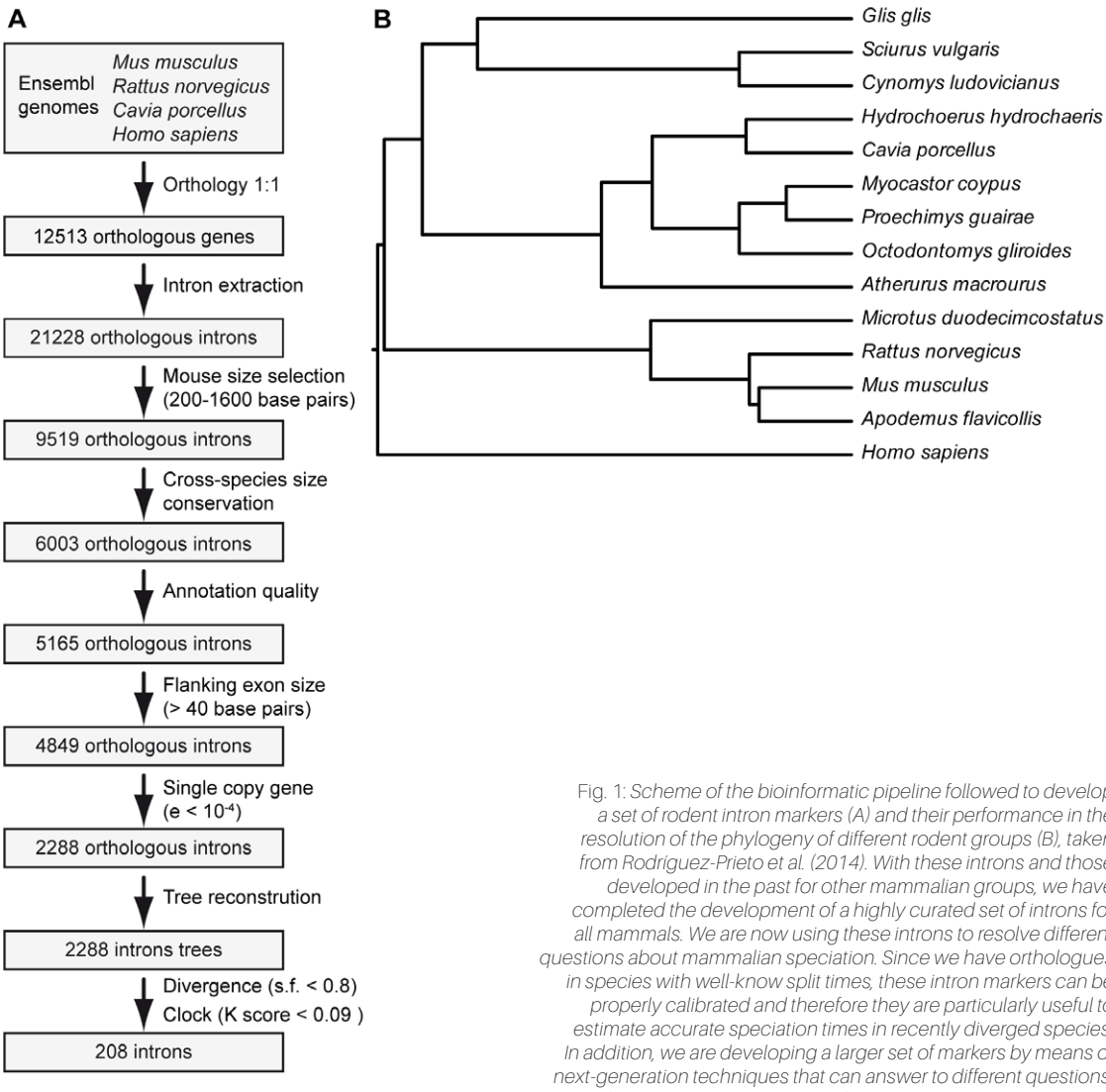


Fig. 1: *Scheme of the bioinformatic pipeline followed to develop a set of rodent intron markers (A) and their performance in the resolution of the phylogeny of different rodent groups (B), taken from Rodríguez-Prieto et al. (2014). With these introns and those developed in the past for other mammalian groups, we have completed the development of a highly curated set of introns for all mammals. We are now using these introns to resolve different questions about mammalian speciation. Since we have orthologues in species with well-know split times, these intron markers can be properly calibrated and therefore they are particularly useful to estimate accurate speciation times in recently diverged species. In addition, we are developing a larger set of markers by means of next-generation techniques that can answer to different questions. Therefore, these will be two sets of highly complementary markers for evolutionary studies of mammals.*

group

SYSTEMATICS, BIOGEOGRAPHY AND EVOLUTION OF REPTILES AND AMPHIBIANS

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

group members

Salvador Carranza, *Group Leader*
Tenured Scientist, CSIC

Pedro Tarroso, Postdoctoral Researcher, FCT Scholarship, Portugal
Raquel Vasconcelos, Postdoctoral Researcher, FCT Scholarship, Portugal
Duarte Gonçalves, PhD Student co-supervised with Dr. José Carlos Brito, CIBIO, Portugal, FCT Scholarship, Portugal
Emilio Valbuena Ureña, PhD Student, Teaching Assistant UAB, Barcelona
Joana Mendes, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Joan Garcia-Porta, PhD Student, JAEPRE-CSIC Fellowship
João Campos, PhD Student co-supervised with Dr. José Carlos Brito, CIBIO, Portugal, FCT Scholarship, Portugal
João Maia, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Luis Machado, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Marc Simó, PhD Student, FPI Scholarship, MEC
Margarita Metallinou, PhD Student, FPU Scholarship, MEC
Philip de Pous, PhD Student co-supervised with Delfi Sanuy, UDL, FI Scholarship
Santiago Montero, MSc Student, Master in Biodiversity, University of Barcelona
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 main research sublines focus mainly on the faunas of the Mediterranean Basin and Arabia, including some oceanic and continental island, as for instance the Canary and the Cape Verde islands in the Atlantic Ocean and, since 2010, the unique archipelago of Socotra in the Indian Ocean.

Fig. 1: Pristurus guichardi *from Socotra Island, Yemen.*

Photo: *Fabio Pupin*

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.

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 reptile islands faunas 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 2014

ISI Articles

Badiane, A., Garcia-Porta, J., Cervenka, J., Kratochvíl, L., Sindaco, R., Robinson, M.D., Morales, H., Mazuch, T., Price, T., Amat, F., Shobrak, M.Y., Wilms, T., Simó-Riudalbas, M., Ahmadzadeh, F., Papenfuss, T.J., Cluchier, A., Viglione, J., and Carranza, S. 2014. Phylogenetic relationships of Semaphore geckos (Squamata: Sphaerodactylidae: *Pristurus*) with an assessment of the taxonomy of *Pristurus rupestris*. *Zootaxa* 3835: 33-58.

Brito, J.C., Godinho, R., Martínez-Freirería, F., Pleguezuelos, J.M., Rebelo, H., Santos, X., Vale, C.G., Velo-Antón, G., Boratynski, Z., Carvalho, S.B., Ferreira, S., Gonçalves, D.V., Silva, T.L., Tarroso, P., Campos, J.C., Leite, J.V., Nogueira, J., Álvares, F., Sillero, N., Sow, A.S., Fahd, S., Crochet, P.A., and Carranza, S. 2014. Unravelling biodiversity, evolution and threats to conservation in the Sahara-Sahel. *Biological Reviews* 89: 215-231.

Maia, J.P., Harris, D.J., Carranza, S., and Gómez-Díaz, E. 2014. A comparison of multiple methods for estimating parasitemia of Hemogregarine Hemoparasites (Apicomplexa: Adeleorina) and its application for studying infection in natural populations. *PLOS ONE* 9: e95010.

Oromí, N., Amat, F., Sanuy, D., and Carranza, S. 2014. Life history trait differences between a lake and a stream-dwelling population of the Pyrenean brook newt (*Calotriton asper*). *Amphibia-Reptilia* 35: 53-62.

Tamar, K., Carranza, S., Sindaco, R., Moravec, J., and Meiri, S. 2014. Systematics and phylogeography of *Acanthodactylus shreiberi* and its relationships with *Acanthodactylus boskianus* (Reptilia: Squamata: Lacertidae). *Zoological Journal of the Linnean Society* 172: 720-739.

Valbuena-Ureña, E., Steinfartz, S., and Carranza, S. 2014. Characterization of microsatellite loci markers for the critically endangered Montseny brook newt (*Calotriton arnoldi*). *Conservation Genetics Resources* 6: 263-265.

Vasconcelos, R., and Carranza, S. 2014. Systematics and biogeography of *Hemidactylus homoeolepis* Blanford, 1881 (Squamata: Gekkonidae), with the description of a new species from Arabia. *Zootaxa* 3835: 501-527.

Vences, M., de Pous, P., Nicolas, V., Díaz-Rodríguez, J., Donaire, D., Hugemann, K., Hauswaldt, J.S., Amat, F., Barnestein, J.A.M., Bogaerts, S., Bouazza, A., Carranza, S., Galán, P., González de la Vega, J.P., Joger, U., Lansari, A., El Mouden, E.H., Ohler, A., Sanuy, D., Slimani, T., and Tejedo, M. 2014. New insights on phylogeography and distribution of painted frogs (*Discoglossus*) in northern Africa and the Iberian Peninsula. *Amphibia-Reptilia* 35: 305-320.

Vences, M., Sanchez, E., Hauswaldt, J.S., Eikelman, D., Rodríguez, A., Carranza, S., Donaire, D., Gehara, M., Helfer, V., Lötters, S., Werner, P., Schultz, S., and Steinfartz, S. 2014. Nuclear and mitochondrial multilocus phylogeny and survey of alkaloid content in true salamanders of the genus *Salamandra* (Salamandridae). *Molecular Phylogenetics and Evolution* 73: 208-216.

Other Publications

Amat, F., Carranza, S., Valbuena-Ureña, E., and Carbonell, F. 2014. Saving the Montseny Brook Newt (*Calotriton arnoldi*) from extinction: an assessment of eight years of research and conservation. *FrogLog* 22, n 111: 55-57.

Amat, F., Oromí, N., Sanuy, D., Palau, A., and Carranza, S. 2014. La neotenia del tritón pirenaico en lagos de alta montaña *Quercus* 344: 26-33.

Carranza, S. 2014. Chapter 44: Sauropsids: Reptilian relationships, including Aves. In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates, Sunderland, MA.

Martínez-Silvestre, A., Amat, F., and Carranza, S. 2014. Natural incidence of body abnormalities in the Montseny newt, *Calotriton arnoldi* Carranza and Amat, 2005. *Herpetology Notes* 7: 277-279.

Metallinou, M., Amat, F., and Carranza, S. 2014. Amantes del desierto. *Investigación y Ciencia* 455: 44-45.

Metallinou, M., Vasconcelos, R., Smid, J., Sindaco, R., and Carranza, S. 2014. Filling in the gap: two new records and an updated distribution map for the Gulf Sand gecko *Pseudoceramodactylus khobarensis* Haas, 1957. *Biodiversity Data Journal* 2: e4011.

Fig. 3: Haemodracon trachyrhinus *endemic to Socotra Island, Yemen.*
Photo: *Fabio Pupin*

Fig. 4: Pristurus sokotranus*, Socotra Island, Yemen.*
Photo: *Raquel Vasconcelos*

Fig. 5: *Panoramic view of a mountain crossing in the Eastern Hajars of Oman.*
Photo: *Salvador Carranza*

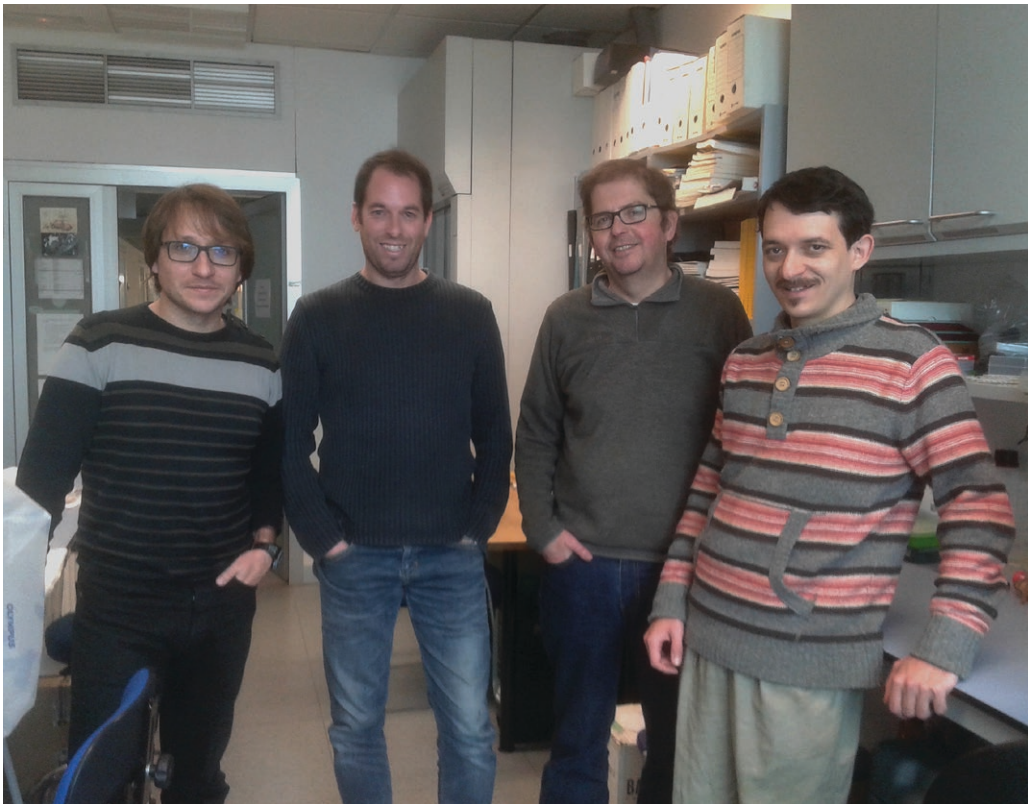
Funded Projects

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Suport als Grups de Recerca de Catalunya, 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 Economia y Competitividad MINECO (CGL2012-36970)
  Years: 2013-2015
  PI: Salvador Carranza

- **Project Title:** Case study on the Dragon Blood Tree's gecko (*Hemidactylus dracaenacolus*)
  Financed by: Mohamed bin Zayed Species Conservation Fund (Ref: 13055714)
  Years: 2013-2014
  PI: Raquel Vasconcelos
  More info: www.speciesconservation.org/case-studies-projects/dragon-blood-trees-gecko/5714

group WATER AND CAVE BEETLE EVOLUTION



From left to right:
David Sánchez-Fernandez, David García, Ignacio Ribera, Andrey Rudoy

group members

Ignacio Ribera, *Group Leader*
Research Scientist, CSIC

David Sánchez-Fernández, Postdoctoral Researcher, Juan de la Cierva Program
Andrey Rudoy, PhD Student, JAE Scholarship, CSIC
David García Vázquez, PhD Student, MICINN Scholarship

Research Outline

We study evolutionary processes using different groups of beetles, the most diverse group of animals. Their 250 MY of evolutionary history and a vast ecological and morphological variation allow to use them to undertake virtually every problem in evolutionary biology, from global macroecological and macroevolutionary patterns to phylogenetics and biogeography down to population genetics and physiology. We use different groups of water and cave beetles to address some of these questions, centred in 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

Thermal tolerance and Pleistocene range expansions

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

Origin of widespread species of European lotic water beetles

A particularly intriguing case is that of species under some constraint that reduces their dispersal abilities, but nonetheless manage to expand their geographic ranges to continental scales. This is the case of some species of beetles typical of running waters that are widespread in central and northern Europe. We investigate the origin of these species, trying to figure out how they came to have their current distributions.

Fig. 1: *The Age of Discovery may be over, but there are still blank areas in our maps of knowledge. One of these no more - the Limnichidae of the Arabian peninsula, from which nothing was known until our description of five new species, in collaboration with Carles Hernando. In the image, part of their type material.*

Photo: *Ignacio Ribera*

Fig. 2: *Azerbaijan is another place with a very incomplete knowledge of its insect fauna, despite sitting in one of the most interesting places in Europe - the Caucasus. In this stream Andrey Rudoy (in the photo) collected the first known* Limnebius *for the country, the genus subject of his PhD.*

Photo: *Arnaud Faille*

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 extreme uniformity in external morphology with a magnificent repertoire of aedeagal extravaganza. Using a comparative phylogenetic and morphometric approach we aim to discern which are the selective forces shaping the evolution of male genitalia in this group of beetles.

Conservation of Iberian water beetles

Inland waters are one of the most endangered ecosystems in Europe, especially in the south - and one of the most diverse, with disproportionately high species richness in relation to the surface they occupy. Many of the freshwater habitats and their faunas are neglected and poorly known, a situation we try to reverse by increasing their knowledge and visibility. 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.

Evolution of the tolerance to salinity

The Iberian Peninsula is also very rich in an often ignored but extremely interesting system: hypersaline lagoons and streams. Life in water at concentrations many times that of seawater requires extreme physiological adaptations, which only few organisms managed to acquire - among them several lineages of beetles.
In a new project starting in 2014, also in collaboration with the Aquatic Ecology group of the University of Murcia, we study the evolution of these adaptations using phylogenies and experimental approaches in order to determine the mechanisms involved and how they were originated.

Publications 2014

ISI Articles

Arribas, P., Andújar, C., Abellán, P., Velasco, J., Millán, A., and Ribera, I. 2014. Tempo and mode of the multiple origins of salinity tolerance in a water beetle lineage. *Molecular Ecology* 23: 360-373.

Bruno, D., Belmar, O., Sánchez-Fernández, D., and Velasco, J. 2014. Environmental determinants of woody and herbaceous riparian vegetation patterns in a semi-arid mediterranean basin. *Hydrobiologia* 730: 45-57.

Bruno, D., Belmar, O., Sánchez-Fernández, D., Guareschi, S., Millán, A., and Velasco, J. 2014. Responses of Mediterranean aquatic and riparian communities to human pressures at different spatial scales. *Ecological Indicators* 45: 456-462.

Fig. 3: Troglocharinus elongatus, *a troglobitic species exclusive of the deep subterranean environment.*
Photo: *Alfonso Gonzalez Meseguer*

Cieslak, A., Fresneda, J., and Ribera, I. 2014. Developmental constraints in cave beetles. *Biology Letters* 10: 20140712.

Cieslak, A., Fresneda, J., and Ribera, I. 2014. Life history evolution and diversification in Leptodirini cave beetles. *Proceedings of the Royal Society of London. Series B* 281: 20132978.

Faille, A., Andújar, C., Fadrique, F., and Ribera, I. 2014. Late Miocene origin of an Ibero-Maghrebian clade of ground beetles with multiple colonisations of the subterranean environment. *Journal of Biogeography* 41: 1979-1990.

Hernando, C., and Ribera, I. 2014. The Limnichidae of the Arabian Peninsula and the Island of Socotra (Coleoptera). *Acta Entomologica Musei Nationalis Pragae* 54 (supp): 173-189.

Hidalgo-Galiana, A., Monge, M., Biron, D.G., Canals, F., Ribera, I., and Cieslak, A. 2014. Reproducibility and consistency of proteomic experiments on natural populations of a non-model aquatic insect species. *PLOS ONE* 9 (8): e104734.

Hidalgo-Galiana, A., Sánchez-Fernández, D., Bilton, D.T., Cieslak, A., and Ribera, I. 2014. Thermal niche evolution and geographic range expansion in a species complex of western Mediterranean diving beetles. *BMC Evolutionary Biology* 14: 187.

Mega, Y.S., and Sánchez-Fernández, D. 2014. A new species of *Desmopachria* Babington (Coleoptera: Dytiscidae) from Cuba with a prediction of its geographic distribution and notes on other Cuban species of the genus. *Zootaxa* 3753: 585-596.

Books / Book Chapters

Beutel, R.G., and Ribera, I. 2014. Chapter 29: Hexapods: Insects and their closely related groups. In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates, Sunderland, MA, pp. 338-351.

Ferreira Jr., N, Lanzellotti Sampaio, B.H., Fernandes, A.S., Clarkson, B., Braga, R.B., dos Passos, M.I.S., Santos, A.D. 2014. Chapter 21: Ordem Coleoptera. In: N. Hamada, J.L. Nessimian, R.B. Querino (Eds) Insetos aquáticos na Amazônia brasileira: taxonomia, biologia e ecologia. Manaus, Editora do INPA, pp. 349-375.

Millán, A., Sánchez-Fernández, D., Abellán, P., Picazo, F., Carbonell, J.A., Lobo, J.M., and Ribera, I. 2014. Atlas de los coleópteros acuáticos de España peninsular. Ministerio de Agricultura, Alimentación y Medio Ambiente. Madrid, 820 pp.

Ribera, I., and Beutel, R.G. 2014. Chapter 33: Coleopterans: Beetles. In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates, Sunderland, MA, pp. 408-418.

Other Publications

Hernando, C., and Ribera, I. 2014. Taxonomic revision of the genus *Caccothryptus* Sharp (Coleoptera: Limnchidae). *Koleopterologische Rundschau* 84: 281-304.

Ribera, I., Sánchez-Fernández, D., and Esteban, I. 2014. Los coleópteros acuáticos de Aragón. *Naturaleza Aragonesa* 31: 26-33.

Fig. 4: *River in the Chilean Patagonia, in the Fiordo Comau, next to the Huinay Biological Station. In 2014 three groups of the Animal Biodiversity and Evolution program conducted a survey to catalogue the local fauna.*

Photo: *Ignacio Ribera*

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: Suport als Grups de Recerca de Catalunya, Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014-2016
  PI: Salvador Carranza

- **Project Title:** El código de barras genético como aproximación a la biodiversidad de insectos de Huinay
  Financed by: CSIC - Fundación ENDESA - Fundación San Ignacio de Huinay
  Years: 2014
  PI: Roger Vila

Fig. 5: *Valeria Rizzo descending to the Avenc Esquerrà, in the Macizo del Garraf, to collect cave beetles of the genus Troglocharinus.*
Photo: *Michele Spada*

PROGRAM

COMPARATIVE AND COMPUTATIONAL GENOMICS

Research groups

Comparative Genomics
Tomàs Marquès, *Group Leader*

Evolutionary and Functional Genomics
Josefa Gonzalez, *Group Leader*

Subgroups
Evolutionary and Functional Genomics
Josefa González, *PI*

Drosophila Telomeres
Elena Casacuberta, *PI*

Evolutionary Genomics
Arcadi Navarro, *Group Leader*

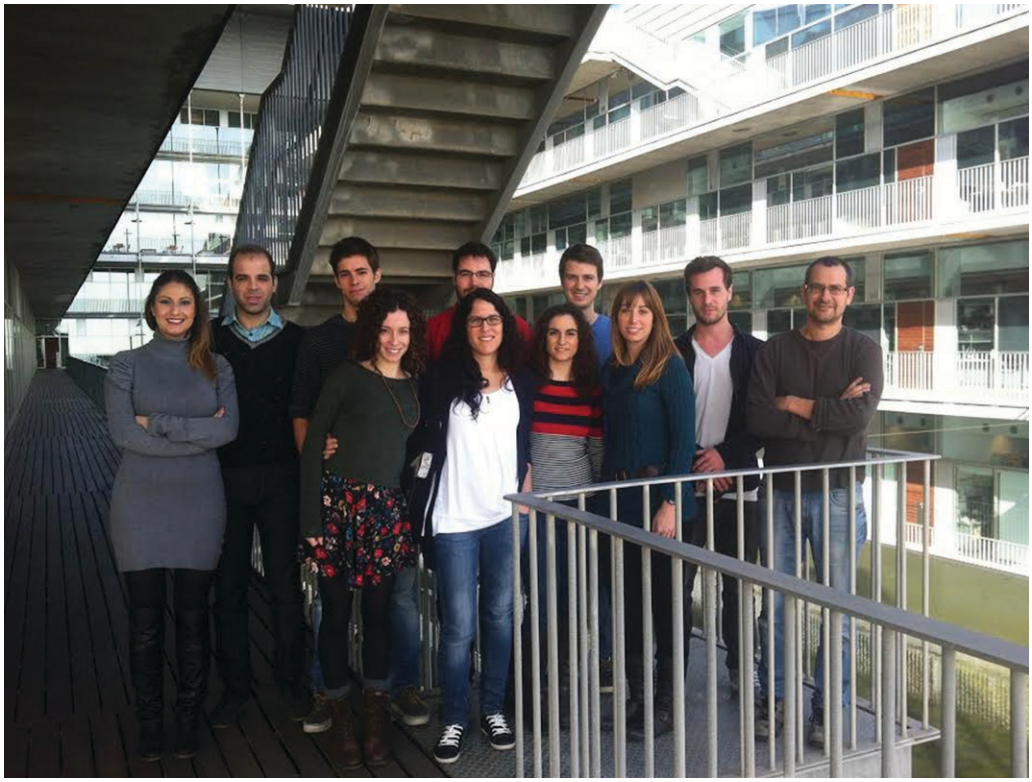
Paleogenomics
Carles Lalueza-Fox, *Group Leader*

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 top to right down:
Serena Tucci, Marcos Fernandez Callejo, Tiago de Loureiro, Irene Hernando, Javier Prado, Belén Lorente-Galdos, Marc de Manuel Montero, Raquel Garcia, Jessica Hernández, Lukas Kuderna, Tomàs Marquès-Bonet

group members

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

Belén Lorente-Galdos, Postdoctoral
Irene Hernando, PhD Student, FI Scholarship, Generalitat de Catalunya
Irene Lobon, PhD Student, (co-directed with Eduardo Soriano, IRB)
Jessica Hernádez, PhD Student, FPI Scholarship, MEC
Marc de Manuel, PhD Student, FI Scholarship, MEC
Raquel Garcia, PhD Student, FI Scholarship, Generalitat de Catalunya
Tiago Carvalho, PhD Student
Lukas Kuderna, Master Student

Research Outline

Our main line of research is centered in the discovery of the extent of all kinds of genome variation within different phenotypically 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. The 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

Despite international efforts to characterize thousands of human genomes to understand the extent of structural variants in the human species, primates (our closest relatives) have somehow been forgotten. Yet, they are the ideal set of species to study the evolution of these features from both mechanistic and adaptive points of view. Most genome projects include only one individual as a reference, but in order to understand the impact of structural variants in the evolution of every species we need to re-sequence multiple individuals of each species. We can only understand the origins of genomic variants and phenotypical differences among species if we can model variation within species and compare it to a proper perspective with the differences among species.

2. Epigenetics and transcriptomics of non-human primates

The recognition of post-genomic modifications with high biological impact has been a focus of research in model and non-model organisms in the last years. However, little has been done combining a three way analysis going from genomic variants, to gene expression and epigenetics in non-human primates. In the coming years I am planning to use different tissues from the same individual comparing human, chimps and rhesus macaque to explore the relationship of these three layers of complexity.

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, SNPs but structural variation, including variation in multicopy gene families, has not been fully characterized in canines.

Publications 2014

ISI Articles

Carbone, L., et al Gibbon Genome Consortium (including Belén Lorente-Galdos, Tomàs Marquès-Bonet). 2014. Gibbon genome and the fast karyotype evolution of small apes. *Nature* 513 (7517): 195-201.

Freedman, A.H., Gronau, I., Schweizer, R.M., Ortega-Del Vecchyo, D., Han, E., Silva, P.M., Galaverni, M., Fan, Z., Marx, P., Lorente-Galdos, B., Beale, H., Ramirez, O., Hormozdiari, F., Alkan, C., Vilà, C., Squire, K., Geffen, E., Kusak, J., Boyko, A.R., Parker, H.G., Lee, C., Tadigotla, V., Siepel, A., Bustamante, C.D., Harkins, T.T., Nelson, S.F., Ostrander, E.A., Marquès-Bonet, T., Wayne, R.K., Novembre, J. 2014. Genome Sequencing Highlights the Dynamic Early History of Dogs. *PLoS Genetics* 10 (1): e1004016.

Montague, M.J., Gang, L., Gandolfi, B., Khan, R., Aken, B.L., Searle, S.M.J., Minx, P., Hillier, L.W., Koboldt, D.C., Davis, B.W., Driscoll, C.A., Barr, C.S., Blackistone, K., Quilez, J., Lorente-Galdos, B., Marquès-Bonet, T., Alkan, C., Thomas, G.W.C., Hahn, M.W., Menotti-Raymond, M., O'Brien, S.J., Wilson, R.K., Lyons, L.A., Murphy, W.J., Warren, W.C. 2014. Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. *Proceedings of the National Academy of Sciences* 111 (48): 17230-17235.

Olalde, I., Allentoft, M.E., Sanchez-Quinto, F., Santpere, G., Chiang, C.W.K., DeGiorgio, M., Prado-Martinez, J., Rodriguez, J.A., Rasmussen, S., Quilez, J., Ramirez, O., Marigorta, U.M., Fernandez-Callejo, M., Prada, M.E., Encinas, J.M.V., Nielsen, R.,

Netea, M.G., Novembre, J., Sturm, R., Sabeti, P., Marquès-Bonet, T., Navarro, A., Willerslev, E., Lalueza-Fox, C. 2014. Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. *Nature* 507 (7491): 225-228.

Olalde, I., Sánchez-Quinto, F., Datta, D., Marigorta, U.M., Chiang, C.W.K., Rodríguez, J.A., Fernández-Callejo, M., González, I., Montfort, M., Matas-Lalueza, L., Civit, S., Luiselli, D., Charlier, P., Pettener, D., Ramírez, O., Navarro, A., Himmelbauer, H., Marquès-Bonet, T., and Lalueza-Fox, C. 2014. Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France. *Scientific Reports* 4: 4666.

Ramirez, O., Olalde, I., Berglund, J., Lorente-Galdos, B., Hernandez-Rodriguez, J., Quilez, J., Webster, M., Wayne, R., Lalueza-Fox, C., Vila, C., Marquès-Bonet, T. 2014. Analysis of structural diversity in wolf-like canids reveals post-domestication variants. *BMC Genomics* 15 (1): 465.

Schubert, M., Jònsson, H., Chang, D., Der Sarkissian, C., Ermini, L., Ginolhac, A., Albrechtsen, A., Dupanloup, I., Foucal, A., Petersen, B., Fumagalli, M., Raghavan, M., Seguin-Orlando, A., Korneliussen, T.S., Velazquez, A.M.V., Stenderup, J., Hoover, C.A., Rubin, C-J., Alfarhan, A.H., Alquraishi, S.A., Al-Rasheid, K.A.S., MacHugh, D.E., Kalbfleisch, T., MacLeod, J.N., Rubin, E.M., Sicheritz-Ponten, T.M, Andersson, L., Hofreiter, M., Marquès-Bonet, T., Gilbert, M.T.P., Nielsen, R., Excoffier, L., Willerslev, E., Shapiro, B., Orlando, L. 2014. Prehistoric genomes reveal the genetic foundation and cost of horse domestication. *Proceedings of the National Academy of Sciences* 111 (52): E5661-E5669.

Tamazian, G., Simonov, S., Dobrynin, P., Makunin, A., Logachev, A., Komissarov, A., Shevchenko, A., Brukhin, V., Cherkasov, N., Svitin1, A., Koepfli, K.P., Pontius, J., Driscoll, C.A., Blackistone, K., Barr, C., Goldman, D., Antunes, A., Quilez, J., Lorente-Galdos, B., Alkan, C., Marquès-Bonet, T., Menotti-Raymond, M., David, V.A., Narfström, K., and O'Brien, S.J. 2014. Annotated features of domestic cat – *Felis catus genome*. *Gigascience* 3: 13.

Venkatesh, B., Lee, A.P., Ravi, V., Maurya, A.K., Lian, M.M., Swann, J.B., Ohta, Y., Flajnik, M.F., Sutoh, Y., Kasahara, M., Hoon, S., Gangu, V., Roy, S.W., Irimia, M., Korzh, V., Kondrychyn, I., Lim, Z.W., Tay, B.H., Tohari, S., Kong, K.W., Ho, S., Lorente-Galdos, B., Quilez, J., Marquès-Bonet, T., Raney, B.J., Ingham, P.W., Tay, A., Hillier, L.W., Minx, P., Boehm, T., Wilson, R.K., Brenner, S., Warren, W.C. 2014. Elephant shark genome provides unique insights into gnathostome evolution. *Nature* 505 (7482): 174-179.

Watson, C.T., Marquès-Bonet, T., Sharp, A.J., Mefford, H.C. 2014. The Genetics of Microdeletion and Microduplication Syndromes: An Update. *Annual Review of Genomics and Human Genetics* 15 (1): 215-244.

Worley, K.C., Warren, W.C., Rogers, J., Locke, D., Muzny D.M., Mardis, E.R., Marquès-Bonet, T., Lorente-Galdos, B., et al The Marmoset Genome, SequencingAnalysis, Consortium. 2014. The common marmoset genome provides insight into primate biology and evolution. *Nature Genetics* 46 (8): 850-857.

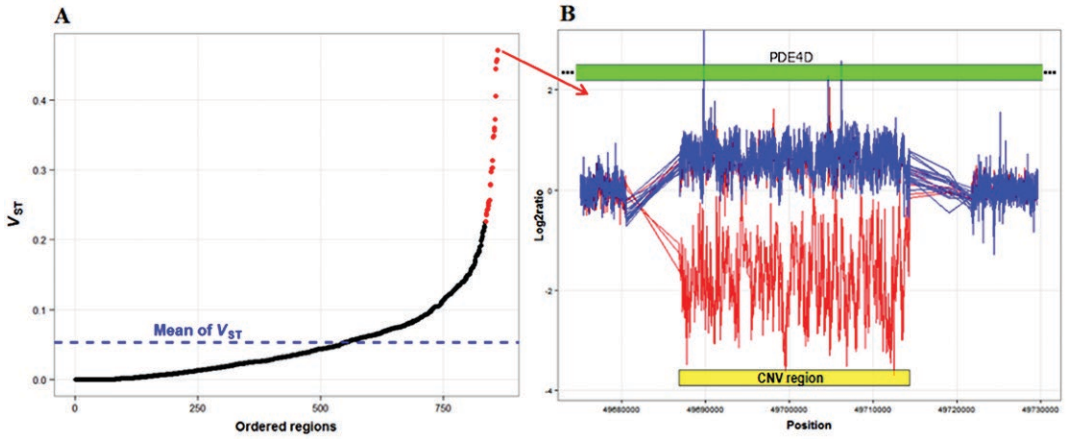


Fig. 1: *High copy number variation between modern dog breeds and wolves. PDEAD gene copy number is related to body weight.*

Image: *Ramirez et al. BMC Genomics 2014*

Funded Projects

- **Project Title:** Identification and characterization of primate structural variation and an assessment of intra-specific patterns of selection and copy-number variation
  Financed by: European Research Council
  Years: 2010-2014
  PI: Tomàs Marquès-Bonet

- **Project Title:** Characterization of Inversions and changes of gene expression in the great-ape evolution (BFU2011-28549)
  Financed by: MICINN (Spain)
  Years: 2011-2014
  PI: Tomàs Marquès-Bonet

group EVOLUTIONARY AND FUNCTIONAL GENOMICS

group members

Josefa González, *Group Leader*
Ramón y Cajal Researcher

Subgroup
Evolutionary and Functional Genomics

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

From left to right:
Elisenda López, Elena Casacuberta, Maite G. Barrón, Quirze Rovira, Lain Guio, Jon Frias, Josefa González, Hung Le Manh, Miriam Merenciano

Subgroup
Drosophila Telomeres

Elena Casacuberta, Tenured Scientist, CSIC

Elisenda López Panadès, PhD Student, UPF Fellowship

Research Outline

The Evolutionary and Functional Genomics group uses transposable elements as a tool to unravel genome function and evolution. The group contains two subgroups: "Evolutionary and Functional Genomics" lead by Josefa González and "Drosophila telomeres" lead by Elena Casacuberta.

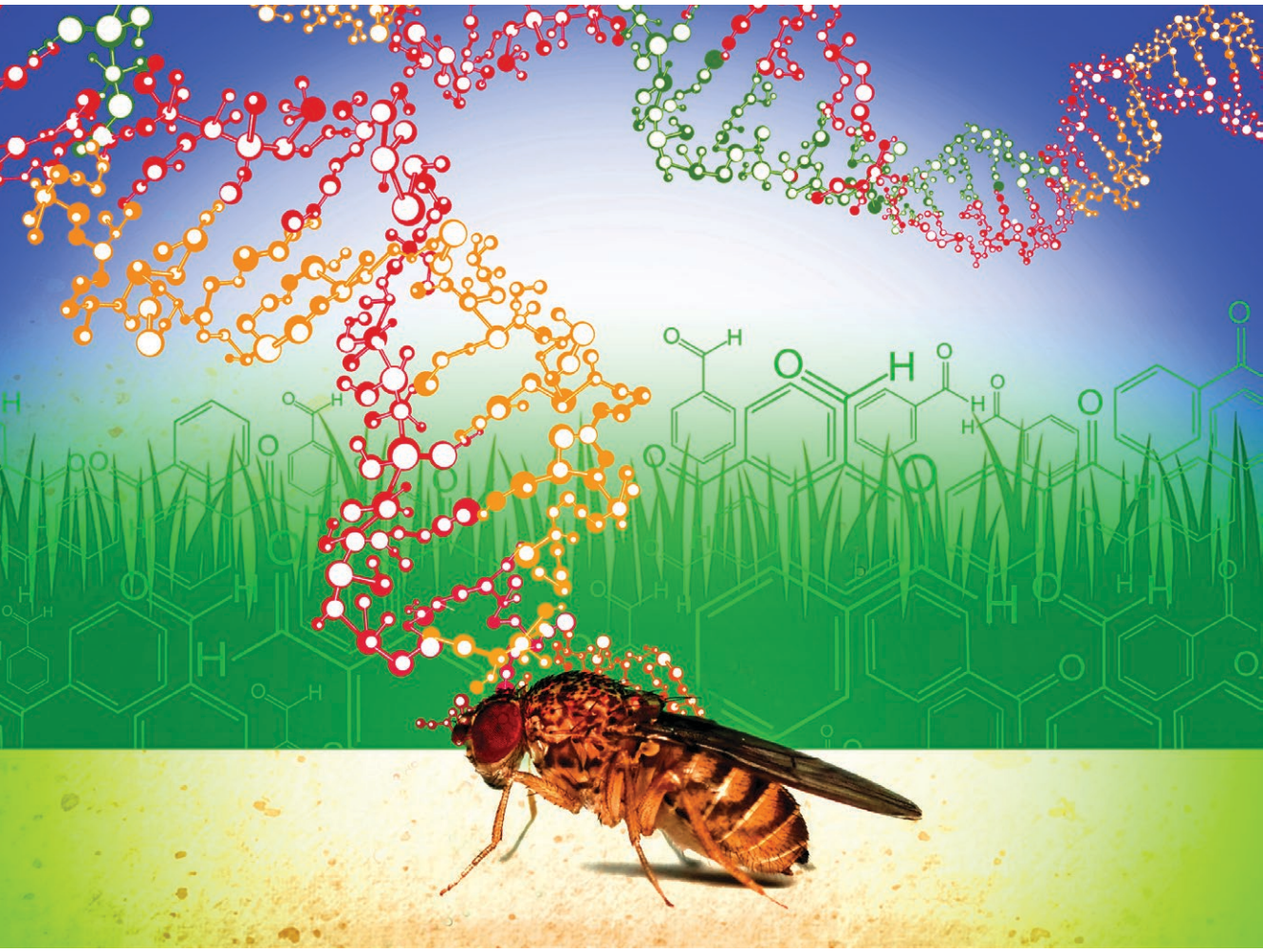
Research Lines

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*.

Fig. 1: *The genetic diversity present in natural populations of fruit flies enables them to adapt to the presence of toxic substances in the environment.*

Image: *Roberto Torres*



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 biology.

Subgroup: ***Drosophila*** Telomeres

1. Host and retrotransposon requirements for telomere elongation and stability in Drosophila

HeT-A, TART, and TAHRE must be integrated into the cellular pathways controlling telomere length and genome stability. Understanding the regulation of the telomeric transposons will shed light on both telomere length control as well as transposon regulation in *Drosophila*. We are currently focused on the regulation of the telomeric chromatin and the consequences for telomere stability. We are also isolating and identifying protein complexes using the telomeric proteins as bait in order to understand which cellular partners assist the telomeric proteins throughout their life cycle.

2. Telomere replication in the *Drosophila* Germ line

We have isolated some interacting partners of the telomere retrotrotransposons that are essential genes for the development of the *Drosophila* germ line and the oocytes. We are currently investigating the life cycle of the telomere retrotransposons in the different germ cells of the developing ovary in wild-type and mutant strains, in order to understand which interactions are necessary for telomere proteins to establish and replicate the telomeres in the germ line tissue.

3. Evolution of the telomere retrotransposons

The sequences of HeT-A and TART, although linked to an essential cellular role, are allowed to change at a fast rate. Studying the level of variability of the telomere retrotransposons is important to better understand their dynamics and the forces that are driving their evolution.

Publications 2014

ISI Articles

Ayala, D., Ullastres, A., and González, J. 2014. Adaptation through chromosomal inversions in Anopheles. *Frontiers in Genetics* 5: 129.

Barrón, M.G., Fiston-Lavier, A.-S., Petrov, D., and González, J. 2014. Population Genomics of Transposable Elements in Drosophila. *Annual Review Genetics* 48 (1): 561-581.

Guio, L., Barrón, M.G., and González, J. 2014. The transposable element Bari-Jheh mediates oxidative stress response in Drosophila. *Molecular Ecology* 23: 2020-2030.

Mateo, L., and González, J. 2014. *Pogo-like* transposases have been repeatedly domesticated into CENP-B related proteins. *Genome Biology and Evolution* 6 (8): 2008-2016.

Mateo, L., Ullastes, A., and González, J. 2014. A transposable element insertion confers xenobiotic resistance in Drosophila. *PLoS Genetics* 10 (8): e1004560.

Preprint Articles

Bergland, A.O., Tobler, R., González, J., Schmidt, P., and Petrov, D.A. 2014. Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in Drosophila melanogaster. bioRxiv. doi: http://dx.doi.org/10.1101/009084

Funded Projects

- **Project Title:** El proceso molecular y las consecuencias funcionales de la adaptación (BFU2011-24397)
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2012-2014
  PI: Josefa González

- **Project Title:** The molecular process and functional consequences of adaptation (PCIG09-GA-2011-293860)
  Financed by: European Commission
  Years: 2011-2014
  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, Josefa González

Outreach Projects

- **Project Title:** The Bio-Pro's Science Meeting: conoce a los protagonistas del mañana (FCT-14-8599)
  Financed by: Fundación Española para la Ciencia y la Tecnologia
  Years: 2014-2015
  PI: Josefa González

- **Project Title:** R(e)volución: acércate a las fronteras del conocimiento (FCT-13-6749)
  Financed by: Fundación Española para la Ciencia y la Tecnologia
  Years: 2013-2014
  PI: Josefa González

- **Project Title:** La conservació de la biodiversitat: el cas dels primats
  Financed by: Professors i Ciència. Fundació Catalunya-La Pedrera.
  Years: 2014
  PI: Josefa González

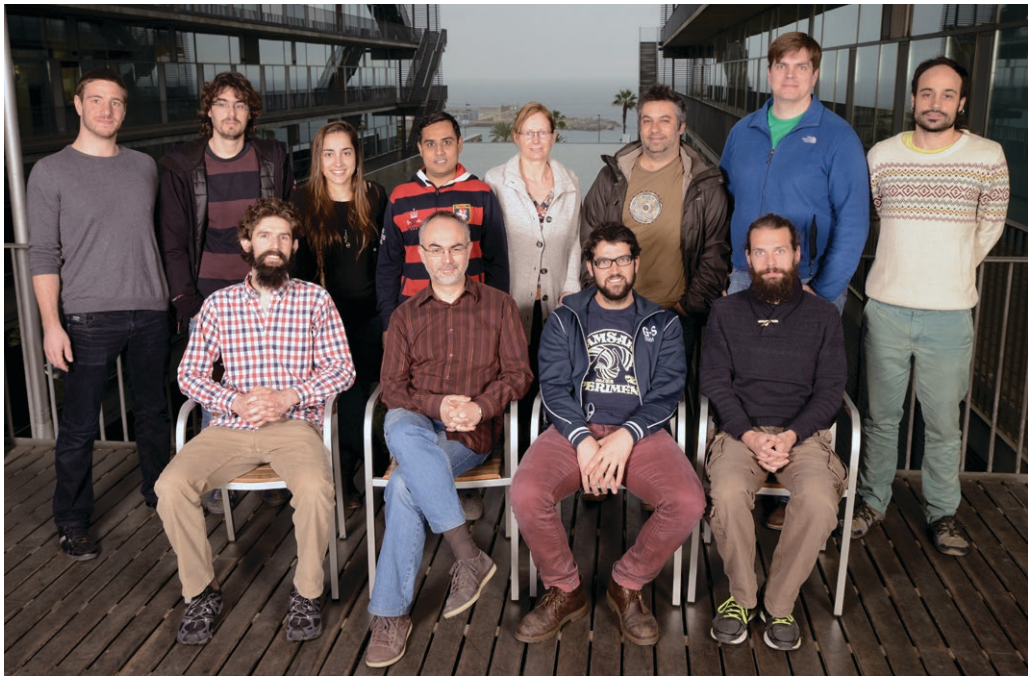
- **Project Title:** Genòmica Evolutiva: Mecanismes, causes i conseqüències de la diversitat genòmica actual de les poblacions humanes
  Financed by: Professors i Ciència. Fundació Catalunya-La Pedrera.
  Years: 2014
  PI: Josefa González

- **Project Title:** Com els organismes s'adapten a l'ambient
  Financed by: Joves i Ciència. Fundació Catalunya-La Pedrera.
  Years: 2014
  PI: Josefa González

- **Project Title:** La genètica posada en pràctica
  Financed by: Joves i Ciència. Fundació Catalunya-La Pedrera.
  Years: 2014
  PI: Elena Casacuberta

- **Project Title:** La setmana de la Ciència i la Tecnologia en el CSIC
  Financed by: CSIC
  Years: 2014
  PI: Elena Casacuberta

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 A. Hughes, Gerard Muntané Medina, Diego 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

Carlos Morcillo, Postdoctoral, Project Contract (INB-ISCIII)
David A. Hughes, Postdoctoral, Marie Curie Fellowship Contract (COFUND - FP7 UE)
Gabriel Santpere, Postdoctoral, Project Contract (RETICS-ISCIII)
Gerard Muntané, Postdoctoral, Project Contract (INB-ISCIII)
Rui Faria, Postdoctoral, FCT Fellowship
Diego Hartasánchez, PhD Student, JAE Contract (CSIC)
Juan Antonio Rodríguez-Pérez, PhD Student, UPF PhD Grant
Marco Telford, PhD Student, Project Contract (INB-ISCIII)
Marina Brasó, PhD Student, Project Contract (Plan Nacional)
Rajendra Mandaje, PhD Student, Project Contract (INB-ISCIII)
Txema Heredia, PhD Student, Project Contract (Plan Nacional)
Xavier Ferré, IT Technician, Project Contract (RETICS-ISCIII)

Research Outline

Life in our planet today has been shaped by many different biological processes during billions of years. These processes leave a signature in our genomes in the form of differences between species, or between individuals of the same species. Interrogating these patterns of genome diversity we can infer what are the forces that affect living organisms, how and when they act, and how do they affect such various things as biodiversity, human emotions or the differential susceptibility of people to disease. All this knowledge empowers us to control our future but, above all, it is fun to obtain.

In practical terms, there are two main kinds of research we do 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. Lately, we have focused on sequencing full viromes, and on studying viral gene expression levels in LCLs to analyze the evolution of virus-host interactions.

Research Lines

1. Molecular evolution of Segmental Duplications

Our genomes contain many Segmental Duplications (SDs), which are sequences with high identity that can vary in copy number and are fundamental for the creation of novel genes. We use both experimental and computational techniques to understand patterns of molecular evolution within SDs.

2. Positive selection in the human lineage

We study the signature of adaptive changes out the usual paradigm of new mutations that arise in single-copy protein-coding regions. Recently, we have been focusing on how natural selection influences regulatory regions within gene networks.

3. Temporal and spatial distribution of human disease variants

We study alleles linked to disease susceptibility to ascertain, for instance, what are the evolutionary causes of senescence.

4. Evolution of Herpesviridae and their relationship with complex disease

Herpesviridae are associated to many complex diseases, including cancers and Multiple Sclerosis. We study full viral sequences and link them with human variability.

5. 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.

Publications 2014

ISI Articles

Faria, R., and Navarro, A. 2014. Pool and conquer: new tricks for (c)old problems. *Molecular Ecology* 23: 1653–1655.

Hartasánchez, D.A, Vallès-Codina, O., Brasó-Vives, M., Navarro, A. 2014. Interplay of interlocus gene conversion and crossover in segmental duplications under a neutral scenario. *G3* 4: 1479-89.

Navarro, A., Faria, R. 2014. Pool and conquer: new tricks for (c)old problems. *Molecular Ecology* 23 (7):1653-1655.

Olalde, I., Allentoft, M.E., Sanchez-Quinto, F., Santpere, G., Chiang, C.W.K., DeGiorgio, M., Prado-Martinez, J., Rodriguez, J.A., Rasmussen, S., Quilez, J., Ramirez, O., Marigorta, U.M., Fernandez-Callejo, M., Prada, M.E., Encinas, J.M.V., Nielsen, R., Netea, M.G., Novembre, J., Sturm, R., Sabeti, P., Marquès-Bonet, T., Navarro, A., Willerslev, E., Lalueza-Fox, C. 2014. Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. *Nature* 507 (7491): 225-228.

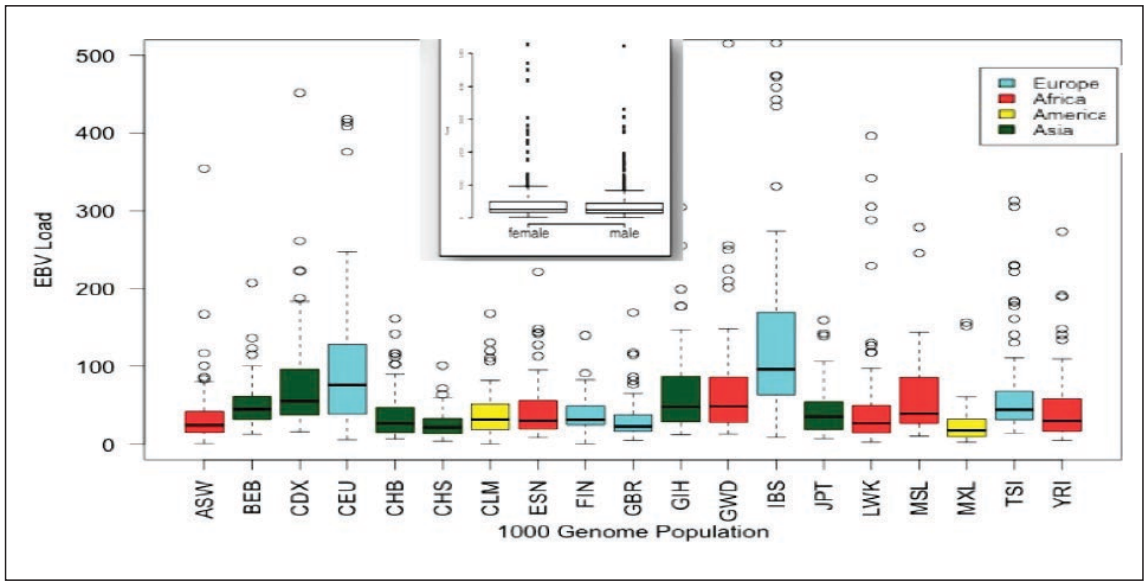
Olalde, I., Sánchez-Quinto, F., Datta, D., Marigorta, U.M., Chiang, C.W.K., Rodríguez, J.A., Fernández-Callejo, M., González, I., Montfort, M., Matas-Lalueza, L., Civit, S., Luiselli, D., Charlier, P., Pettener, D., Ramírez, O., Navarro, A., Himmelbauer, H., Marquès-Bonet, T., and Lalueza-Fox, C. 2014. Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France. *Scientific Reports* 4: 4666.

Pineda, S., Milne, R.L., Calle, M.L., Rothman, N., López de Maturana, E., Herranz, J., Kogevinas, M., Chanock, S.J., Tardón, A., Márquez, M., Guey, L.T., García-Closas, M., Lloreta, J., Baum, E., González-Neira, A., Carrato, A., Navarro, A., Silverman, D.T., Real, F.X., Malats, N. 2014. Genetic Variation in the TP53 Pathway and Bladder Cancer Risk. A Comprehensive Analysis. *PLOS ONE* 9 (5): e89952.

Rodriguez, J.A., Marigorta, U.M., and Navarro, A. 2014. Integrating genomics into evolutionary medicine. *Current Opinion in Genetics and Development* 29: 97–102.

Santpere, G., Darre, F., Blanco, S., Alcami, A., Villoslada, P., Albà, M.M., and Navarro, A. 2014. Genome-wide analysis of wild-type Epstein-Barr virus genomes derived from healthy individuals of the 1000 Genomes Project. *Genome Biology and Evolution published* 6 (4): 846-860.

Fig. 1: *SNPs associated with EBV load detected by GWAS method in European populations (1)*



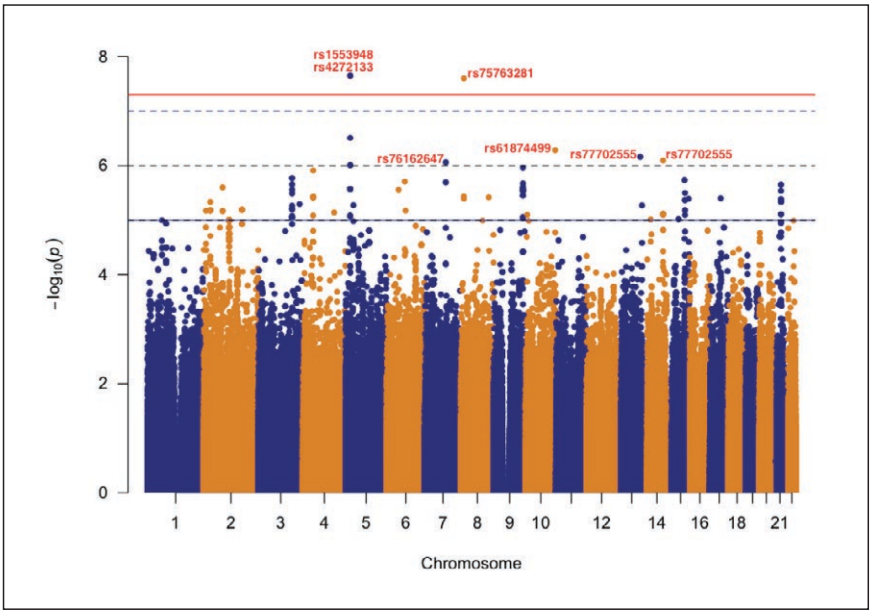


Fig. 2: *SNPs associated with EBV load detected by GWAS method in European populations (2)*

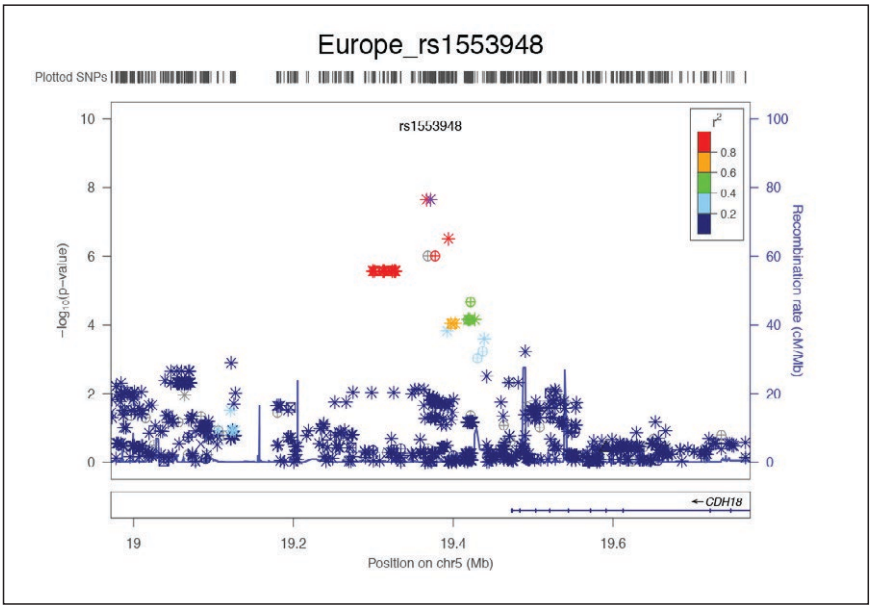


Fig. 3: *SNPs associated with EBV load detected by GWAS method in European populations (3)*

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

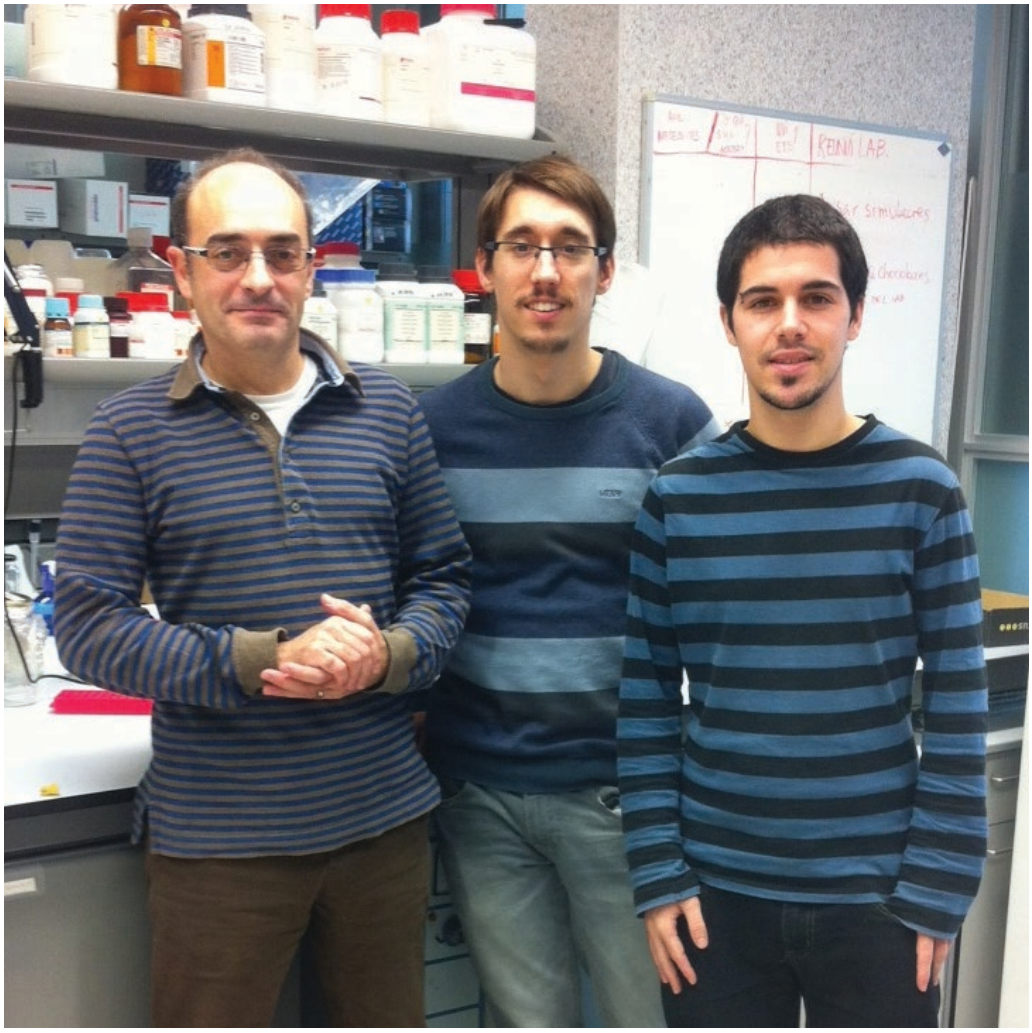
- **Project Title:** Group within the "Red Española de Esclerosis Múltiple" (Spanish Research Network in Multiple Scle-rosis)
  Financed by: Within the RETICS (Redes Españolas de Investigación Cooperativa en Salud) on Multiple Sclerosis (RD12/0032/0011)
  Years: 2013-2015
  PI: Arcadi Navarro (Coordinator: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

- **Project Title:** INB GN8
  Financed by: Instituto de Salud Carlos III (Instituto Nacional de Bioinformática)
  Years: 2014
  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)

group PALEOGENOMICS



From left to right:
Carles Lalueza-Fox, Íñigo Olalde, Andrés Vázquez

group members

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

Íñigo Olalde, PhD Student, Basque Country Scholarship
Andrés Vázquez Figueiras, Undergraduate Student, CSIC JAE-Intro Scholarship

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 individualisation of a Neandertal family group from El Sidrón site (Asturias, Spain). We are also investigating the evolutionary dynamics of the prehistory of Europe through the analysis of Mesolithic, Neolithic, Cooper Age and Bronze Age human genomes.

Research Lines

1. Neandertal genomic diversity

We are analyzing different individuals from 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 help 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 the European prehistory by analyzing past human genomes from different periods –with a special focus on the Iberian peninsula-, including the Mesolithic-Neolithic transition and later periods such as the Cooper and Bronze Age. We have recently retrieved the first pre-agricultural, modern human European genome, that of La Braña-Arintero in León, Spain. We are currently analysing Cardium pottery samples with the goal of retrieving a complete genome from this early Neolithic Mediterranean migration and compare it to other, central European Neolithic expansions. We are also analysing Bell-Beaker Iberian samples for reconstructing the dynamics and nature of the expansion of archaeological horizon and its role in the shaping of modern European genetic diversity.

Publications 2014

ISI Articles

Castellano, S., Parra, G., Sánchez-Quinto, F., Racimo, F., Kuhlwilm, M., Kircher, M., Sawyer, S., Fu, Q., Heinze, A., Nickel, B., Dabney, J., Siebauer, M., White, L., Burbano, H.A., Renaud, G., Stenzel, U., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Rudan, P., Brajkovic, D., Kucan, Z., Gušic, I., Shunkov, M.V., Derevianko, A.P., Viola, B., Meyer, M., Kelso, J., Andrés, A.M., and Pääbo, S. 2014. Patterns of coding variation in the complete exomes of three Neandertals. *Proceedings of the National Academy of Sciences* 111 (18): 6666-6671.

Engelken, J., Carnero-Montoro, E., Pybus, M., Andrews, G.K., Lalueza-Fox, C., Comas, D., Sekler, I., de la Rasilla, M., Rosas, A., Stoneking, M., Valverde, M.A., Vicente, R., and Bosch, E. 2014. Extreme Population Differences in the Human Zinc Transporter ZIP4 (SLC39A4) are Explained by Positive Selection in Sub-Saharan Africa. *PLoS Genetics* 10 (2): e1004128.

Gómez-Sánchez, D., Olalde, I., Pierini, F., Matas-Lalueza, L., Gigli, E., Lari, M., Civit, S., Lozano, M., Vergès, J.M., Caramelli, D., Ramírez, O., and Lalueza-Fox, C. 2014. Mitochondrial DNA from El Mirador Cave (Atapuerca, Spain) Reveals the Heterogeneity of Chalcolithic Populations. *PLOS ONE*. 9 (8):e105105.

Olalde, I., Sánchez-Quinto, F., Datta, D., Marigorta, U.M., Chiang, C.W.K., Rodríguez, J.A., Fernández-Callejo, M., González, I., Montfort, M., Matas-Lalueza, L., Civit, S., Luiselli, D., Charlier, P., Pettener, D., Ramírez, O., Navarro, A., Himmelbauer, H., Marquès-Bonet, T., and Lalueza-Fox, C. 2014. Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France. *Scientific Reports* 4: 4666.

Fig. 1: *Artistic reconstruction of the La Braña 1 Mesolithic individual (Pelopantón-CSIC)*

Olalde, I., Allentoft, M.E., Sanchez-Quinto, F., Santpere, G., Chiang, C.W.K., DeGiorgio, M., Prado-Martinez, J., Rodriguez, J.A., Rasmussen, S., Quilez, J., Ramirez, O., Marigorta, U.M., Fernandez-Callejo, M., Prada, M.E., Encinas, J.M.V., Nielsen, R., Netea, M.G., Novembre, J., Sturm, R., Sabeti, P., Marquès-Bonet, T., Navarro, A., Willerslev, E., Lalueza-Fox, C. 2014. Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. *Nature* 507 (7491): 225-228.

Ramirez, O., Olalde, I., Berglund, J., Lorente-Galdos, B., Hernandez-Rodriguez, J., Quilez, J., Webster, M.T., Wayne, R.K., Lalueza-Fox, C., Vilà, C., and Marquès-Bonet, T. 2014. Analysis of structural diversity in wolf-like canids reveals post-domestication variants. *BMC Genomics* 15: 465.

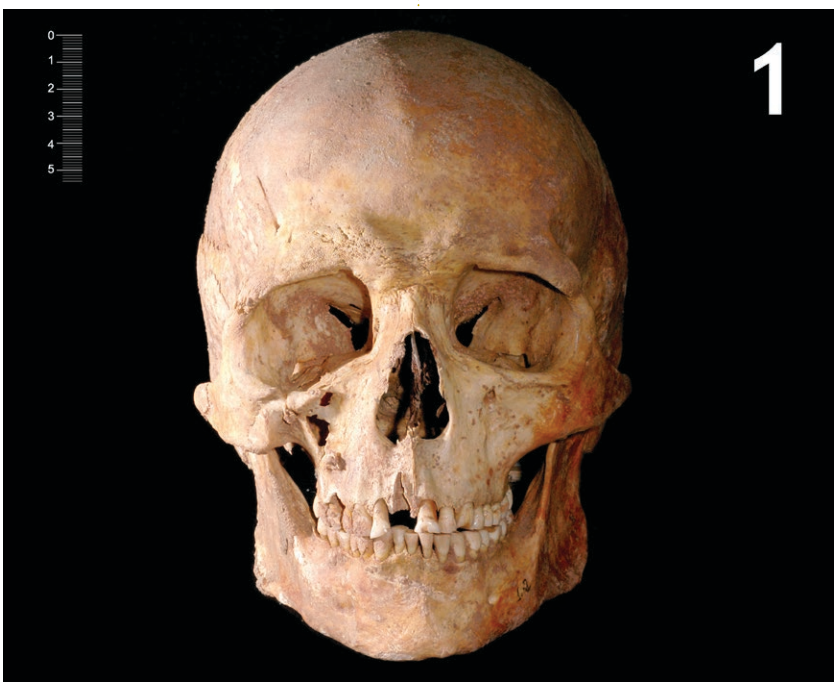
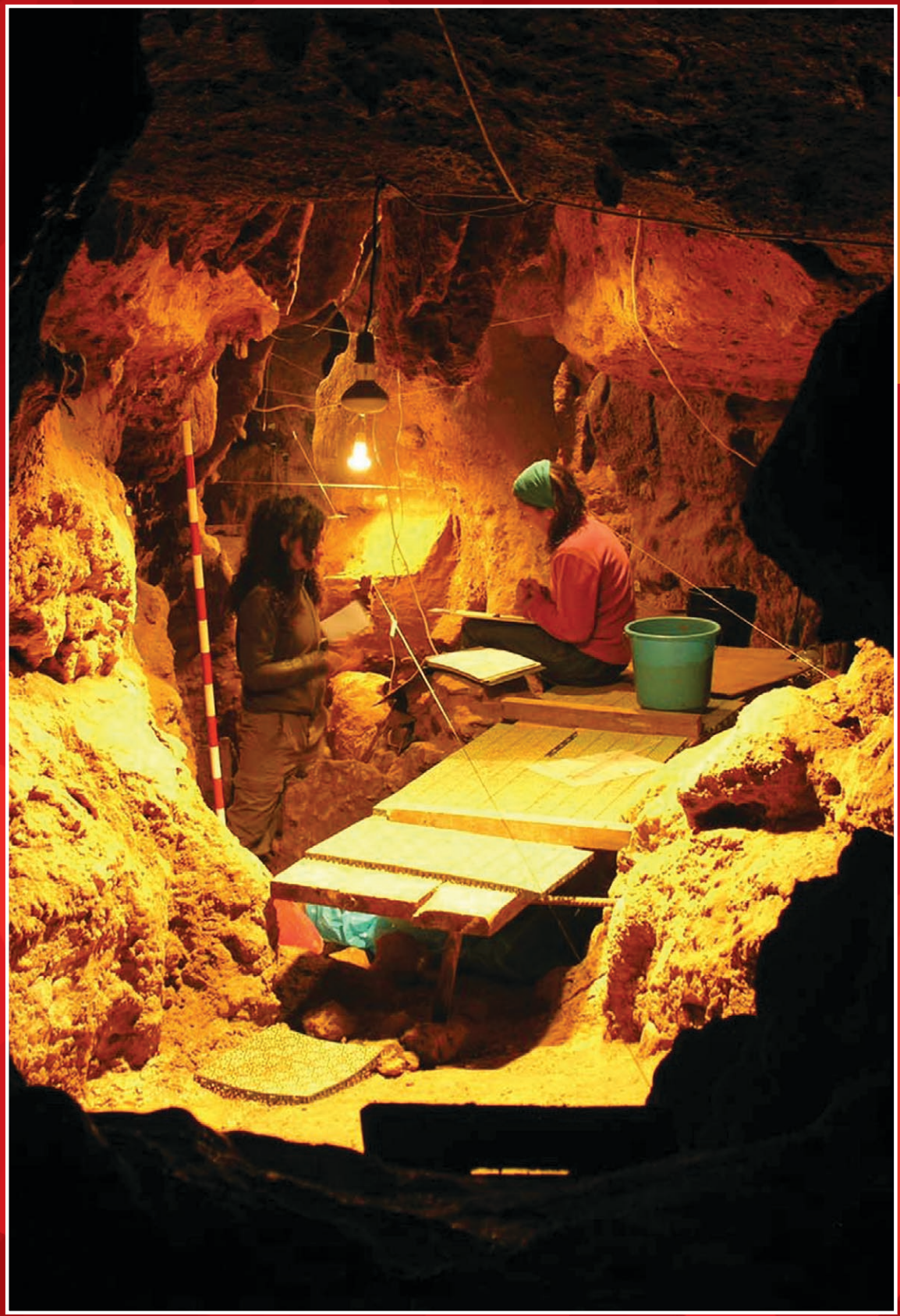


Fig. 2: *Frontal view of the La Braña 1 skull; the full genome of this Mesolithic individual was obtained from the dental root of an upper third molar.*

Funded Projects

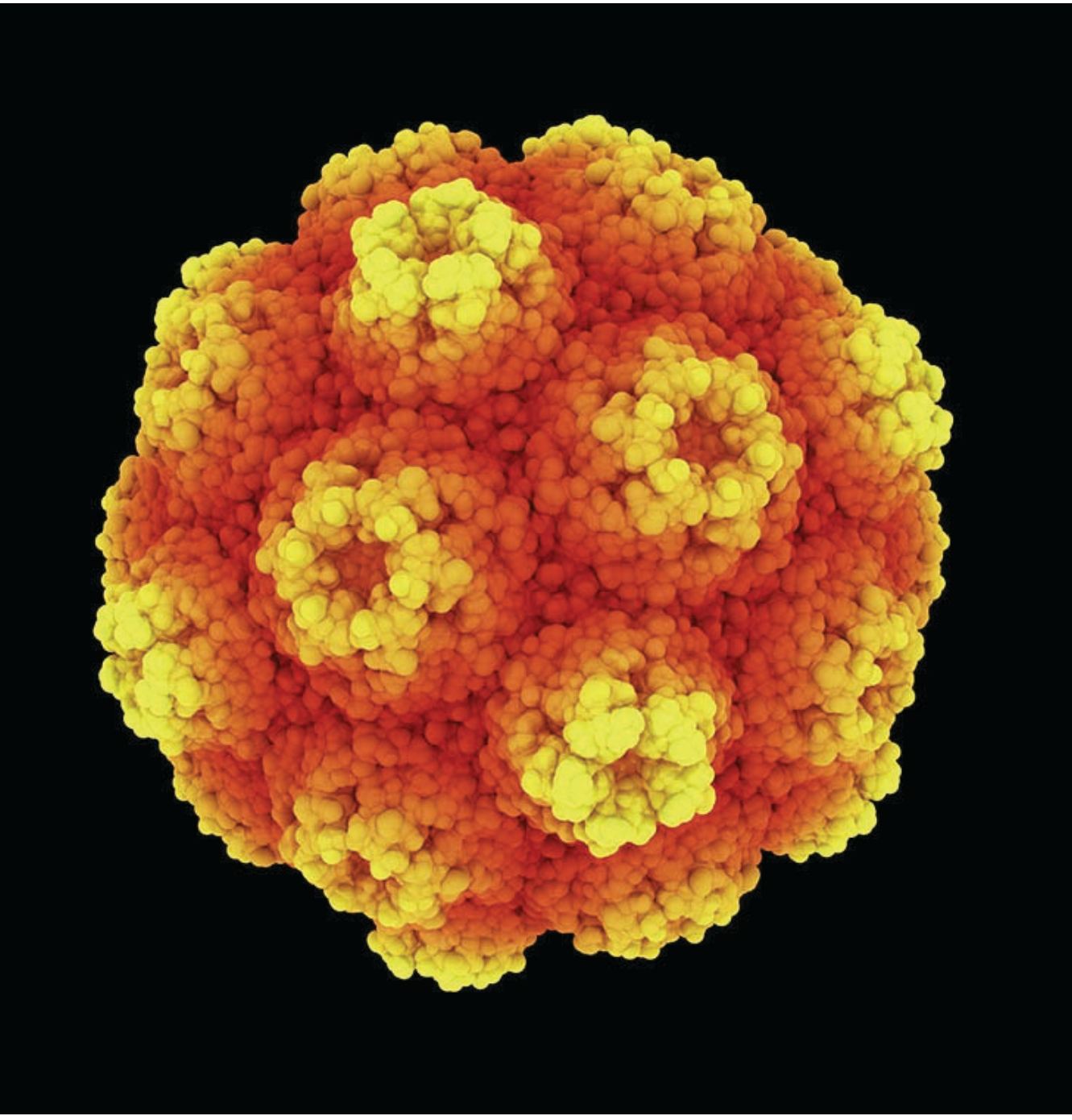
- **Project Title:** Evolutionary inferences from targeted sequence retrieval of Neandertal genomic regions (REF: BFU2012-34157)
  Financed by: Ministry of Economy and Competitivity, Spain.
  Years: 2013-2015
  PI: Carles Lalueza-Fox

- **Project Title:** Grup de Recerca Consolidat en Biologia Evolutiva (2014SGR1311)
  Financed by: Direcció General de Recerca, Comissionat per a Universitats i Recerca, Generalitat de Catalunya
  Years: 2014-2016
  PI: Arcadi Navarro



PROGRAM

COMPLEX SYSTEMS



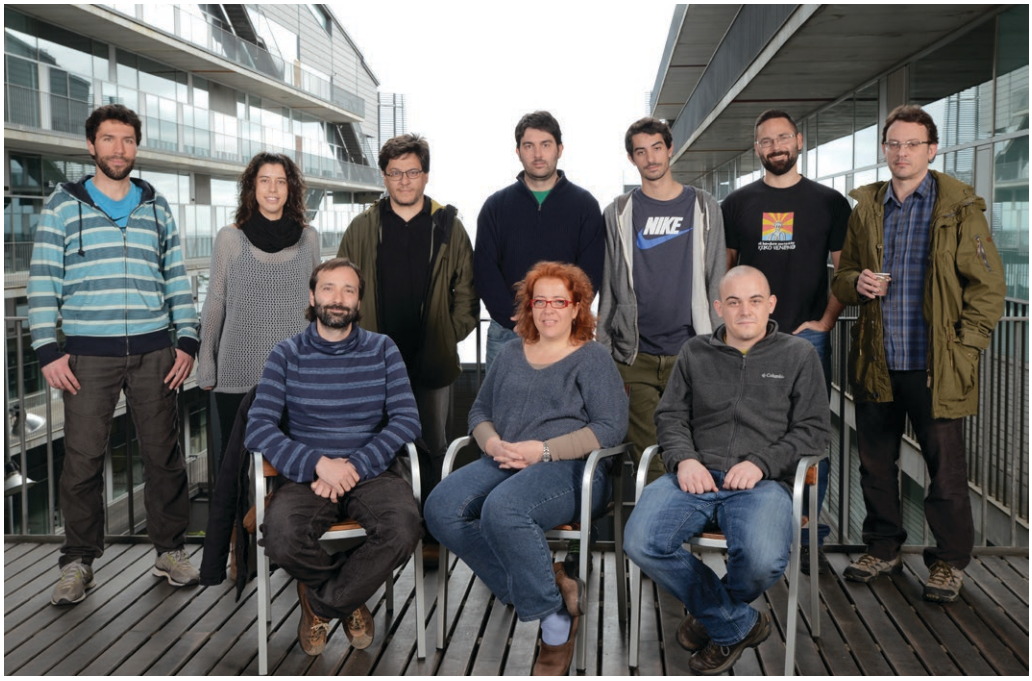
Research groups

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:
Daniel Amor, Aina Ollé, Ricard Solé, Josep Sardanyés, Max Carbonell, Raúl Montañez, Sergi Valverde, Carlos Rodríguez-Caso, Eva García-Ramallo, Salva Durán

group members

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

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

Research Outline

The Complex Systems Lab is an interdisciplinary research team exploring the evolution of complex systems, both natural and artificial, searching for their common laws of organization. We closely work in collaboration with the Santa Fe Institute (USA) and the European Centre of Living Technology (IT). Our research spans a broad range of systems, with special attention to biological computation, protocell biology, synthetic systems and network biology.

Research Lines

1. Evolutionary innovations
We explore theoretical approaches to the origins of evolutionary innovations and major transitions in biological, artificial and technological systems. Using methods from statistical physics we explore potential scenarios for the development of innovations and the potential patterns of universality common to all these disparate classes of systems. Simulated artificial ecosystems, information technology systems, language networks and other case studies are considered.

2. Multicellularity: origins, maintenance and decay
We want t develop a general theoretical framework for the origins and development of complex multicellular systems, including early emergence through evolution (evo-devo), th elegiac of tissue organization and the role played by evolution in cancer development. We also have a theoretical/experimental research approach based on synthetic multicellularity, involving the development of synthetic, engineered cell-cell communication in order to force cells to behave as multicellular entities.

3. Emergence of complex behaviour
We explore the emergence of communication, collective intelligence and language in natural and artificial systems. The main goal here is to understand the nature of the major transitions associated to the shift from single individuals to cooperative systems as well as the emergence of a complex language as a result of interactions among words. Here we also use synthetic biology to study the potential collective behaviors arising from manipulated, single-cell bacterial communities.

4. Biological computation
We study the nature, origins and evolution of living computational systems, both natural and synthetic. Using a number of methods from complex systems theory, we want to make a map of the landscape of computational processes that can occur in nature and how we can move beyond that landscape. This work has several branches, both theoretical and applied to biomedical research.

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

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

7. 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.

8. 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.

9. 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.

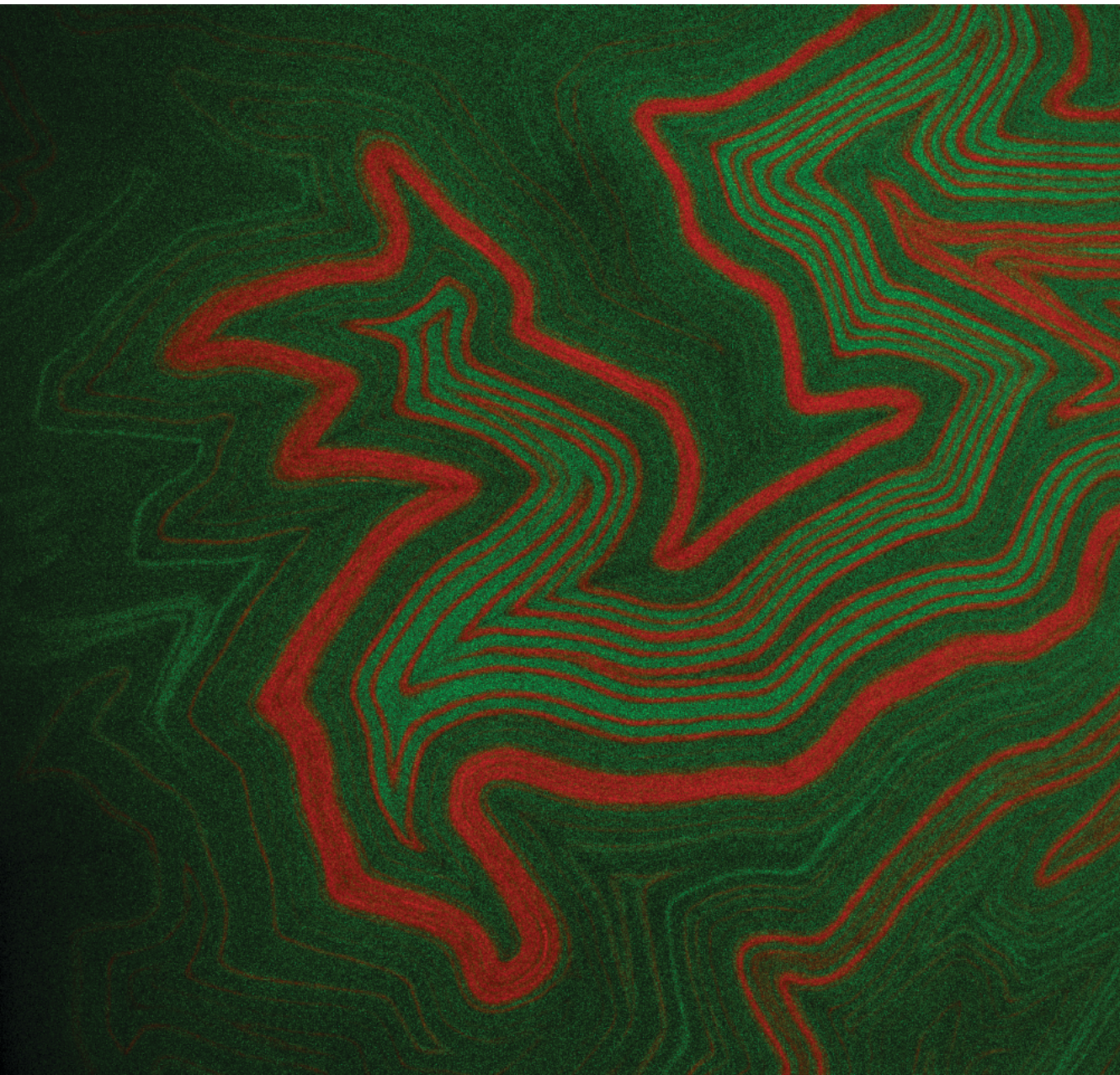
10. Major synthetic transitions

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.

11. Bioengineering the Biosphere

One potential path to restore the balance of endangered ecosystems and fight against climate change could be Terraforming our own planet. We explore (mathematically and experimentally) the potential scenarios that could allow to redesign our biosphere using synthetic biology as a major engineering approach
http://complex.upf.edu/

Fig. 1: *Spatial distribution in a growing colony of two synthetic mutualists of E coli. Two mechanisms affect the growth dynamics in opposite ways. On the one hand, the competition for space favours demixing of phenotypes into growing monostrain sectors. On the other hand, growth is only possible if the two strains remain close enough to maintain their mutualistic interactions. The combination of both effects leads to the observed spatial pattern.*



Publications 2014

ISI Articles

Amor, D.R., Fort, J. 2014. Cohabitation reaction-diffusion model for virus focal infections. *Physica A: Statistical Mechanics and its Applications* 416 (0): 611-619.

Amor, D.S., and Solé, R.V. 2014. Catastrophic shifts and lethal thresholds in a propagating front model of unstable tumor progression. *Physical Review E*. 90 (2): 22710-18.

Azzurro, E., Tusset, V.M., Lombarte, A., Maynou, F., Simberloff, D., Rodríguez-Pérez, A., and Solé, R. V. 2014. External morphology explains the success of biological invasions. *Ecology Letters* 17 (11): 1455-1463.

Carbonell-Ballestero, M., Duran-Nebreda, S., Montañez, R., Solé, R., Macía, J., and Rodríguez-Caso, C. 2014. A bottom-up characterization of transfer functions for synthetic biology designs: lessons from enzymology. *Nucleic Acids Research* 42 (22): 14060-14069.

Corominas-Murtra, B., Fortuny, J., and Sole, R.V. 2014. Towards a mathematical theory of meaningful communication. *Scientific Reports* 4: 4587.

Gautrais, J., Bulh, J., Valverde, S., Kuntz, P., Theraulaz, G. 2014. The Role of Colony Size on Tunnel Branching Morphogenesis in Ant Nests. *PLOS ONE*. 9(10): e109436.

Hillung, J., Cuevas, J.M., Valverde, S., and Elena, S.F. 2014. Experimental evolution of an emerging plant virus in host genotypes that differ in their susceptibility to infection. *Evolution* doi: 10.1111/evo.12458.

Macia, J., and Sole, R.V. 2014. How to Make a Synthetic Multicellular Computer. *PLOS ONE* 9 (2): e81248.

Munteanu, A., Cotterell, J., Solé, R., and Sharpe, J. 2014. Design principles of stripe-forming motifs: the role of positive feedback. N*ature Scientific Reports* 4, 5003.

Notton, T., Sardanyés J., Weinberger, A.D., and Weinberger, L.S. 2014. The case for transmissible antivirals to control population-wide infectious disease. *Trends in Biotechnology* 32 (8), 400-405.

Sardanyes, J., Simó, C., Martinez, R., Sole, R.V., and Elena, S.F. 2014. Variability in mutational fitness effects prevents full lethal transitions in large quasispecies populations. *Scientific Reports* 4: 4625.

Shirt-Ediss, B., Ruiz-Mirazo, K., Mavelli, F., and Solé, R.V. 2014. Modelling Lipid Competition Dynamics in Heterogeneous Protocell Populations. *Scientific Reports* 4: 5675.

Solé R.V., and Macía J. 2014. Synthetic biology: Biocircuits in synchrony. *Nature* 508 (7496), 326-327.

Solé, R.V., and Sardanyés, J. 2014. Red Queen Coevolution on Fitness Landscapes.In: Recent Advances in the Theory and Application of Fitness Landscapes. H. Richter and A. Engelbrecht.(ed). pp. 301-338.

Solé, R.V., Valverde, S., Rodriguez-Caso, C., and Sardanyés, J. 2014. Can a minimal replicating construct be identified as the embodiment of cancer? *BioEssays* 36 (5): 503-512.

Books / Book Chapters

Solé, R.V., and Duran, S. 2014. In silico transitions to multicellularity. In: Evolutionary transitions to multicellular life. A. Nedelcu, Ruiz-Trillo, I.(ed). Springer-Verlag London.

Funded Projects

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

- **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:** Assessment of topological vulnerability of infrastructural systems based on extended complex network technique.
  Financed by: Stichting Next Generation Infrastructure
  Years: 2012-2014
  PI: Ricard Solé

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

group LANGUAGE EVOLUTION

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

group members

Luc Steels, *Group Leader*
Research Professor, ICREA

Emília García Casademont, Pre-doctoral Researcher
Maria Ferrer Bonet, 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 should answer 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 explaining 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 behavior 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 of 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 to handle variation, flexibility, and change. We are therefore working in collaboration with other research centers on the development of such formalism. The formalism takes a construction grammar viewpoint which is more appropriate for modeling language evolution. It consists of data structures for representing linguistic knowledge and mechanisms for parsing, production, and language learning. FCG has been released in open source and is being used by a growing community (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.

Publications 2014

ISI Article

Garcia Casademont, E., and Steels, L. 2014. Strategies for the emergence of first-order phrase structure. In E. A. Cartmill, S. Roberts, H. Lyn & H. Cornish (Eds.) The evolution of language - Proceedings of the 10th International Conference (Evolang-X - Vienna), pp. 50-57. *World Scientific*. DOI: 10.1142/9789814603638_0005.

Steels, L. 2014. Robot tutoring. In: Cohn, A., B. Neumann, A. Saffiotti and M. Vincze (eds). Robots Learning from Experience. Dagstuhl Report 4 (3). ISSN 2192-5283.

Book Chapters

Steels, L. 2014. False dichotomies. In: Dor, D., C. Knight and J. Lewis. The Social Origins of Language: Early Society, Communication and Polymodality. Oxford University Press, Oxford. pp. 336-393.

Steels, L. 2014. The Computational Art of Peter Beyls. In: Beyls, P. (ed) Simple Thoughts. MER, Ghent.

Steels, L., and Beuls, K. 2014. How to Explain the Origins of Complexity in Language: A Case Study for Agreement Systems. In: Mufwene, S. (ed) Complexity in Language: Developmental and Evolutionary Perspectives. Cambridge University Press, Cambridge Ma.

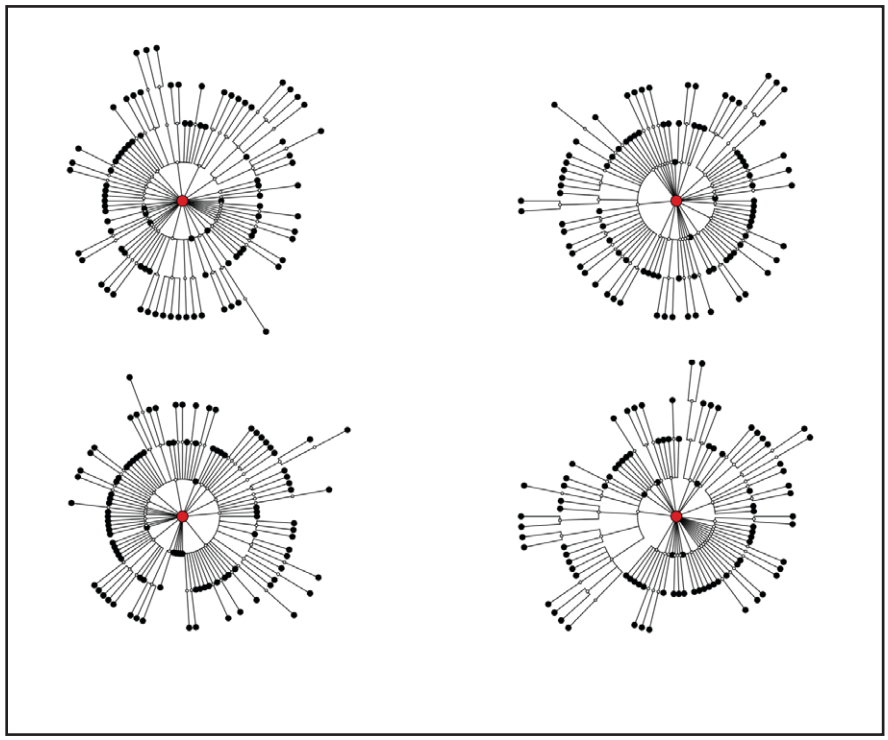


Fig. 1: *Various methods from evolutionary biology have been identified to study the evolutionary dynamics of language: analysis of a linguistic fitness landscape, glossogenetic trees analogous with phylogenetic trees, semiotic webs, and genotype-phenotype mappings. Here we show glossogenetic trees of 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.*

Image: *Steels, 2014*

Funded Projects

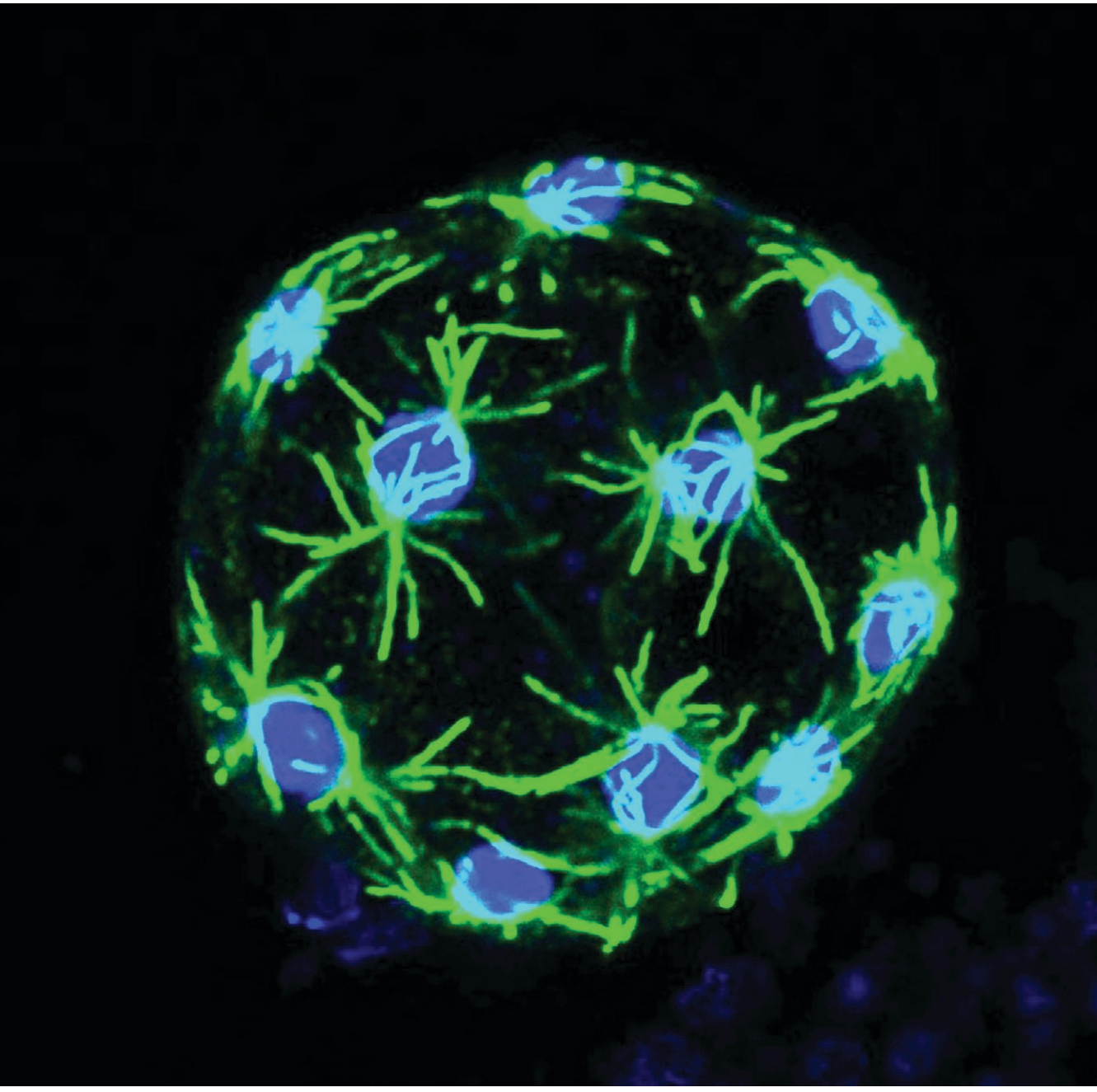
- **Project Title:** LANGEVO
  Financed by: EU Marie Curie Integration Grant
  Years: 2011-2015
  PI: Luc Steels

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

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

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

From left to right and top to bottom:
Marc Torra, Xavier Franch-Marro, David Martín, Alex Subías, Juan Gómez, Noemi Tomsen, Silvia Chafino, Cristina de Miguel, Neus Botas, Eulàlia Rovira, Cecilia Albor

group members

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

Subgroup
Morphology and Signalling

Xavier Franch-Marro, Group Leader, Tenured Scientist, CSIC
Cristina de Miguel Vijandi, PhD Student, FPI Scholarship, MEC
Neus Bota Rabassedas, PhD Student, FPI Scholarship, MEC
Marc Torra, Undergraduate Student, UB
Victoria Rodríguez Marcé, Undergraduate Student, UdV

Hormonal Control of Insect Development

David Martín, Principal Investigator, Tenured Scientist, CSIC
Cecilia Albor, Postdoctoral Researcher, Juan de la Cierva Program
Silvia Chafino, Master Student, UB
Alex Subías, Undergraduate Student, UB

Research Outline

Throughout the history of the Earth evolution has developed a great number of different organisms with a consequent incredible variety of forms and sizes. Those morphologies are tailored during development, by modifying the expression pattern of key genes as well as by the modulation of hormone activation, which controls the timing of development. Thus, our main goal is to understand how changes in gene expression and hormone regulation affect morphology evolution. We also challenge to identify which genes and what kinds of changes and their sequences are responsible for the evolution of the mentioned morphological diversity. We address these questions by using insects as experimental model, particularly comparing *Drosophila melanogaster*, *Tribolium castaneum*, and *Blattella germanica* development.

Research Lines

Subgroup: Morphology and Signalling

1. Tracheal System Remodeling and Morphogenesis

The tracheal system is the *Drosophila* respiratory organ and consists of epithelial tubes, the morphogenesis of which is controlled by distinct sets of signalling pathways and transcription factors. During embryogenesis, the tracheal system develops from segmentally repeated groups of ~ 80 cells that express the *Trachealess* transcription factor and invaginate, forming sacs attached to the epidermis by a stalk of Spiracular Branch (SB) cells. Branches bud from the sacs and cells diversify primarily under control of the Fibroblast Growth Factor (FGF) signalling pathway. At metamorphosis, the tracheal system undergoes a deep remodelling stage, giving rise to pupae and the tracheal system. This remodelling involves proliferation of both a classical imaginal cell population, as in SB, and a population of differentiated functional larval tracheal cells, as in Tr2 that re-enters the cell cycle and regains development potency. The genetic circuits controlling tracheal cell proliferation and dedifferentiation are only now beginning to emerge. Therefore, we aim to discover new genes and signalling pathways involved in such interesting processes (see Publications 2014).

2. Tracheal System Evolution

The tracheal system is the respiratory organ of insects. It consists of a network of tubes that transport oxygen to all the tissues. Insects present different morphology of the tracheal network depending on their habitat. For instance, we have found that the *Drosophila* tracheal network presents some morphological innovations compared to the tracheal morphology of a more primitive insect such as *Tribolium*. The main goal of this project is to discover the genetic changes that have allowed the generation of those morphological adaptations along evolution.

3. Wingless signaling in size control and evolution

How organ size and shape are regulated is a remaining outstanding question in developmental biology. Recently, we have shown that Wg signaling has an important role in controlling growth in *Drosophila* wing imaginal discs. New experimental approaches have allowed us to find that a mild increase of Wg signaling over and above the endogenous level causes wing overgrowth by promoting cell proliferation. However, how this Wg signaling activation controls cell proliferation at a transcriptional level is still elusive. Using a microarray approach we have identified new target genes of the signaling pathway that would explain mechanistically the way Wg controls cell proliferation in the *Drosophila* wing disc. In parallel, we study these genes in *Tribolium castaneum* in order to gain further insights into developmental processes occuring during beetle and fly development, leading to more general conclussions for arthropod evolution.

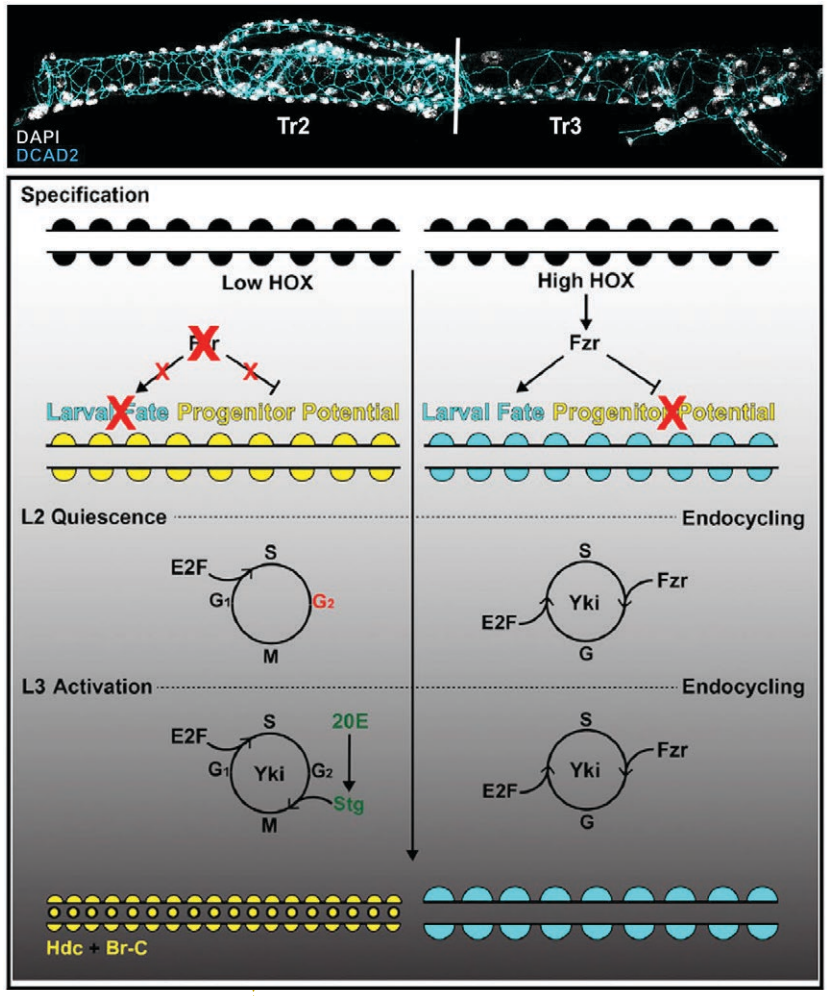


Fig. 1: *Our group described the genetic mechanisms mediating the specification, quiescence, and activation of a subset of differentiated tracheal cells as adult progenitors in* Drosophila. *We also showed that a single factor Fzr, is necessary and sufficient to couple cell-cycle mode with expression of adult progenitor markers. Djabrayan et al., 2014,* Cell Reports *9, 859–865.*

Subgroup: Hormonal Control of Insect Development

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

Based on phylogenetic analysis, Holometabolous insects (complete metamorphosis) evolved from hemimetabolan ancestors (incomplete metamorphosis), although the mechanisms underlying this transition remain to be identified. The main question our group is trying to answer is: What types of mechanistic and regulatory changes underlie the evolution of insect metamorphosis? Interestingly, despite the dramatic differences between hemimetaboly and holometaboly, both types of metamorphosis are controlled by a reduced number of genes (*E93*, *Kr-h1* and *Br-C*) that form a conserved regulatory metamorphic toolkit, and whose expression is controlled by two hormones, 20-hydroxyecdysone and juvenile hormone (JH). *Kr-h1* is a JH-response gene that prevents premature adult differentiation during juvenile stages, while Br-C is a transcription factor that directs pupal development in holometabolous insects. Recently, our group has identified the transcription factor *E93* as the critical master gene of the toolkit that promotes adult differentiation during the metamorphic period in both hemimetabolous and holometabolous insects (see Publications 2014). In order to understand the evolution of Holometaboly, our

group is currently characterizing the evolutionary conservation of the metamorphic toolkit genes in ametabolous insects. By doing so, we want to assess the presence and the ancestral role of the metamorphic genes in a non-metamorphic insect. Furthermore, we are characterizing in detail the transcriptional regulation and the mode of action, from a molecular point of view, of E93 during metamorphosis in hemimetabolous and holometabolous insects.

2. Molecular analysis of nuclear hormone receptors in insects

Two hormones control all the developmental changes associated with the metamorphic process in insects. The steroid hormone 20-hydroxyecdysone (20E) triggers major developmental transitions through a genetic cascade of transcription factors that belong to the Nuclear Hormone Receptor superfamily (NRs). Our group has cloned and functionally characterized the entire repertoire of 20E-dependent NRs in the hemimetabolous insects *Blattella germanica*. Furthermore, Juvenile Hormone (JH), the other hormones of paramount importance in development, prevents metamorphosis by coordinating multiple 20E-dependent developmental and physiological processes. The main goal of this project is the molecular characterization of the mechanisms underlying the regulatory roles of both, 20E and JH in the metamorphosis of the hemimetabolous insect *B. germanica* (using RNAi *in vivo* and parental RNAi procedures) and the holometabolous insects *Tribolium castaneum* and *Drosophila melanogaster* (RNAi and mutational analysis). These studies have already demonstrated critical roles of 20E-dependent NRs on ecdysteroid production, programmed cell death, tissue growth and morphogenesis, ovary follicle proliferation, and molting behavior in both types of insects. In summary, this project aims to define the molecular mechanisms underlying the action of NRs during insect metamorphosis to understand the evolutionary conservation of the molecular program determining the developmental transition to adulthood in animals.

3. Insect body plan evolution

The body plan is highly conserved in hemimetabolous and holometabolous insects, although the molecular mechanisms underlying body patterning during embryogenesis are very different. The holometabolous *D. melanogaster* is an example of a long germ band insect. The embryonic primordium of the embryo, the germ band, spreads through the entire egg and all of the body segments are specified simultaneously. In contrast, hemimetabolous insects present short germ band development where the germ band occupies a relatively short portion of the body, and segments are added sequentially during the embryonic development from a posterior proliferation zone. The main goal of this project is to characterize how ecdysteroids and juvenile hormone control the major morphogenetic events in short germ band hemimetabolous insects, which mainly occur during early-embryogenesis. For that, we are analyzing the role of each 20E-dependent NR on the morphogenetic events during the embryogenesis of the insect model *B. germanica*. This project will provide a valuable model to understand the molecular basis for how shifts in the hormonal context can lead to the creation of different body forms.

4. Evolution of SUMO protein functions in insect metamorphosis

Post-translational modification with small ubiquitin-related modifier, SUMO, is a widespread mechanism for rapid and reversible changes in protein function, especially in nuclear hormone receptors. In this project, in collaboration with the laboratory of Dr. Rosa Barrio (CIC bioGUNE, Vizcaya), we are addressing the functional analysis of sumoylation on the development of the hemimetabolous model insect, *B. germanica* (which contains two SUMO genes), and its relationship with nuclear hormone receptor function. Furthermore, we are testing whether the functions of SUMO proteins are evolutionarily conserved between hemimetabolous and holometabolous insects by performing functional analysis of the two *B. germanica* Sumo homologues using *D. melanogaster* (which contains a single SUMO gene) as model system.

Publications 2014

ISI Articles

Djabrayan, N. J. V., Cruz, J., de Miguel, C., Franch-Marro, X., and Casanova, J. Specification of Differentiated Adult Progenitors via Inhibition of Endocycle Entry in the Drosophila Trachea. *Cell Reports* 9, 859–865 (2014).

Ureña, E., Manjon, C., Franch-Marro, X., and Martín, D. Transcription factor E93 specifies adult metamorphosis in hemimetabolous and holometabolous insects. *Proceedings of the National Academy of Sciences USA* 111, 7024-7029 (2014).

Fig. 2: *Our group found the transcription factor E93 as the master gene that induces adult metamorphosis in all winged insects. Adult cockroach (Blattella germanica) with functional wings (left part) compared with a wingless* E93*-depleted supernumerary nymph of the same age (right part). In the absence of E93, nymphs of Blattella germanica molts to a new supernumerary nymphal stage instead of molting into the adult form.*

Photo: *Enric Ureña, Xavier Franch-Marro and David Martín*

Funded Projects

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

group INSECT PHYSIOLOGY AND MOLECULAR BIOLOGY

From left to right:
José Luis Maestro, Xavier Bellés, Mahboobeh Naghdi, Carolina G. Santos, Elena Navas, Guillem Ylla, Jesús Lozano

group members

Xavier Bellés, *Group Leader*
Research Professor, CSIC

Subgroup
Evolution of Insect Metamorphosis

Xavier Bellés, Group Leader, Research Professor, CSIC
Carolina G. Santos, Postdoctoral Researcher, CNPq (Brazil) Fellowship
Sheila Ons, Postdoctoral Researcher, CONICET (Argentina) Fellowship
Ana Fernández Nicolas, PhD Student, Scholarship MICINN
Jesús Lozano, PhD Student, Scholarship MICINN
Elena Navas, Graduate Student, Project Contract, Universitat de Vic
Mahboobeh Naghdi, Graduate Student, University of Tehran Fellowship
Guillem Ylla, Bioinformatician, Project Contract
Núria Sanchez, Lab Manager, Project Contract

Subgroup
Nutritional Signals in Insects

José Luis Maestro, Tenured Scientist, CSIC
Sheila Ons, Postdoctoral Researcher, CONICET (Argentina) Fellowship
Ainoa Marín, Undergraduate Student, UB
Claudia Domínguez, Master Student

Research Outline

Our goals and interests embrace a number of subjects around the physiology of the insect, but most of the work focuses on physiological processes regulated by hormones. Therefore, we have studied the biochemical and regulatory aspects of the hormones themselves (juvenile hormone, ecdysteroids and regulatory peptides), the signalling pathways (especially that of juvenile hormone) and the processes dependent on these hormones.

At present, we concentrated on the origin and evolution of insect metamorphosis, a research line headed by Xavier Bellés, and on the study of the physiological and developmental effects of nutritional signals, line headed by José Luis Maestro. We are interested in the regulation of these processes from a mechanistic point of view and from an evolutionary perspective. As most information has been obtained in highly modified, holometabolan species (mainly in the fly *Drosophila melanogaster*), we currently use the cockroach *Blattella germanica* as model, which is a phylogenetically basal, hemimetabolan species. Therefore, results obtained in this cockroach can be used as a reference baseline when establishing comparisons with other evolutionarily more modified insect species.

Research Lines

Subgroup: Evolution of Insect Metamorphosis

We aim to elucidate the mechanisms regulating metamorphosis in *B. germanica* and then comparing them with those operating in holometabolan species. The idea is to infer the evolutionary history underlying the transition from hemimetaboly to holometaboly. Currently, we have been working on the following five main subjects.

1. Using the development of cockroach tergal glands as a minimal model of metamorphosis

The male tergal gland of cockroaches is a complex morphologic structure that forms during the imaginal molt in the tergites 7 and 8 (T7-8). In 2014, we have compared mRNA libraries from T7-8 in metamorphic and non-metamorphic transitions, and also from metamorphic transitions after juvenile hormone treatment. A number of transcripts that appeared differentially expressed at the beginning of the last instar nymph have been identified, like the transcription factor E93, which is a promoter of metamorphosis, and Nejire, which is a factor that contributes to regulate food consumption in the last nymphal instar, as well as the quality of the imaginal molt.

2. Transcription factors and hormonal signalling

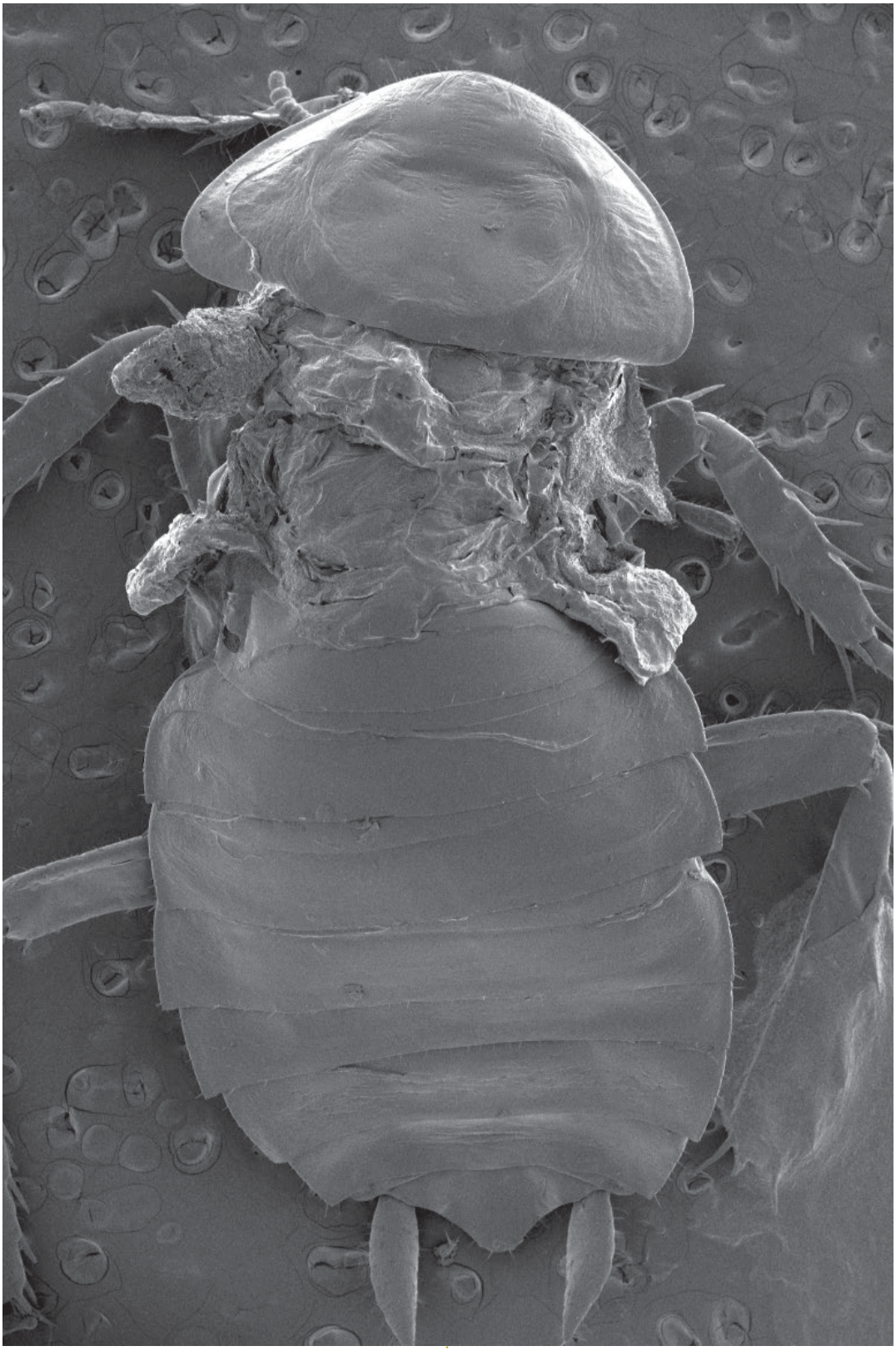
Metamorphosis is mainly regulated by two hormone types: ecdysteroids and juvenile hormones. We are interested in the transcription factors involved in the signalling pathways elicited by both hormone types but focusing on that of juvenile hormone, which is less known. During 2014 we have finished and published the functional characterization of the aforementioned E93, which is repressed by the factor Krüppel-h1, the master repressor of metamorphosis, and which was previously characterized in *B. germanica* by our group. Also in our cockroach model, we have finished and published the functional study of the two components of the JH receptor: the bHLH-PAS proteins Methoprene-tolerant and Taiman.

3. Small RNAs and metamorphosis

Our hypothesis is that miRNAs play a modulatory role in the shift from juvenile to adult developmental programs. Comparing miRNA libraries from penultimate and last instar nymph we identified a number of miRNAs that where differentially expressed and can thus play significant roles in adult morphogenesis. Among these were miR-8, miR-100, miR-123, let-7 and miR-2. In 2014 we have been investigating the contribution of miR-2 family

Fig. 1: *SEM micrography of an intermediate nymph-adult of* B. germanica*, obtained after depleting Taiman expression by RNAi in the penultimate nymphal instar. Notice the wings only rudimentarily developed and the general shape of a nymph (Lozano et al., 2014).*

Photo: *Jesus Lozano and Xavier Bellés*



miRNAs on the decrease of Krüppel-h1 mRNAs that occurs at the beginning of the last nymphal instar of *B. germanica*. Our results show that miR-2 miRNAs regulate this decrease, thus crucially contributing to the correct progress of metamorphosis.

4. Developmental transitions during embryogenesis

This line is related to lines 1, 2 and 3, but extended to the study of the regulation of developmental transitions occurring along embryo development. The idea is that crucial information about the origin of holometaboly from hemimetabolan ancestors will be revealed from the comparison of embryogenesis in species representing both metamorphosis modes. During 2014 we have prepared transcriptomes from six key stages of *B. germanica* embryogenesis in order to identify differentially expressed genes in these stages, and we have started the functional study of the components of the MEKRE93 pathway in the embryo, using parental RNAi.

Fig. 2: B. germanica *Precocious adult obtained after depleting Methoprene tolerant expression by RNAi in the penultimate nymphal instar. Notice the wing partially developed and extended, and blackish color of the teguments, which still resemble that of a nymph (Lozano and Bellés, 2014).*

Photo: *Jesus Lozano and Xavier Bellés*

5. Determination of wing identity

In 2014 we have continued a project addressed to identify factors determining the identity of wing structure (wings and tegmina) in *B. germanica*. Our functional studies using RNAi have confirmed that *ultrabithorax* gene largely determines the membranous structure of the metathoracic wings, *apterous* is crucial for the formation of the coriaceous structure of the mesothoracic tegmina, whereas *sex comb reduced* represses the formation of wings in the prothorax.

Subgroup: Nutritional Signals in Insects

Insulin and insulin-like peptides interact with the insulin receptor, activating its signalling pathway and informing the organisms about their nutritional status. The main interest of our research line is to unveil how this nutritional signalling pathway regulates reproductive processes, particularly juvenile hormone production and vitellogenin synthesis. Our research subjects during 2014 and to the present include:

1. Regulatory effect of the insulin receptor pathway on longevity and starvation resistance

During 2014 we have evaluated the effect of the insulin receptor itself and that of the protein FoxO, the main transcriptional effector of the insulin receptor pathway, on longevity and starvation resistance. We have demonstrated that depletion of the activity of the insulin receptor pathway provides a higher resistance to starvation. The effects on longevity were more ambiguous.

2. Insulin-like peptides (ILPs)

During 2014 we continued our studies in order to understand the function of the seven different ILPs identified in *B. germanica*. We are interested in the relationships between each of the ILPs and the processes of juvenile hormone production, and vitellogenin synthesis. Until now, and according to preliminary results, our hypothesis is that only one of the ILPs is responsible for activating juvenile hormone production and that the other ones, although their expression may be regulated by juvenile hormone levels, play different functions.

3. Orkokinin function in insects

We have also investigated the function of two peptide families, OKA and OKB, on cockroach reproduction. Our results show that OKB peptides are involved in the regulation of vitellogenin synthesis directly in the fat body.

Publications 2014

ISI Articles

Abrisqueta, M., Süren-Castillo, S., Maestro, J.L. 2014. Insulin receptor-mediated nutritional signalling regulates juvenile hormone biosynthesis and vitellogenin production in the German cockroach. *Insect Biochemistry and Molecular Biology* 49: 14-23.

Bellés, X., Santos, C.G. 2014. The MEKRE93 (Methoprene tolerant-Krüppel homolog 1-E93) pathway in the regulation of insect metamorphosis, and the homology of the pupal stage. *Insect Biochemistry and Molecular Biology* 52: 60-68.

Lozano, J., Bellés, X. 2014. Role of Methoprene-tolerant (Met) in adult morphogenesis and in adult ecdysis of *Blattella germanica*. *PLOS ONE* 9 (7): e103614.

Lozano, J., Kayukawa, T., Shinoda, T., Bellés, X. 2014. A role for taiman in insect metamorphosis. *PLoS Genetics* 10 (10): e1004769.

Patiño-Navarrete, R., Piulachs, M.D., Bellés, X., Moya, A., Latorre, A., Peretó, J. 2014. The cockroach *Blattella germanica* obtains nitrogen from uric acid through a metabolic pathway shared with its bacterial endosymbiont. *Biology Letters* 10 (7). pii: 20140407.

Süren-Castillo, S., Abrisqueta, M., Maestro, J.L. 2014. FoxO is required for the activation of hypertrehalosemic hormone expression in cockroaches. *Biochimica et Biophysica Acta: General Subjects* 1840: 86-94.

Fig. 3: *From right to left, normal sixth (last) instar male nymph, supernumerary (seventh) instar male nymph obtained after depleting E93 expression by RNAi in the last nymphal instar, and normal adult* B. germanica *male (Bellés and Santos, 2014).*

Photo: *Carolina G. Santos and Xavier Bellés*

Funded Projects

- **Project Title:** Global change and physiological diversity
  Finaced by: International Laboratory of Global Change (LINC Global), CSIC and Pontificia Universidad Católica de Chile
  Years: 2008-2014
  PIs: Xavier Bellés (España) and Francisco Bozinovic (Chile)

- **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:** Nutritional signals and reproduction in insects. Role of the transcription factor FoxO
  Finaced by: MINECO (BFU2010-15906)
  Years: 2011-2014
  PI: José Luis Maestro Garriga

group INSECT REPRODUCTION

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

group members

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

Nashwa Elshaer, PhD Student, JAEPRE-CSIC Fellowship
Carlos Vásquez, PhD Student, CONICYT Fellowship Contract
Elena Navas, Graduate Student, Universitat de Vic
Guillem Ylla, Bioinformatician, Project Contract
Nuria Sánchez, Lab Manager, Project Contract

Research Outline

In our group, we aim at understanding 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 between insects. The next step in our research will be to study how to regulate the function of these genes and which are the relationships between them that allow the proper development of the oocyte. Comparison of the results obtained with those already described in other, more modified insect species, suggests that some functions are conserved in evolution, although the regulation of these functions could have changed.

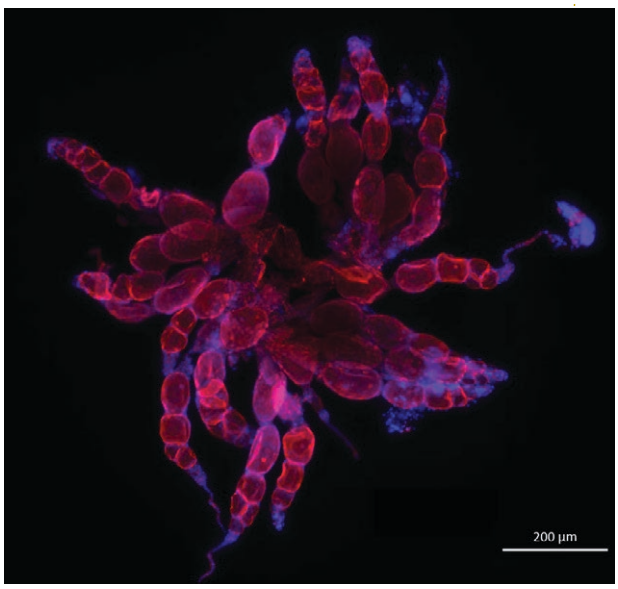


Fig. 1: *Ovary from* Blattella germanica *fifth instar nymph. Blue: DNA stained by DAPI, red: actins stained by TRITC.*
Photo: *Paula Irles and M. Dolors Piulachs*

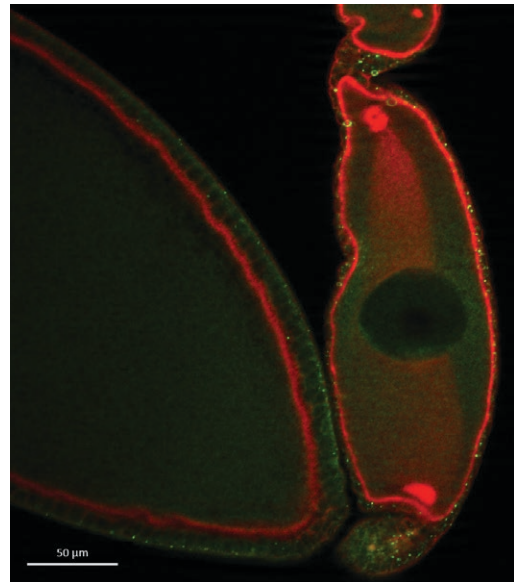
Research Lines

During the last year our research has focused on two main subjects, using *B. germanica* as 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 steps 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 conserved or has changed in the transition from the panoistic to the meroistic ovarian type.

Fig. 2: *Sub-basal ovarian follicles from* Blattella germanica *sixth instar nymph, showing the network of actins connecting the oocyte poles. Green: immunolocalization of epidermal growth factor receptor (EGFR), red: actins stained by TRITC.*
Photo: *Nashwa Elshaer and M. Dolors Piulachs*



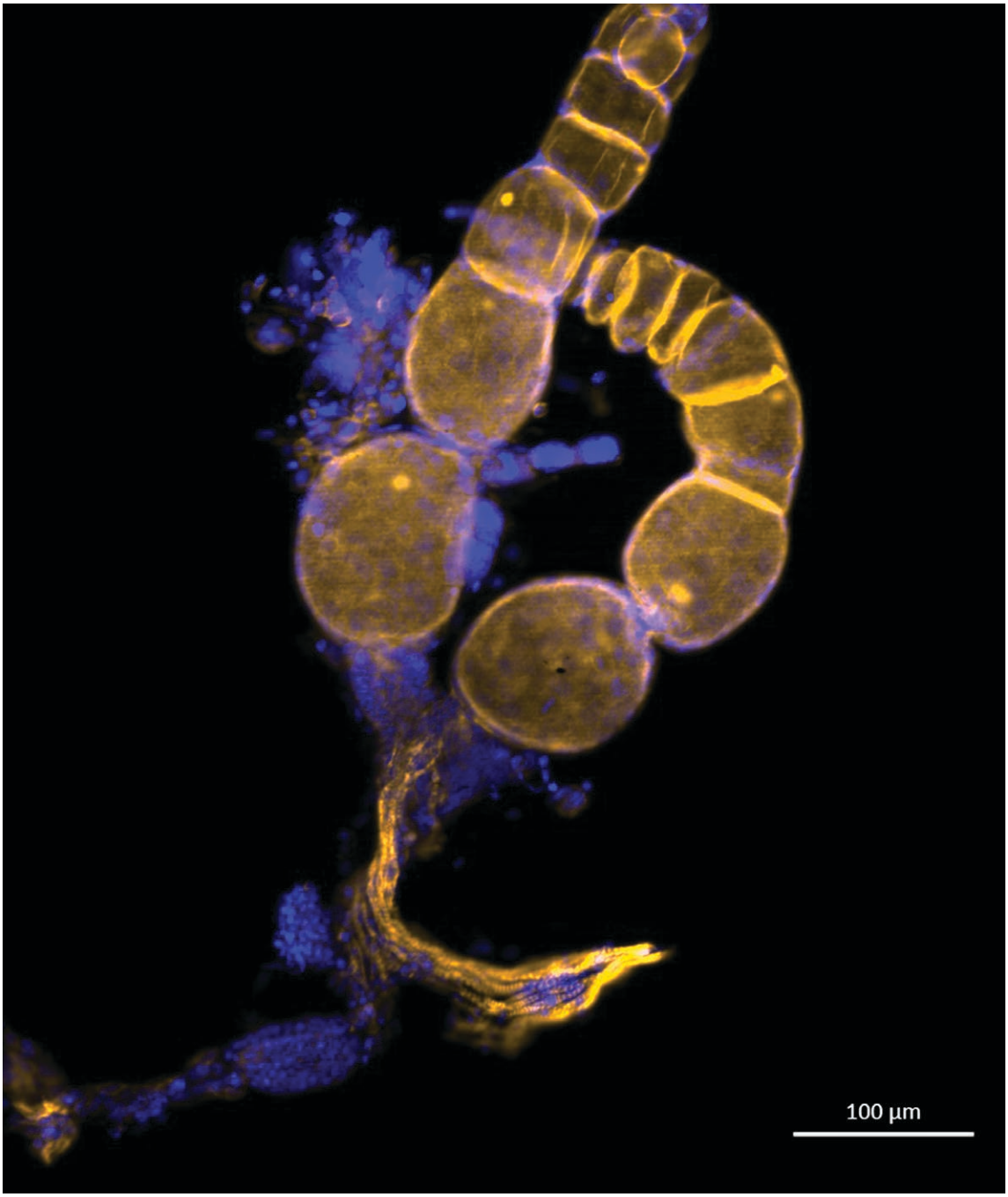


Fig. 3: *Ovarioles from* Blattella germanica *fifth instar nymph. Blue: DNA stained by DAPI, yellow: actins stained by TRITC.*

Photo: *Paula Irles and M. Dolors Piulachs*

2. Studying the regulation of cell proliferation during oogenesis.

The rate between cell proliferation and cell death is a critical parameter determining tissue growth, and the Hippo pathway is crucial to understand the dynamics of the growth process. Understanding the regulation of the Hippo pathway is important to study not only how do cells proliferate, but also how do they avoid overproliferation, which could lead to tumorigenesis. Our objective has been to study the Hippo pathway and its relationships with EGFR and Notch signaling 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 the 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 2014

ISI Articles

Herraiz, A., Bellés, X., Piulachs, M.D. 2014. Chorion formation in panoistic ovaries requires windei and trimethylation of histone 3 lysine 9. *Experimental Cell Research* 320: 46-83.

Irles, P., Piulachs, M.D. 2014. Unlike in Drosophila meroistic ovaries, Hippo represses Notch in Blattella germanica panoistic ovaries, triggering the mitosis-endocycle switch in the follicular cells. *PLOS ONE* 9 (11): e113850.

Patiño-Navarrete, R., Piulachs, M.D., Bellés, X., Moya, A., Latorre, A., Peretó, J. 2014. The cockroach *Blattella germanica* obtains nitrogen from uric acid through a metabolic pathway shared with its bacterial endosymbiont. *Biology Letters* 10 (7). pii: 20140407.

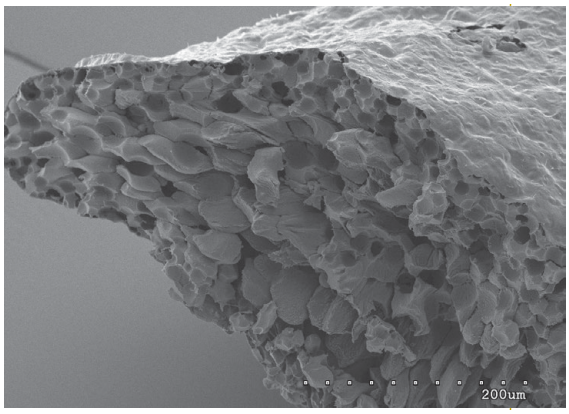


Fig. 4: Blattella germanica *oocyte observed at the scanning microscope. The oocyte was broken to show the distribution of the yolk platelets.*

Photo: *Nashwa Elshaer and M. Dolors Piulachs*

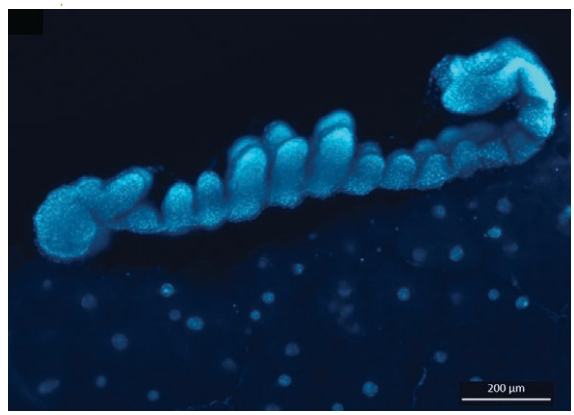


Fig. 5: Blattella germanica *4-day-old embryo stained with DAPI.*

Photo: *Paula Irles and M. Dolors Piulachs*

Funded Projects

- **Project Title:** Searching the origin of oocyte polarization in insects
  Financed by: MINECO
  Years: 2012-2014
  PI: M. Dolors Piulachs

- **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

Fig. 6: *Ovarioles from* Blattella germanica *sixth instar nymph. Green: Fasciclin III, DNA stained by DAPI, red: actins stained by TRITC.*

Photo: *Paula Irles and M. Dolors Piulachs*

group MULTICELL GENOME

First row, from left to right:
Helena Parra, Núria Sánchez, Azusa Nakata

Second row, from left to right:
David López-Escardó, Meritxell Antó, Matija Harcet, Arnau Sebé-Pedrós, Sebastián Najle, Iñaki Ruiz-Trillo

group members

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

Arnau Sebé-Pedrós, Postdoctoral Researcher
Hiroshi Suga, Postdoctoral Researcher
Matija Harcet, Marie Curie Postdoctoral Researcher
Sebastián Najle, Postdoctoral Researcher
Alex de Mendoza, PhD Student
David López-Escardó, PhD Student
Guifré Torruella, PhD Student
Helena Parra, PhD Student
Núria Ros, PhD Student
Xavier Grau-Bové, PhD Student
Meritxell Antó, Research Technician

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.

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

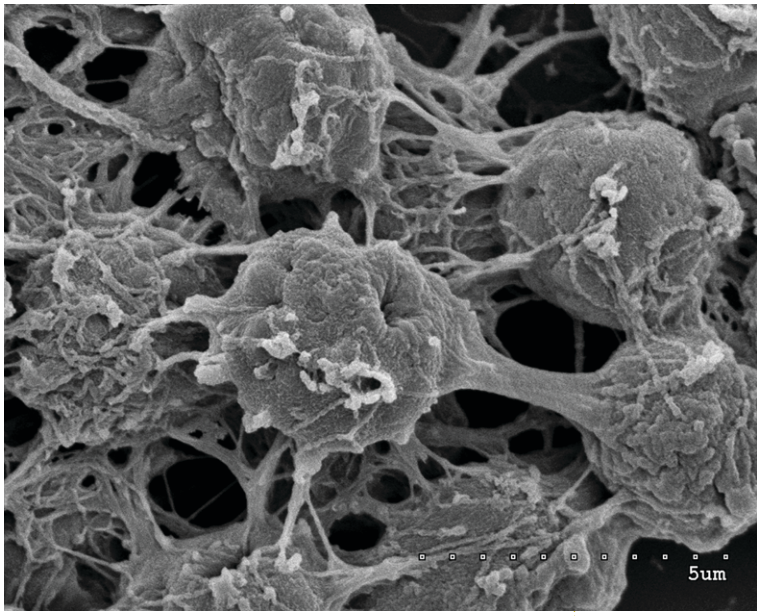


Fig. 1: *Capsaspora owczarzaki (Filasterea) SEM microscopy image; aggregative multicellular stage.*

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 analysing 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 aim, we are part of the UNICORN (UNICellular Opisthokonts at Broad). 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 analysed 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 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. Unraveling 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-signaling and cell-adhesion genes played in the origin of Metazoa.

To make this happen 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 of the opisthokonts (i.e., the clade that comprises Metazoa, Fungi and their closes 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 the most taxon-rich phylogenomic analysis of the opisthokonts.

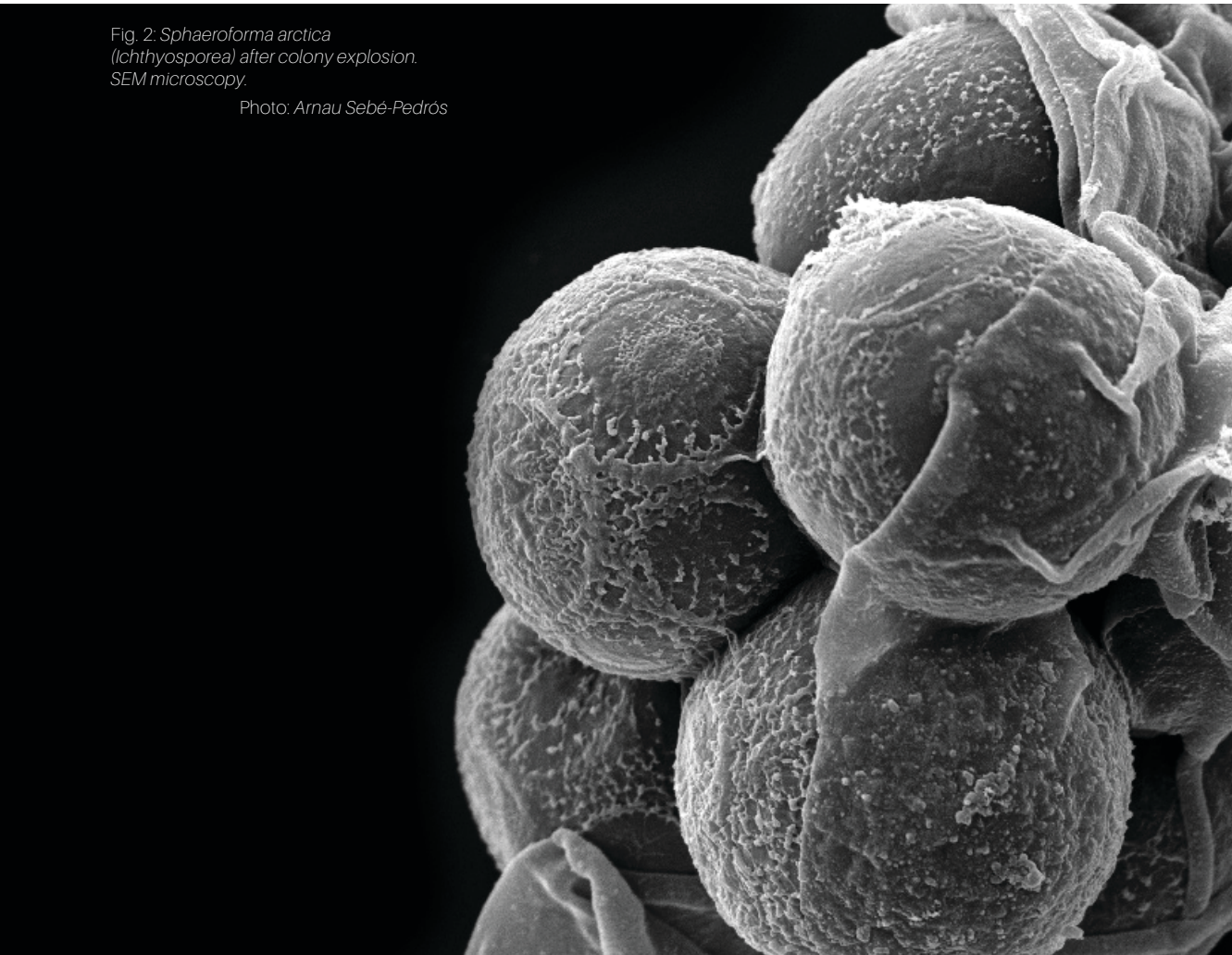
Publications 2014

ISI Articles

de Mendoza, A., and Ruiz-Trillo, I. 2014. Forward genetics for back-in-time questions. *eLife* 3: e04070.

de Mendoza, A., Sebé-Pedrós, A., and Ruiz-Trillo, I. 2014. The evolution of the GPCR signalling system in eukaryotes: modularity, conservation and the transition to metazoan multicellularity. *Genome Biology and Evolution* 6 (3): 606-19.

Fig. 2: *Sphaeroforma arctica (Ichthyosporea) after colony explosion. SEM microscopy.*
Photo: *Arnau Sebé-Pedrós*



del Campo, J., Sieracki, M.E., Molestina, R., Keeling, R., Massana, R., and Ruiz-Trillo, I. 2014. The others: our biased perspective of eukaryotic genomics. *Trends in Ecology and Evolution* 29 (5): 252-259.

Desvoyes, B., de Mendoza, A., Ruiz-Trillo, I., and Gutierrez, C. 2014. Novel roles of plant RETINOBLASTOMA-RELATED (RBR) protein in cell proliferation and asymmetric cell division. *Journal of Experimental Botany* 65 (10): 2657-66.

Schultheiss, K.P., Craddok, B.P., Suga, H., and Miller, W.T. 2014. Regulation of Src and Csk Nonreceptor Tyrosine Kinases in the Filasterean Ministeria vibrans. *Biochemistry* 53 (8): 1320-1329.

Sebé-Pedrós, A., Grau-Bové, X., Richards, T.A., and Ruiz-Trillo, I. 2014. Evolution and classification of myosins, a paneukaryotic whole genome approach. *Genome Biology and Evolution* 6 (2): 290-305.

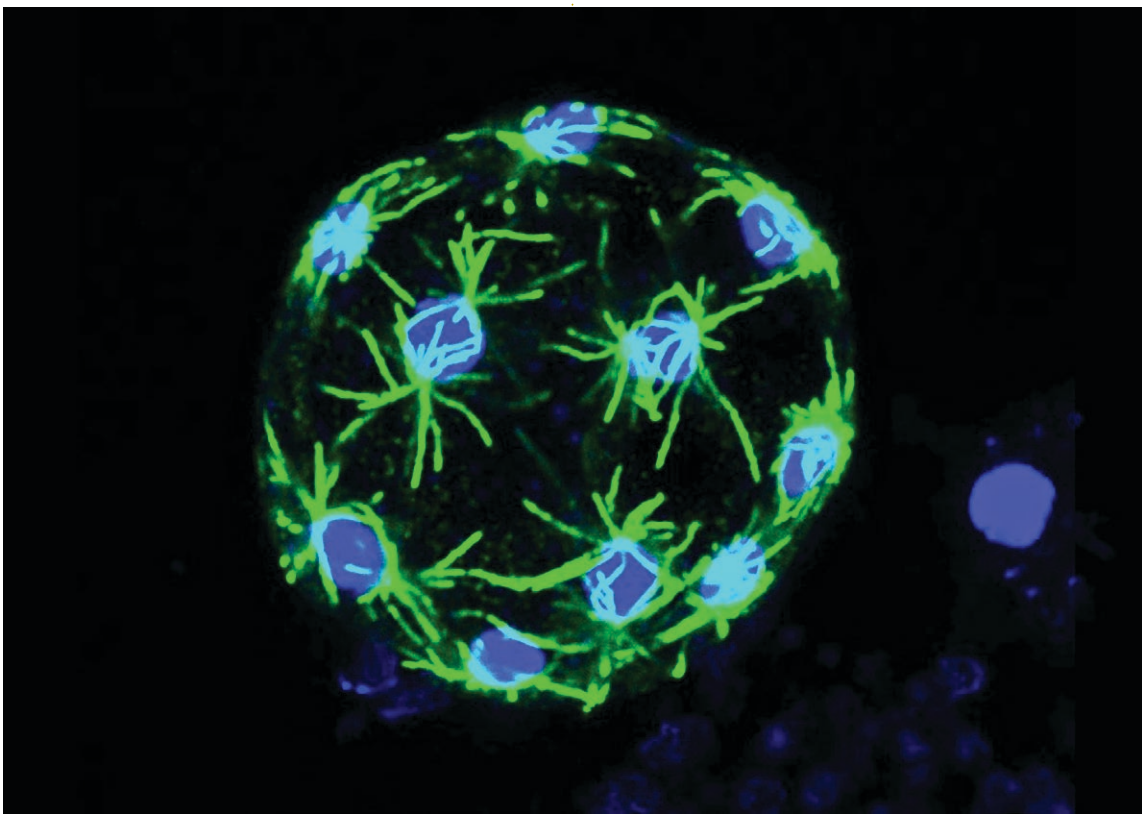
Suga, H., Torruella, G., Burger, G., Brown, M.W., and Ruiz-Trillo, I. 2014. Earliest holozoan expansion of phosphotyrosine signaling. *Molecular Biology and Evolution* 31 (3): 517-528.

Other Publications

Riutort, M., Paps, J., and Ruiz-Trillo, I. 2014. *Bilaterians. The Evolutionary Advantage of Being Two-Sided.* In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates.

Rodríguez-Ezpeleta, N., Moreira, D., and Ruiz-Trillo, I. 2014. *The Former "Protists". Amoebozoa, Rhizaria, Excavata, Haptophyta, Cryptophyta, Heterokonta, and Alveolata.* In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates.

Torruella, G., Moreira, D., and Ruiz-Trillo, I. 2014. *The Domain Eucarya. The Rise of Organisms with Nucleated Cells.* In: Vargas, P. and Zardoya, R. (Eds) *The tree of life*. Sinauer Associates.



Funded Projects

- **Project Title:** El origen del reino animal: un análisis genómico, filogenómico y de biodiversidad de los linajes unicelulares más cercanos a los animales
  Financed by: Ministerio de Ciencia e Innovación
  Years: 2012-2014
  PI: Iñaki Ruiz-Trillo

- **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

Fig. 3: *Sphaeroforma arctica (Ichthyosporea) confocal microscopy, stained with DAPI and tubulin. 3D projection.*

PROGRAM

POPULATION GENETICS

Research groups

Evolutionary Population Genetics Group
Elena Bosch, *Group Leader*

Evolutionary Systems Biology Group
Jaume Bertranpetit, *Group Leader*

Genomics of Individuallity Group
Francesc Calafell, *Group Leader*

Human Genome
David Comas, *Group Leader*

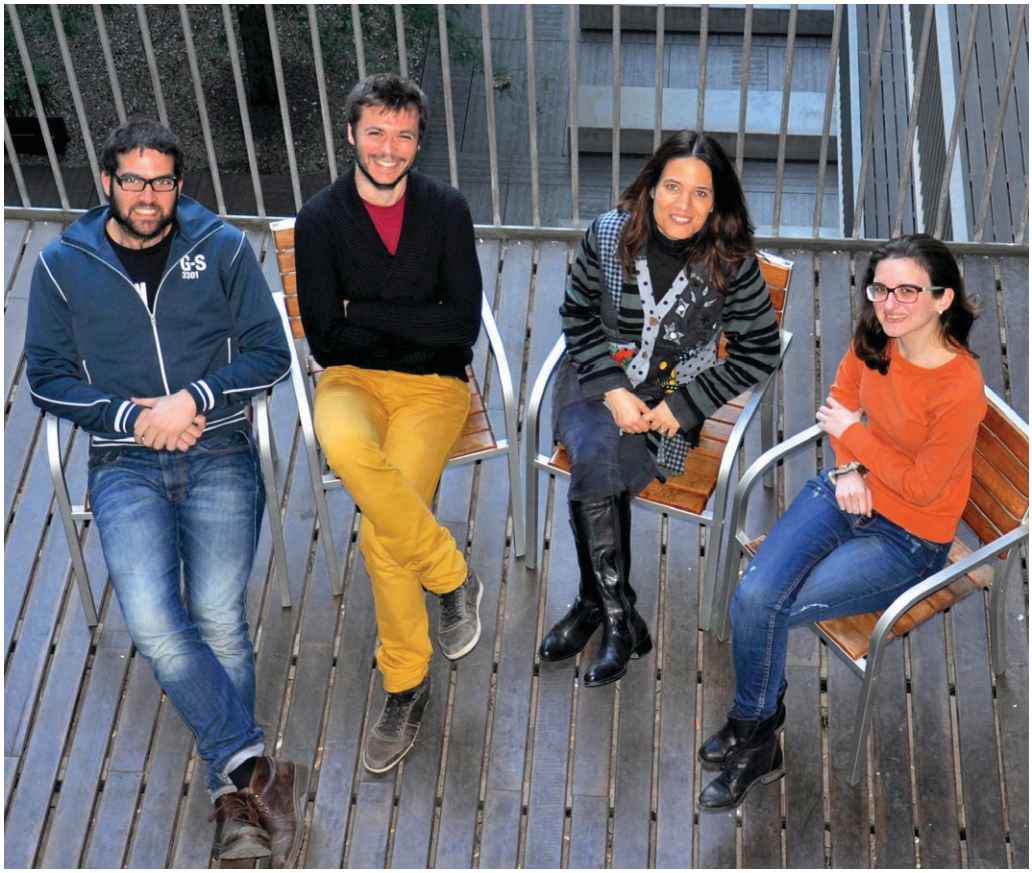
Subgroups

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 Rodríguez, Nino Spataro, Elena Bosch, 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 unraveling the genetic contribution to them.

Research Lines

1. Recent human adaptation and immunity

We are experimentally testing a number of functional variants for candidate genes related to immunity which do show signatures of recent adaptation in human populations, possibly as an adaptive response to pathogen interaction. As an example, we have identified a non-synonymous polymorphism in the human ZIP4 transporter with a strong geographical population differentiation. Further, we speculate that the reduced zinc uptake we detected for the derived variant may have been advantageous in Sub-Saharan Africa, possibly by reducing access of a geographically restricted pathogen to this micronutrient.

2. 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 describe the interplay between genetic variation, mRNA and protein expression, together with trace elements content in different human tissue samples in order to gain insight into possible adaptive responses to nutrient availability and diet changes occurred in our past.

3. Role of selection in coding and non-coding regions of the genome

We are analyzing sequence data at both intraspecific and interespecific levels in order to investigate the role of natural selection in all coding and regulatory elements of particular gene pathways. This project is done in collaboration with Arcadi Navarro (Evolutionary Genomics Lab) and with Hernán Dopazo (Centro de Investigación Príncipe Felipe, Valencia).

4. Natural selection on human disease genes

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

5. 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. From targeted sequencing data in multiple individuals we are also detecting and characterizing structural variants on different Mendelian and susceptibility genes for Parkinson.

Publications 2014

ISI Articles

Cenit, M.C., Martínez-Florensa, M., Consuegra, M., Bonet, L., Carnero-Montoro, E., Armiger, N., Caballero-Baños, M., Arias, M.T., Benitez, D., Ortego-Centeno, N., de Ramón, E., Sabio, J.M., Garcia-Hernádez, F.J., Tolosa C., Suárez, A., González-Gay, M.A., Bosch, E., Martín, J., Lozano, F. 2014. Analysis of Ancestral and Functionally Relevant CD5 Variants in Systemic Lupus Erythematosus Patients. *PLOS ONE* 9 (11): e113090.

Engelken, J., Carnero-Montoro, E., Pybus, M., Andrews, G.K., Lalueza-Fox, C., Comas, D., Sekler, I., de la Rasilla, M., Rosas, A., Stoneking, M., Valverde, M.A., Vicente, R., and Bosch, E. 2014. Extreme Population Differences in the Human Zinc Transporter ZIP4 (SLC39A4) are Explained by Positive Selection in Sub-Saharan Africa. *PLoS Genetics* 10 (2): e1004128.

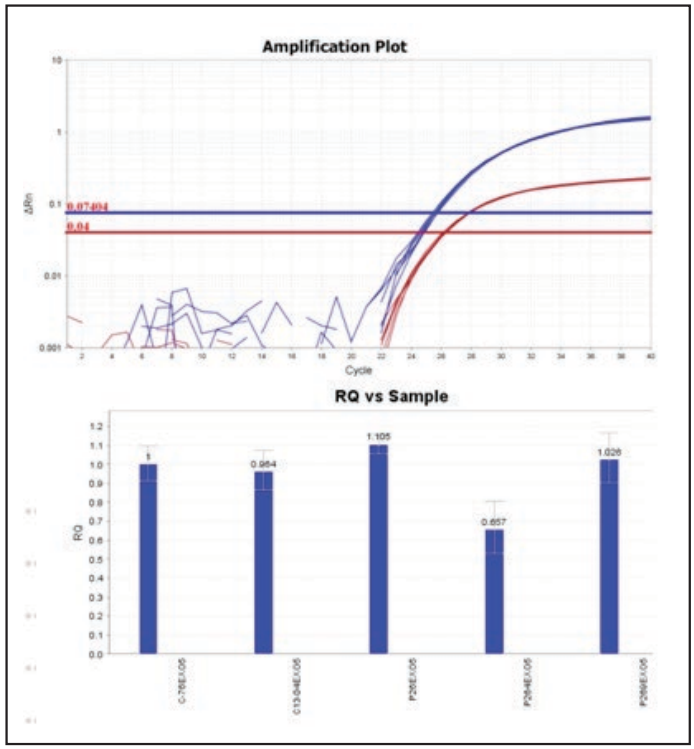


Fig. 1: *Real time analysis of gene copy number differences with Taqman probes.*

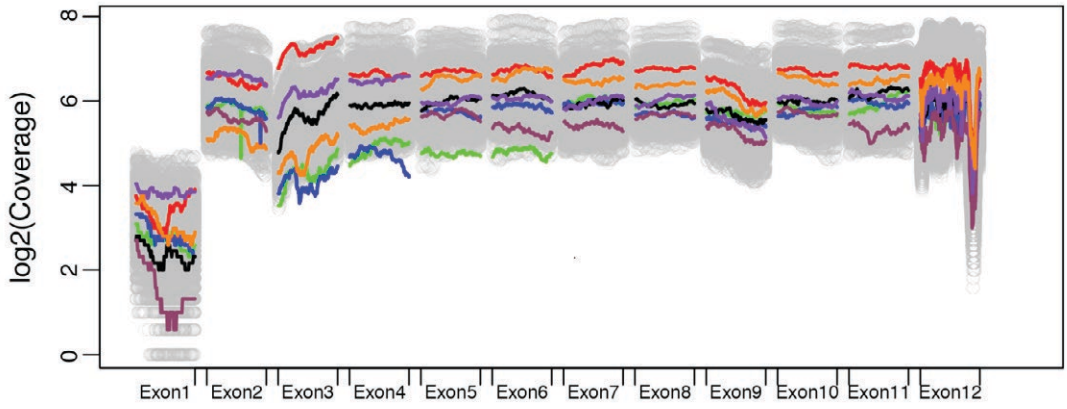


Fig. 2: *Structural variation on the PARK2 gene detected from regional coverage differences after targeted sequencing on multiple individuals.*

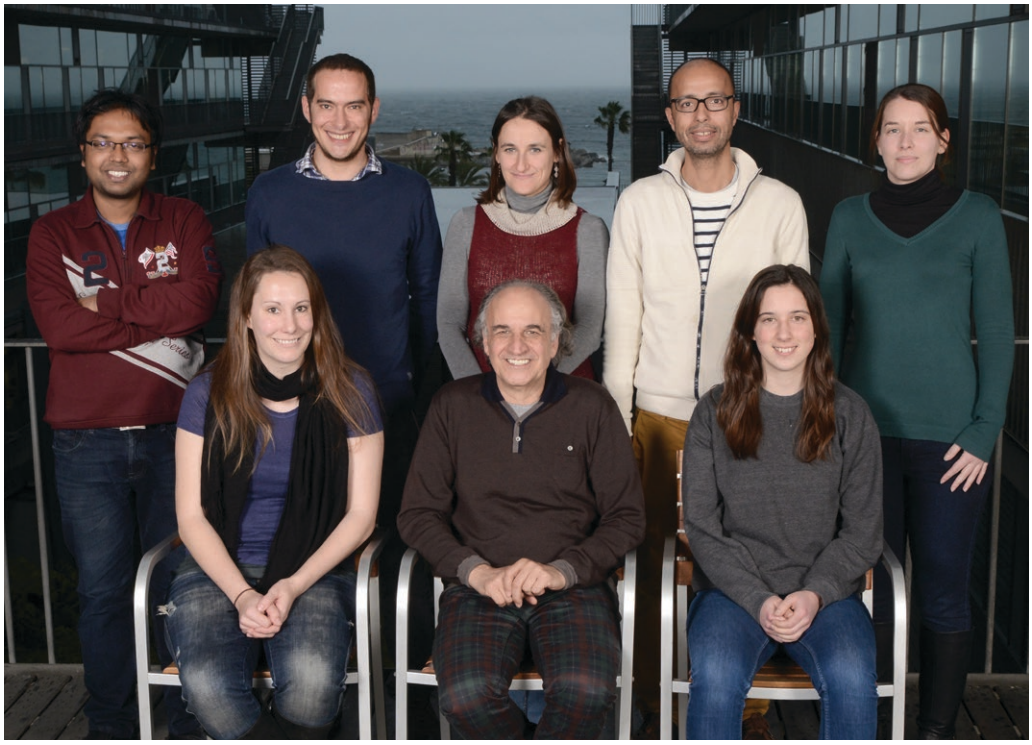
Funded Projects

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

- **Project Title:** Variantes genéticas raras en la enfermedad de Parkinson: Aproximación evolutiva y re-secuenciación de alto rendimiento
  Financed by: Subdirección General de Proyectos de Investigación (SAF2011-29239)
  Years: 2012-2014
  PI: Elena Bosch

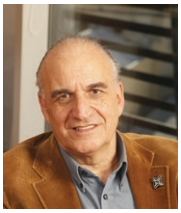

PRH
ASC
AGC Group
PVC RESIN
ASNYL
FJ - 65R
Net Weight : 25 kg
PT. Asahimas Chemical
Banten - Indonesia

group EVOLUTIONARY SYSTEMS BIOLOGY



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

group members



Jaume Bertranpetit, *Group Leader*
Professor, UPF

Hafid Laayouni, Senior Scientist, UPF Contract
Ludovica Montanucci, Postdoctoral, Juan de la Cierva Contract
Brandon Invergo, PhD Student, FI Scholarship, Generalitat de Catalunya
Giovanni Dall'Olio, PhD Student, FI Scholarship, MICINN
Marc Pybus, PhD Student, FI Scholarship, MICINN
Pierre Luisi, PhD Student, ISCIII Scholarship
Mayukh Mondal, PhD Student, FI Scholarship, Generalitat de Catalunya
Begoña Dobón Berenguer, Master Student from UPF

Research Outline

Our present 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 by genome wide analyses of the footprints that natural selection has left in the genomes after its action and not only detecting single signals (in one specific gene or genome region) but trying to put 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.

The action of selection is measured and understood beyond single lists of genes, and integrated in molecular physiological pathways or networks and the aim is, in a given pathway, to understand the complex basis of adaptation and how networks have been shaped by natural selection. At the end we are trying to uncover rules and laws in the action of selection in its primary source: the molecular action.

As a huge amount of genomic information is being produced for humans, there are ample possibilities of studying differential adaptation among human populations, as different human groups have been adapting in different environments; this is the intra-specific level of analysis of natural selection. Moreover, genomic information is being produced for other species, allowing increasing possibilities of understanding differential adaptation of different species and opening the possibility of asking a key question: which has been the adaptive history of a given species, say humans?
This question may allow tackling the intriguing questions of which are the genome bases for our own (or any other) species.

We also have ongoing work in understanding recombination and in reconstructing population history by studying human genetic diversity.
We are collaborating with David Comas in human population studies, including studies of India and Sudan; and with Tomàs Marquès-Bonet on detecting selection in the genome of apes.

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 genetic 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) that will be population-specific (in the case of human diversity) or species-specific (in the case of genetic divergence). The action of selection is measured and understood not in terms of single lists of genes, but integrated in molecular physiological pathways or networks and the aim is, in a given pathway, to understand the complex basis of adaptation and how networks have been shaped by natural selection. Indeed to understand the complex basis of adaptation it is necessary to integrate the knowledge derived from evolutionary studies into a network framework since biological function is the result of a large number of interacting molecules organized in complex networks and arises as an emergent property from a combined effect of many different genes. The final goal is, on 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.

Data is either retrieved from pre-existing databases (HapMap or 1000genomes project) or produced (*Immunochip*, WGS Illumina chip or whole genome sequences). We are collaborating with colleagues that produce new data that may be analyzed trough our pipelines.

For the analysis of selection among humans (intra-specific), we have developed a pipeline for the detection of positive selection that calculates 21 tests and, through simulation, are integrated in a machine-learning algorithm (boosting) that produces a single score for specific selection footprints. The goal is to produce a map of positive selection in the human genome for three populations (Europe, Asia and Africa) that will be used afterwards for other studies, mainly for the analysis of ape genomes.

Among primates and mammals we have produced a pipeline of analysis of selection that may be used either for studying positive selection or for purifying selection.

The pathways that we have analyzed are: N-glycosylation pathway; innate immunity; phototransduction; obesity through adiposity signals; and the whole human metabolome. Special attention has been put in the quality of databases for metabolic pathways, as their quality is worse than most studies assume and manual curation is needed in all cases.

We are also trying to go beyond the topology of pathways and go into the modeling and the dynamics of the molecular biological systems.

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 whole genome sequences for 70 individuals. In collaboration with Mihai Netea (Nijmegen Medical Center, The Netherlands) we have studied adaptation in Gypsies and Romanians, in a project that now includes whole genome sequences.

Publications 2014

ISI Articles

Colonna, V., Ayub, Q., Chen, Y., Pagani, L., Luisi, P., Pybus, M., Garrison, E., Xue, Y., Tyler-Smith, C. 2014. Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. *Genome Biology* 15 (6): R88.

Colombo, M., Laayouni, H., Invergo, B.M., Bertranpetit, J., and Montanucci, L. 2014. Metabolic flux is a determinant of the evolutionary rates of enzyme-encoding genes. *Evolution* 68 (2): 605-613.

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Julià, A., Domènech, E., Chaparro, M., García-Sánchez, V., Gomollón, F., Panés, J., Mañosa, M., Barreiro-De Acosta, M., Gutiérrez, A., Garcia-Planella, E., Aguas, M., Muñoz, F., Esteve, M., Mendoza, J.L., Vera, M., Márquez, L., Tortosa, R., López-Lasanta, M., Alonso, A., Gelpí, J.L., García-Montero, A.C., Bertranpetit, J., Absher, D., Myers, R.M., Gisbert, J.P., and Marsal, S. 2014. A genome-wide association study identifies a novel locus at 6q22.1 associated with ulcerative colitis. *Human Molecular Genetics* 23 (25): 6927-34.

Juyal, G., Mondal, M., Luisi, P., Laayouni, H., Sood, Aj., Midha, V., Heutink, P., Bertranpetit, J., Thelma, B.K., and Casals, F. 2014. Population and genomic lessons from genetic analysis of two Indian populations. *Human Genetics* 133 (10): 1273-1287.

Laayouni, H., Oosting, M., Luisi, P., Ioana, M., Alonso, S., Ricaño-Ponce, I., Trynka, G., Zhernakova, A., Plantinga, T.S., Cheng, S., van der Meer, J.W.M., Popp, R., Sood, A., Thelma, B.K.,

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Pybus, M., Dall'Olio, G.M., Luisi, P., Uzkudun, M., Carreño-Torres, A., Pavlidis, P., Laayouni, H., Bertranpetit, J., and Engelken, J. 2014. 1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. *Nucleic Acids Research* 42 (D1): D903-D909.

Solé-Morata, N., Bertranpetit, J., Comas, D., and Calafell, F. 2014. Recent Radiation of R-M269 and High Y-STR Haplotype Resemblance Confirmed. *Annals of Human Genetics* 78 (4): 253-254.

Yamamoto, F., Cid, E., Yamamoto, M., Saitou, N., Bertranpetit, J., and Blancher, A. An integrative evolution theory of histo-blood group ABO and related genes. *Scientific Reports* 4: 6601.

Publications as part of The Genographic Consortium

Elhaik E, et al. 2014. Geographic population structure analysis of worldwide human populations infers their biogeographical origins. *Nature Communications* 5: 3513.

Clarke, A.C., Prost, S., Stanton, J.A., White, W.T., Kaplan, M.E., Matisoo-Smith, E.A., Genographic Consortium. 2014. From cheek swabs to consensus sequences: an A to Z protocol for high-throughput DNA sequencing of complete human mitochondrial genomes. *BMC Genomics* 15: 68.

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Vilar, M.G., Melendez, C., Sanders, A.B., Walia, A., Gaieski, J.B., Owings, A.C., Schurr, T.G., Genographic Consortium. 2014. Genetic diversity in Puerto Rico and its implications for the peopling of the Island and the West Indies. *American Journal of Physical Anthropology* 155 (3): 352-68.

Non ISI

Bertranpetit, J. 2014. Sydney Brenner's Gift to Science. Laudatio of Professor Sydney Brenner as Doctor Honoris Causa. Universitat Pompeu Fabra.

Bertranpetit, J. 2014. Reptes de país: La Universitat i la Recerca. Diari ARA.

Bertranpetit, J. 2014. Qüestions d'estat. Reflexions per al país del futur. Seminari de Ciència. Publicacions de l'Institut d'Estudis Catalans.

Bertranpetit, J. 2014. Universities and research in Catalonia, the challenges that lie ahead. Catalan International View. An European Review of the World.

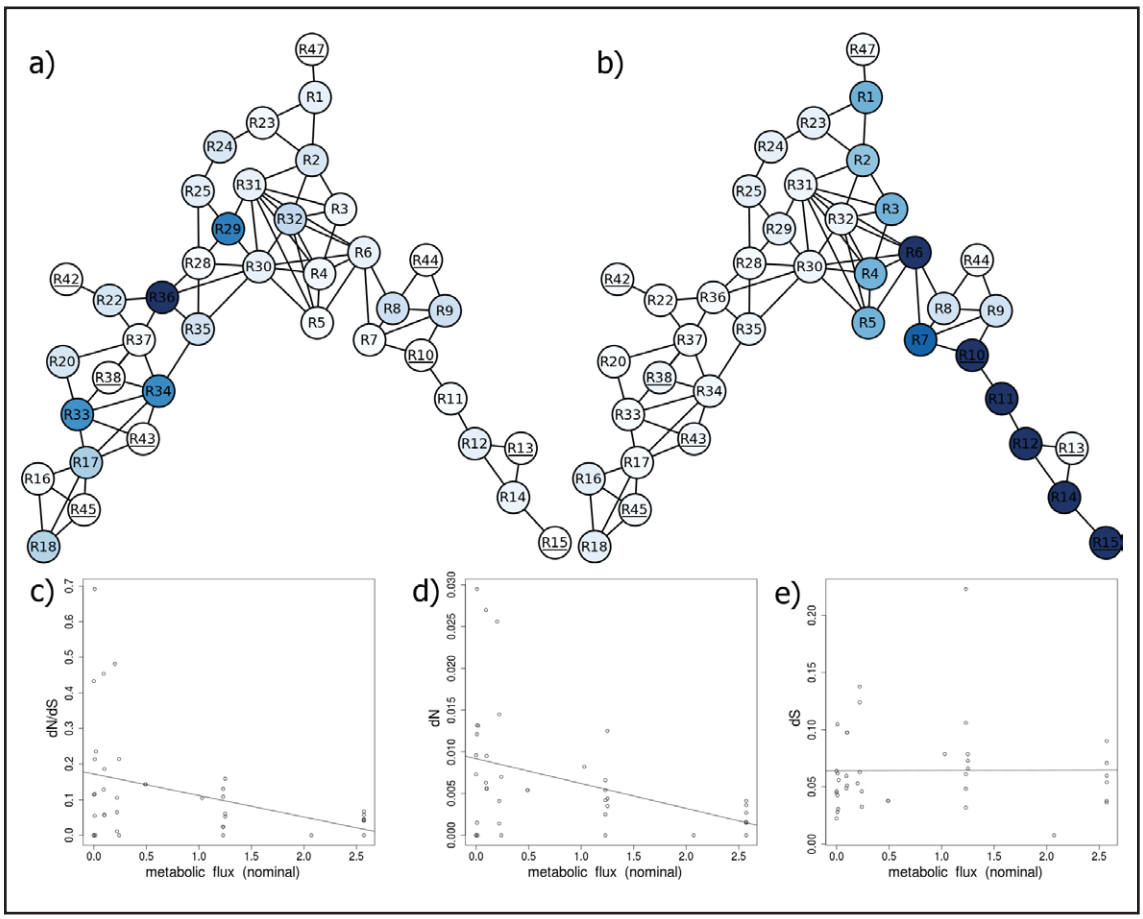
Fig. 1: Distribution of evolutionary rates and flux over the reaction graph.
a) Reaction graph of the erythrocyte core metabolic network. Nodes represent reactions (the numbers on the nodes refer to the number of the reactions as listed in Supplementary Table S1 and S2), and edges represent the sharing of a common metabolite between two reactions. White nodes with underlined reaction names correspond to transport reactions (and therefore have no associated genes). Each node is colored according to the *dN/dS* ratios of the gene encoding the enzyme that catalyze the corresponding reaction. The color ranges from white (*dN/dS* equal to 0) to dark blue (*dN/dS* equal to 0.69)
b) Reaction graph colored according to a gradient of flux ranging from white (low flux, toward 0) to dark blue (high flux, toward the maximum value of 2.6). It can be seen that the region of the graph characterized by lower *dN/dS* values (node color toward white in figure a) are characterized by high values of flux (node color toward dark blue in figure b).
c) d) e) Scatter plot of evolutionary rates versus flux measures in the nominal condition: c) *dN/dS*; d) *dN*; e) *dS*.

Funded Projects

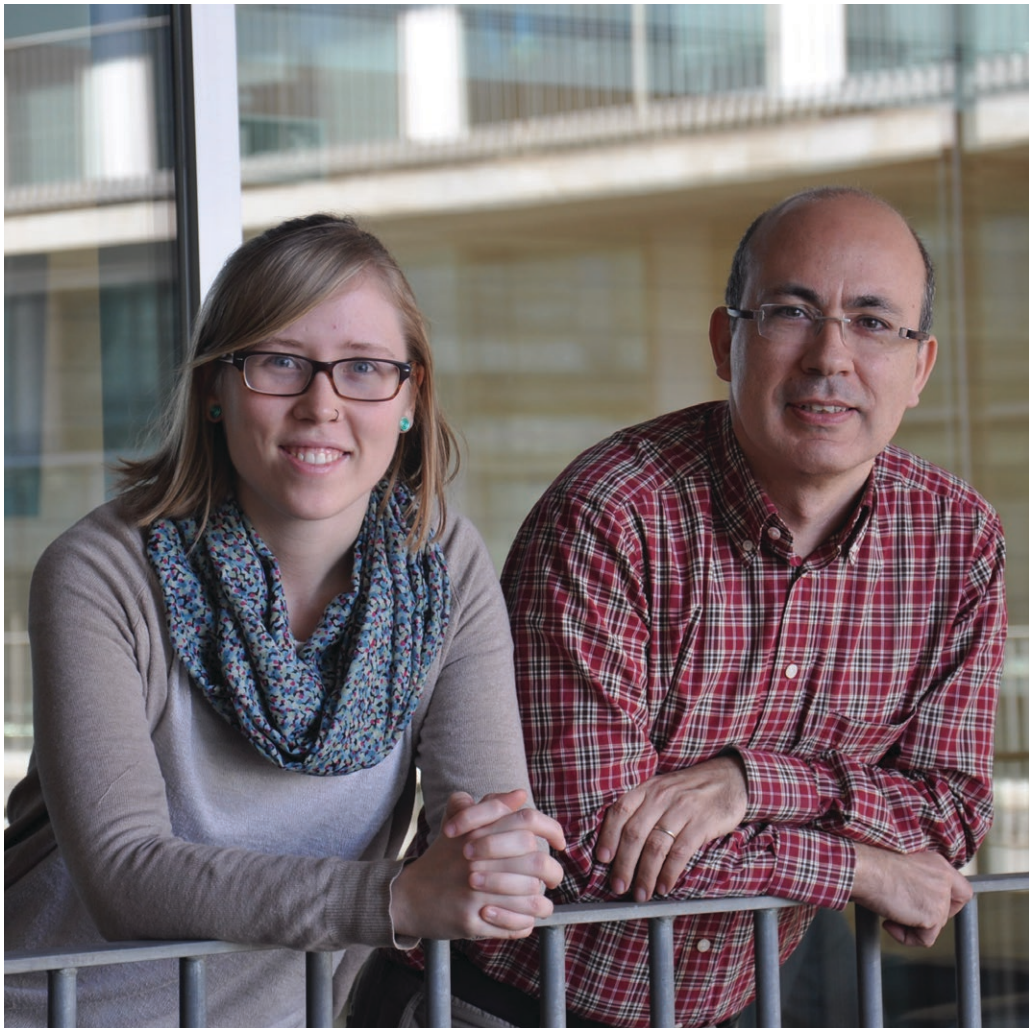
- **Project Title:** Detección y comprensión de las huellas de selección natural en el genoma de humanos y simios
  Financed by: Ministerio de Ciencia y Tecnología (BFU2013-43726-P)
  Years: 2014-2016
  PI: Jaume Bertranpetit

- **Project Title:** : Population genetic and functional analyses of maintenance of DNA sequence variability in response to infectious agents (human innate immune system and other responses)
  Financed by: MICINN acciones integradas con India
  Years: 2012-2014
  PI: Jaume Bertranpetit

- **Project Title:** : Human Population Genetics
  Financed by: Generalitat de Catalunya (Consolidate Research Group 2014 SGR 866)
  Years: 2014-2016
  PI: Jaume Bertranpetit



group GENOMICS OF INDIVIDUALITY



From left to right:
Neus Solé Morata, Francesc Calafell

group members

Francesc Calafell, *Group Leader*
Associate Professor, UPF

Neus Solé Morata, Support Personnel, UPF Contract

Research Outline

The general topics that interest us revolve around the genomics of individuality: what is there in our genomes that make us the way we are? What does it tell about our ancestry? How does it affect our susceptibility to diseases? How can this be applied in practical settings (i.e., in forensic genetics)? Lately, we have 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 the Y chromosome, which marks paternal lineages, and to another (cultural) marker of the same lineages, namely the surname.

Research Lines

1. A genetic atlas of Catalan surnames

Given their transmission, surnames behave as alleles at a locus in the Y chromosome, and they also carry linguistic, social, and historic information. We selected a list of 50 Catalan surnames and gathered ~50 men for each of those surnames, for a total sample of 2,550. We typed 17 Y-chromosome STRs and 68 SNPs in those samples, and we addressed the following questions: 1) How are surname frequency and genetic diversity related? The frequency of a surname may be the result of polyphiletism, namely, the fact that it may have been founded multiple times (think of *Smith* or *Jones*, John's son); in that case, surname frequency and its internal genetic diversity should be positively correlated. Alternatively, certain surnames may have become more common by natural

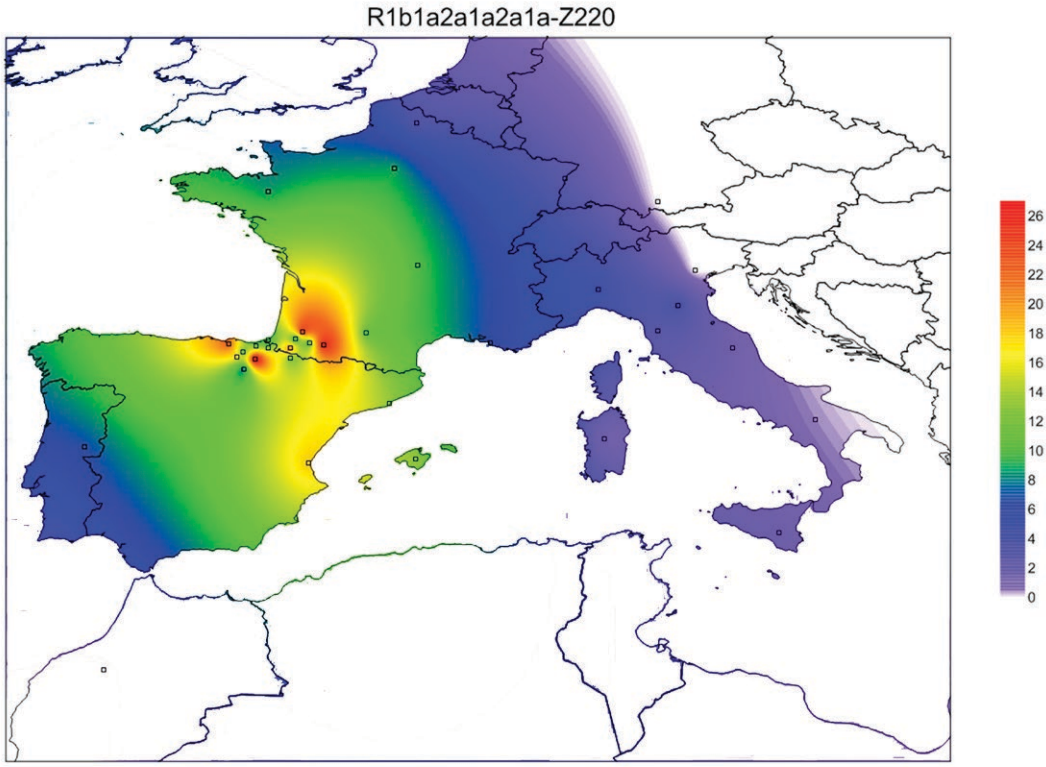


Fig. 1: *Estimated population frequencies (in percent) of haplogrup R1b-Z220 in Western Europe.*

selection: surnames may be markers of social status, which, quite often, determined survival and fertility. We have recently found that Catalan surnames follow the first model. 2) Were the carriers of German patronymic surnames of a different genetic origin from the rest of the population? In Catalonia, as in France, a frequent source of surnames is former first names of Germanic origin (Albert, Robert, Grau, etc).

We compared some of those to patronymic surnames of Latin origin (Oriol, Pons, etc), and found that they are not different from each other. 3) Is that also the case for ethnonym surnames? Some Catalan surnames (Alemany, Danés, Anglès, Guasch) denote geographic origin (they mean German, Dane, English, and Gascon, respectively). However, the Alemany or Danès Y chromosomes are much more similar to those of the general Catalan population than to those of Germans or Danes. 4) What is the probability of identifying the surname of the anonymous donor of a biological sample, in a forensic situation? What would be the false positive rate? The answers are 60% and 17%, and we found evidence that false positives may reveal an old surname in the same biological paternal lineage that subsequently changed by false paternity, adoption or transmission of the maternal surname.

This project is in collaboration with David Comas and Jaume Bertranpetit (IBE), and is mostly undertaken by Neus Solé.

2. Phylogeography of the Y chromosome in the Iberian Peninsula

The genetic diversity available in the Y chromosome can be arranged easily into a phylogenetic tree, with differences branches found with different frequencies and diversities in different populations. This pattern, called phylogeography, can be used to make inferences on the origin and dispersal of Y chromosome tree branches, and, more importantly, on the history of the populations carrying these Y chromosomes. 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. We are genotyping STRs and recently discovered SNPs in this branch in populations of Iberia, France and Italy, in order to trace the origin and history of this main branch of the Y chromosome diversity.

Publications 2014

ISI Articles

Džunková, M., Garcia-Garcerà, M., Martínez-Priego, L., D'Auria, G., Calafell, F., and Moya, A. 2014. Direct sequencing from the minimal number of DNA molecules needed to fill a 454 picotiterplate. *PLOS ONE* 9 (6): e97379.

Garcia-Etxebarria, K., Garcia-Garcerà, M., and Calafell, F. 2014. Consistency of metagenomic assignment programs in simulated and real data. *BMC Bioinformatics* 15: 90.

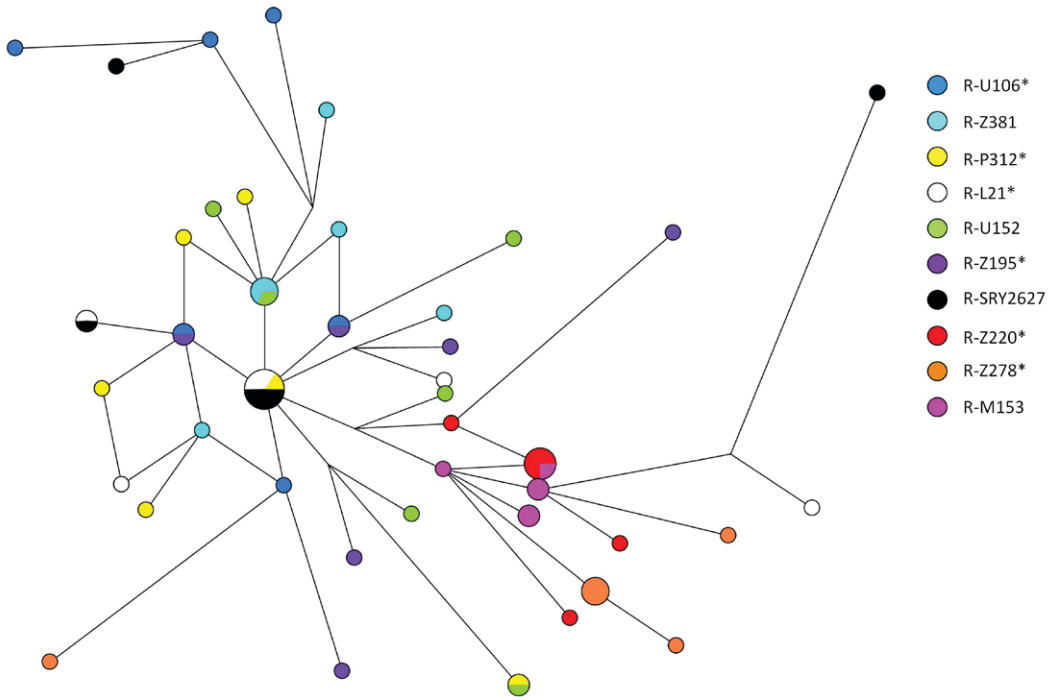
Solé-Morata, N., Bertranpetit, J., Comas, D., and Calafell, F. 2014. Recent Radiation of R-M269 and High Y-STR Haplotype Resemblance Confirmed. *Annals of Human Genetics* 78 (4): 253-254.

Funded Projects

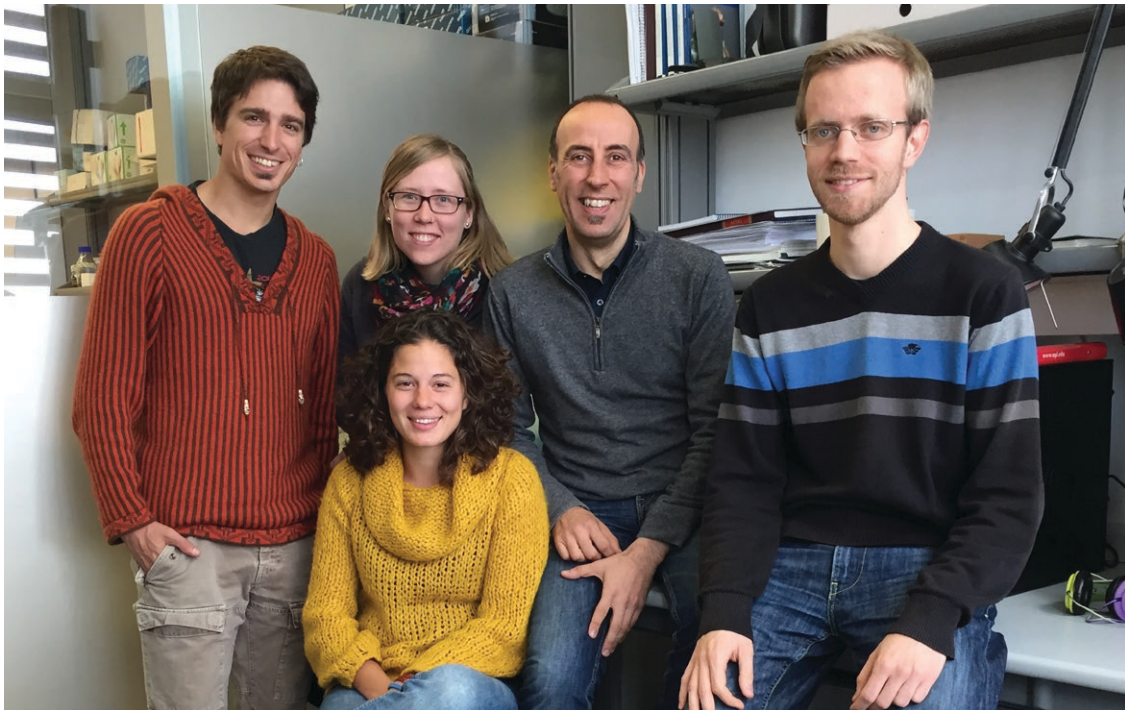
- **Project Title:** Grup de Recerca Consolidat-SGR
  Financed by: Generalitat de Catalunya (2014 SGR-866)
  Years: 2014-2018
  PI: Jaume Bertranpetit

- **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

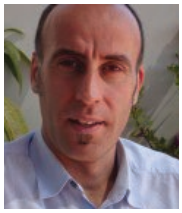
Fig. 2: *Network of haplotypes and carrying the Y-chromosome R1b-P312 haplogroup. Each circle represents a 17 Y-STR haplotype, and are connected by edges proportional to the number of mutations. Colors indicate subhaplogroups.*



group HUMAN GENOME



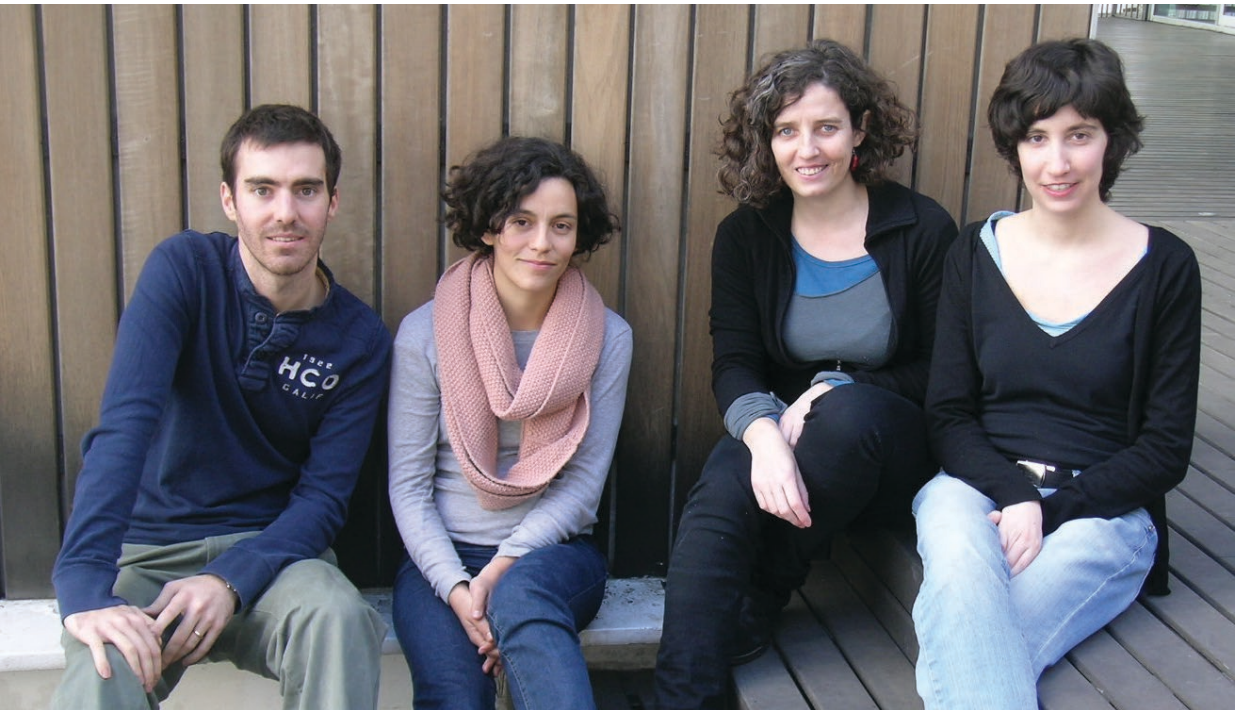
group members



David Comas, *Group Leader*
Associate Professor, UPF

Subgroup
Human Genome Diversity

David Comas, Associate Professor, UPF
Lara Rubio Arauna, PhD Student, UPF Scholarship
Neus Solé-Morata, PhD Student
Àlex Mas, Master Student, UPF
Gerard Serra, Master Student, UPF



From left to right:
Àlex Mas, Lara Rubio Araúna (sitting), Neus Solé-Morata, David Comas, Gerard Serra, Ignasi Torruella, Maria López-Valenzuela, Yolanda Espinosa-Parrilla, Ingrid Balcells, Alicia Gallego

Subgroup
microRNAs in Human Adaptation and Disease

Yolanda Espinosa-Parrilla, Visitor Professor, UPF

Alicia Gallego, PhD Student, FPU-MEC Scholarship

Ignasi Torruella, PhD Student, FPI-MINECO Scholarship

Maria López-Valenzuela, PhD Student, FI-AGAUR Scholarship

Research Outline

Our group is focused on the analysis of the human genome and closest related species in order to understand the processes that have modeled the extant genetic diversity of humans. We are interested in unraveling the demographic and adaptative processes that have given place 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**

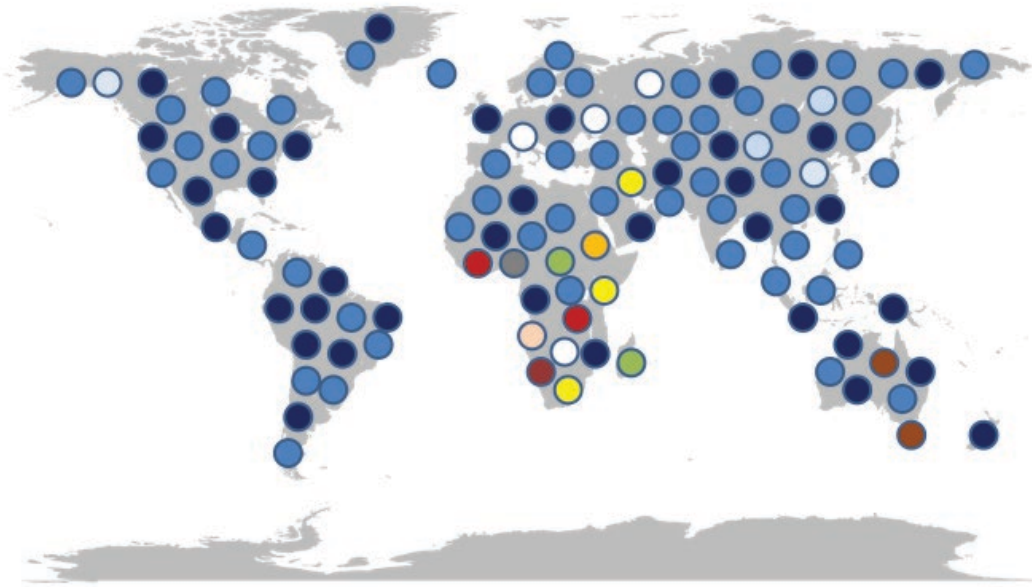
1. Involvement of microRNA related mechanisms in human disease susceptibility
2. Molecular evolution of microRNAs in primates

Publications 2014

ISI Articles

Ballantyne, K., Ralf, A., Aboukhalid, R., Achakzai, N.M., Anjos, J., Ayub, Q., Balažic, J., Ballantyne, J., Berger, B., Bobillo, C., Bouabdellah, M., Burri, H., Capal, T., Caratti, S., Cárdenas, J., Cartault, F., Carvalho, E.F., Carvalho, M., Cheng, B., Coble, M.D., Comas, D., Corach, D., D'Amato, M.E., Davison, S., et al. 2014. Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. *Human Mutation* 35 (8): 1021-1032.

Fig. 1: *Geographical representation of the human genome diversity. Color circles represent genetic variants in human populations. Sub-Saharan groups exhibit larger genome diversity due to our African origin and the larger effective population size of African groups.*



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Other Publications

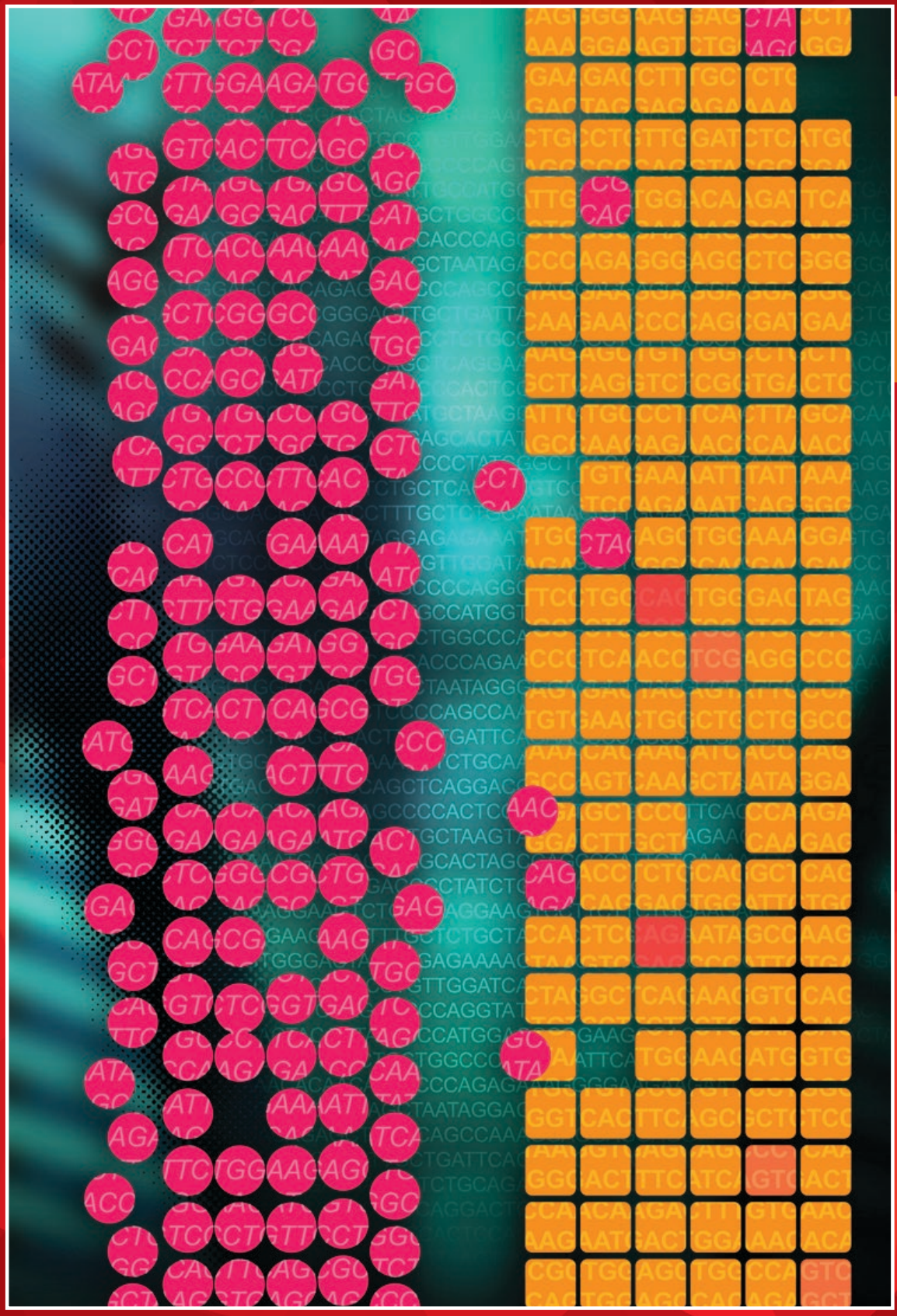
Comas, D. 2014. La genètica de les migracions humanes. *Mètode* 81: 41-47.

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:** Grup de Recerca Consolidat-SGR
  Financed by: Generalitat de Catalunya (2014 SGR-866)
  Years: 2014-2018
  PI: Jaume Bertranpetit



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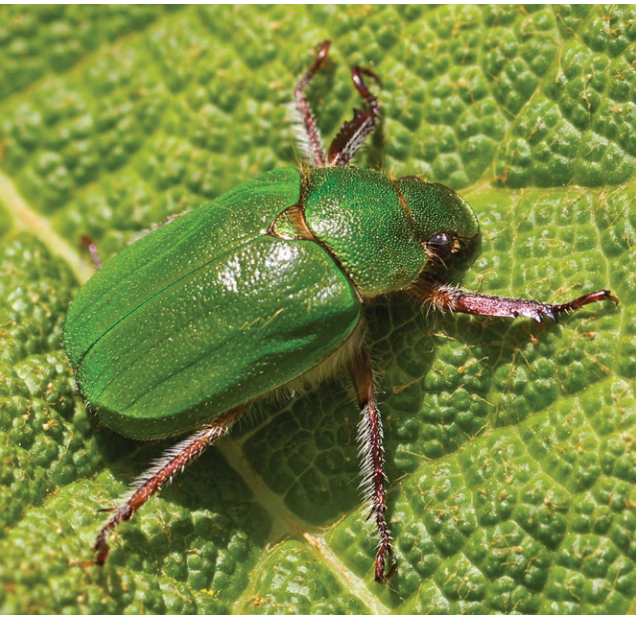

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Engelken, J., Carnero-Montoro, E., Pybus, M., Andrews, G.K., Lalueza-Fox, C., Comas, D., Sekler, I., de la Rasilla, M., Rosas, A., Stoneking, M., Valverde, M.A., Vicente, R., and Bosch, E. 2014. Extreme Population Differences in the Human Zinc Transporter ZIP4 (SLC39A4) are Explained by Positive Selection in Sub-Saharan Africa. *PLoS Genetics* 10 (2): e1004128.

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IBE HIGHLIGHTED PAPERS

Genome references from new species

One of the many benefits of the affordable cost of genome sequencing is the application of comparative genomics to a set of species that are recognized as model organisms (i.e. Marmoset) or species with traits of specific interest (i.e bone formation in elephant shark or chromosomal rearrangements in gibbons).

In this year 2014 we have seen the publication of three manuscripts in comparative genomics that represent the release of three new genome references. As a technical note, the marmoset and gibbon genome assemblies will be remembered as the last primate genomes to be reconstructed with Sanger capillary sequencing. The elephant shark was built based on the "almost expired" Roche pyrosequencing 454 technology.

The elephant shark genome (a cartilaginous fish) taught us about the oldest living group of jawed-vertebrates. Unlike humans and other bony vertebrates, cartilaginous fishes are unable to replace cartilage with bone. Analysis of the elephant shark genome was able to highlight a family of genes that are absent in elephant shark but present in all bony vertebrates. A significant reduction in bone formation was observed when a member of this gene family was knocked out in zebrafish, thereby indicating the importance of this gene family in bone formation. This finding has important implications for our understanding of bone diseases such as osteoporosis and for developing effective therapeutic strategies.

In the analysis of the gibbon genome, we gained insight into the evolution of the ancestral ape genome and the gibbon genome and its extraordinary number of chromosomal rearrangements. The analysis of the gibbon genome exposed an intriguing role for a new repetitive DNA sequence that emerged exclusively in the gibbon genome. It's called the "LAVA" element and more than one thousand copies have been found in the gibbon genome. Several LAVA elements have been inserted in a group of genes that are important for guaranteeing the correct separation of chromosomes when cells divide thus providing a testable hypothesis about how this repeat element might had contributed to the elevated rate of rearrangements in the gibbon lineage.

Finally, the genome sequence of the common marmoset, the first sequence of a New World Monkey, provided novel information about unique features of the marmoset such as a unique rapid reproductive system with multiple births and rapid growth. The study revealed several genes that are likely responsible for their ability to consistently reproduce multiple births and associated to chimerism. The dizygotic (or fraternal) twins in marmosets exchange blood stem cells called hematopoietic stem cells in utero, which leads to chimerism, a single organism composed of genetically distinct cells. Also, the genome sequence showed this may be the result of positive selection in five growth hormone/insulin-like growth factor axis genes (GH-IGF) with potential roles in producing small body size.

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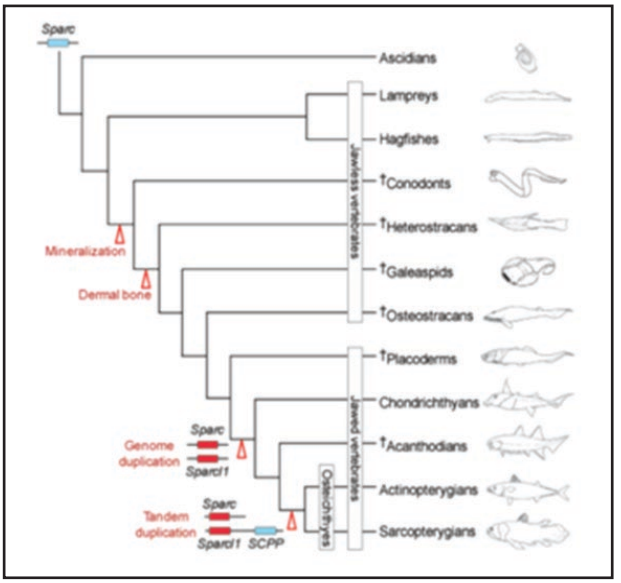

Fig. 1: *(from Venkatesh, B. et al. 2014. Elephant shark genome provides unique insights into gnathostome evolution.* Nature. *505 (7482): 174-179). The duplication of* Sparc *gene and subsequent tandem duplication of the paralogous copy (*Sparcl1*) gave rise to the SCPP gene family responsible for endochondral ossification.*

A bottom-up characterization of transfer functions for synthetic biology designs: lessons from enzymology

After the hype phase that come out from the foundation of the synthetic biology field a decade ago, the inherent complexity of living systems has proven to be a big barrier for the success of this emerging discipline. Following an engineering perspective, building up genetic complex devices requires the adequate understanding and characterization of their constituting simpler parts. The way on how genetic parts function is often described in terms of their input-output response, i.e. transfer functions. Often they are modeled by the use of Hill-shaped curves regardless their biological ground. This approximation inevitably reduces the behavior predictability of the parts providing limited information for the construction of larger genetic devices.

In Carbonell-Ballestero et al. (2014) we provide a novel mathematical formalization that allows prediction of the global behavior of a synthetic device by considering the actual information from the involved biological parts. This is achieved by adopting an enzymology-like framework, where transfer functions are described in terms of their input affinity constant and maximal response. As a proof of concept, we characterize a set of Lux homoserinelactone-inducible genetic devices with different levels of Lux receptor and signal molecule. Our model fits the experimental results and predicts the impact of the receptor's ribosome-binding site strength, as a tunable parameter that affects gene expression. Such a principle of design may give insights about the evolutionary implications of shaping the response affinity of natural signaling pathways by just the variation of receptor concentration.

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Neandertal genomic diversity

After the retrieval of the Neandertal draft in 2010 and the subsequent publication of a high coverage genome (that from Altai Neandertal) in 2013, it become evident that to explore the genomic diversity of these extinct hominins in a wide geographic range was the next scientific step. To explore this issue, two exomes -including more than 17,000 protein-coding genes en encompassing 27 million nucleotides- from two Neandertal samples from Vindija (in Croatia) and El Sidrón (in Spain) have been captured and sequenced. The analysis of these two exomes -together with the one previously available from Altai- has uncovered a remarkably low genetic diversity among Neandertals and the accumulation of deleterious mutations resulting from a small long-term effective population size. This, in combination with a social structure based on small, family-related groups, may have contributed to its final extinction.

In addition, different mutations in genes associated to some relevant phenotypic traits -both in the Neandertal and the modern human lineages- have been discovered. In the former group, these genes are related to skeletal features, while in the later, these genes seem to be involved in pigmentation and behavioural aspects. Functional studies are needed to better understand the precise impact of these genetic changes in Neandertals and modern humans.

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Detection of population structure in modern human populations

Population differentiation has proved to be effective for identifying loci under geographically localized positive selection, and has the potential to identify loci subject to balancing selection. The first study (Colonna et al. 2014) investigates novel genetic variation from the last release of The 1000 Genomes Project, in order to survey sites with low levels of differentiation, and evaluate the extent to which highly differentiated sites are likely to result from selective or other processes. The study demonstrates that while sites with low differentiation represent sampling effects rather than balancing selection, sites showing extremely high population differentiation are enriched for positive selection events and that one half may be the result of classic selective sweeps. Among these, the study finds previously known examples, where it can actually identify the established functional SNP, and discovers novel examples including the genes ABCA12, CALD1 and ZNF804, which we speculate may be linked to adaptations in skin, calcium metabolism and defense, respectively. The work identifies known and many novel candidate regions for geographically restricted positive selection, and suggests several directions for further research. This study has established a comprehensive catalog of most of the variants, including SNPs, INDELS and SVs, that are highly differentiated between the major populations of sub-Saharan Africa, Europe and East Asia.

Within a different framework, Elhaik *et al.* 2014 correlates the population structure of human populations with geography in order to infer the biogeographical origin of human samples through genetic markers. A Geographic Population Structure (GPS) algorithm is proposed to be applied to 40-130 thousand SNPs, which reveals high accuracy in the geographic localization of different data sets. More than 80% of the worldwide individuals tested are correctly geolocalized to their country of origin. The accuracy and power of the GPS algorithm overcomes challenges of population origins, ancestry and admixture in current human groups.

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The genetic prehistory of european populations

The Neolithic transition to agriculture has been a major social and demographic episode in European prehistory. It also represented adaptive challenges triggered by the adoption of a carbohydrate-based diet and the infectious diseases brought by domestic animals. Therefore, the retrieval and analysis of human Mesolithic and Neolithic genomes, now possible with the new Next Generation Sequencing technologies, is of great scientific interest for trying to understand this crucial transition.

In 2014, two papers published at Nature have explored for first time this subject. In the first, the retrieval of a complete genome from a 7,000 years-old Mesolithic hunter from La Braña in León (Spain) has shown that this individual was genetically distinct to modern Europeans although it clusters closer to modern Scandinavians. The most plausible explanation to this pattern is that hunters were quickly replaced in southern Europe by the incoming farmers but they persisted longer in northern latitudes that are less favourable to farming, admixing there

with the Neolithic people. Remarkably, this study has uncovered also some phenotypic traits of the Mesolithic people, such a combination of dark skin pigmentation alleles and blue eyes alleles that are not currently present in modern Europeans. In addition, numerous immunological derived alleles thought to have been selected for its resistance to zoonotic infectious diseases were already present in this individual.

The scenario changes radically with the arrival of the Neolithic. The first Neolithic groups entered Europe through Anatolia around 8,500 years BP, coming originally from the Near East. These pioneers established in Greece and the Balkans, and subsequently spread west and northwest, following two different routes: the Mediterranean coast to the west (with the Cardial ware culture) and the Danube river to the centre and north of Europe (with the LBK or Linear Pottery culture). In the second paper, the retrieval of complete genomes from Mesolithic hunter-gatherers from Luxembourg and Sweden, and from a LBK farmer from Germany has allowed the proposal of a three ancestral population model to explain the current diversity of European populations. Current Europeans might be the result of the admixture of west European hunter-gatherers, ancient north Eurasians, and early European farmers. This study has challenged the hypothesis of the origin of Europeans as a single admixture of hunter-gatherers and farmers, suggesting a much more complex scenario as proposed previously.

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Recent selection in modern humans

Searching for Darwinian selection in natural populations has been the focus of multiple studies over the last decades. The creation of the 1000 Genomes Selection Browser (http://hsb.upf.edu) is a resource for detecting signatures of recent natural selection in modern humans. In this browser, a large number of neutrality tests as well as summary statistics informative for the action of selection have been implemented and applied to low coverage sequencing data from The 1000 Genomes Project. The information is provided in UCSC-style

format to facilitate the integration with the rich UCSC browser tracks and an access page is provided with instructions and for convenient visualization. This online resource will facilitate the interpretation of signals of selection on different temporal, geographical and genomic scales.

Another study aims to identify signals of convergent evolution of the immune system, based on the peculiar demographic history in which two populations with different genetic ancestry, Europeans and Rroma (Gypsies), have lived in the same geographic area and have been exposed to similar environments, during the last millennium. We identified several genes under evolutionary pressure in European/Romanian and Rroma/Gipsy populations, but not in a Northwest Indian population, the geographic origin of the Rroma. Three Toll-like receptor genes (*TLR1*, *TLR6*, and *TLR10*) showed a strong signal of adaptive selection. Their gene products are functional receptors for *Yersinia pestis*, the agent of Plague. Immunogenetic analysis showed that single-nucleotide polymorphisms of these genes modulate *Y. pestis*-induced cytokine responses. Thus, we identified immune system genes as being shaped by convergent evolution in two different human populations.

A third work reports an unusual case of positive natural selection for an amino acid replacement in the human intestinal zinc uptake transporter ZIP4. This substitution had been previously recognized as one of the most strongly genome-wide differentiated polymorphisms between different human populations. However, since this extreme population differentiation was not accompanied by additional signatures of natural selection, it was unclear whether it resulted from genetic adaptation. Using computer simulations we demonstrate that such an unusual pattern can be explained by the effect of the local recombination, together with positive selection in Sub-Saharan Africa. Moreover, we provide evidence to suggest functional differences between the two ZIP4 isoforms in terms of the transporter cell surface expression and zinc uptake. This result is the first genetic indication that zinc regulation differs among modern human populations, a finding that may have implications for health research. Further, we speculate that reduced zinc uptake mediated by the derived variant may have been advantageous in Sub-Saharan Africa, possibly by restricting access of this micronutrient to a geographically restricted pathogen.

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New advances in insect metamorphosis

Insect metamorphosis is one of the most fascinating processes of animal development. However, the mechanisms governing metamorphosis only started to be unveiled in the last century, when physiological research revealed that the main factor involved is juvenile hormone (JH), which represses metamorphosis

in juvenile stages. Further steps to elucidate the molecular mechanisms underlying the action of JH remained elusive until recently, when the transcription factor Methoprene-tolerant (Met) was reported to be the JH receptor in the context of metamorphosis. Experiments in vitro suggested that Met did not act alone as the JH receptor, but had to heterodimerise with another protein, Taiman (Tai). Unfortunately, Tai depletion experiments to demonstrate this protein's involvement in metamorphosis proved unsuccessful because they resulted in 100% mortality. The paper by Lozano et al. (2014) reports that in the cockroach *Blattella germanica* Tai is expressed in a number of isoforms, and selective depletion has shown that at least some of these are involved in transducing the JH signal that represses metamorphosis. These results additionally show that the whole range of isoforms should be considered when studying Tai functions. Once the complex JH-Met+Tai is formed, it induces the expression of the transcription factor Krüppel homolog 1, which transduces the JH signal that represses metamorphosis. Indeed, these data summarizes the molecular basis regulating insect metamorphosis reported until now, and that was limited to describe how metamorphosis is repressed.

Despite the characterization of the molecular mechanisms underlying metamorphosis repression, it was still required to identify the nature of the long-elusive factor that promotes metamorphosis. In this regard, the paper by Ureña et al. (2014) unveils, for the first time, the key factor that instructs cells to differentiate into the adult fate. The protagonist is the transcription factor E93, which regulates juvenile-to-adult transition in insects as shown by functional genomics experiments. When E93 expression was depleted in last instar nymphs of the hemimetabolan *B. germanica*, rather than molting to the adult stage, they molted to successive supernumerary new nymphal stages, even in the absence of JH. To check whether this function was conserved in holometabolan species, the expression of E93 was depleted during the pupal stage of the beetle *Tribolium castaneum* and the fly *Drosophila melanogaster*. As in the case of the cockroach, both insects were not able of differentiating adult forms and instead produced new supernumerary pupae. The research work also showed that E93 inhibits the expression of two transcription factors that are key repressors of adult morphogenesis: Krüppel-homolog 1 and Broad-Complex, which ensures the proper juvenile-adult transition. In summary, these findings represent a significant step toward defining the molecular mechanisms underlying insect metamorphosis.

Reference Articles

Lozano, J., Kayukawa, T., Shinoda, T., Belles, X. 2014. A role for Taiman in insect metamorphosis. *PLoS Genetics* 10 (10): e1004769.

Ureña, E., Manjón, C., Franch-Marro, X. Martín, D. 2014. Transcription factor E93 specifies adult metamorphosis in hemimetabolous and holometabolous insects. *Proceedings of the National Academy of Sciences USA* 111 (19): 7024-7029.

Genome sequencing highlights the dynamic early history of dogs

Still today, the precise origin of dog domestication is quite uncertain. Different evidences (both archaeological and genetic) provide conflicting support for Southeast Asia, the Middle East or Europe. In order to generate novel evidence for the origin and demographic history of the dog domestication, a variety of wolves from three genetically distinct origins that overlaps with the potential centers for domestication, two basal dog breeds (Basenji, a hunting dog originating in central Africa and Dingo from Australia) and a golden jackal were sequenced using Next-Generation Sequencing technologies to a deep coverage. Surprisingly, none of the wolves lineages sequenced was found to be the potential center of domestication for modern dog breeds supporting further evidences that the wolf population from which dogs originated is now extinct. Demographic analyses performed indicated the existence of strong bottlenecks in both lineages (stronger in dogs than wolves).

In addition, the initial duplication of the Amylase gene, previously associated to exposure to agriculture, was found to predat in fact the initial dog domestication. Finally, we dated the initial dog domestication event between 11–16 thousand years ago, a date that predates the rise of agriculture and would suggest that the earliest dogs most likely appeared along Upper Paleolithic hunter-gatherers.

Reference Article

Freedman, A.H., Gronau, I., Schweizer, R.M., Ortega-Del Vecchyo, D., Han, E., Silva, P.M., Galaverni, M., Fan, Z., Marx, P., Lorente-Galdos, B., Beale, H., Ramirez, O., Hormozdiari, F., Alkan, C., Vilà, C., Squire, K., Geffen, E., Kusak, J., Boyko, A.R., Parker, H.G., Lee, C., Tadigotla, V., Siepel, A., Bustamante, C.D., Harkins, T.T., Nelson, S.F., Ostrander, El.A., Marquès-Bonet, T., Wayne, R.K. Novembre, J. 2014. Genome Sequencing Highlights the Dynamic Early History of Dogs. *PLoS Genetics* 10 (1): e1004016.

Linking natural genetic mutations to its ecologically relevant phenotype helps understanding the adaptive process

Given the predictions of future environmental fluctuations, it is crucial to understand how organisms adapt to changing environments. The fruit fly *Drosophila melanogaster* is an ideal model organism to study environmental adaptation because of our deep understanding of developmental, physiological, and metabolic networks, as well as the ease of experimental manipulation.

Xenobiotics are widely used in this adaptation studies. They are chemicals to which an organism is exposed that are extrinsic to the normal metabolism of that organism. Without metabolism, many xenobiotics would reach toxic concentrations. In Mateo et al (2014),

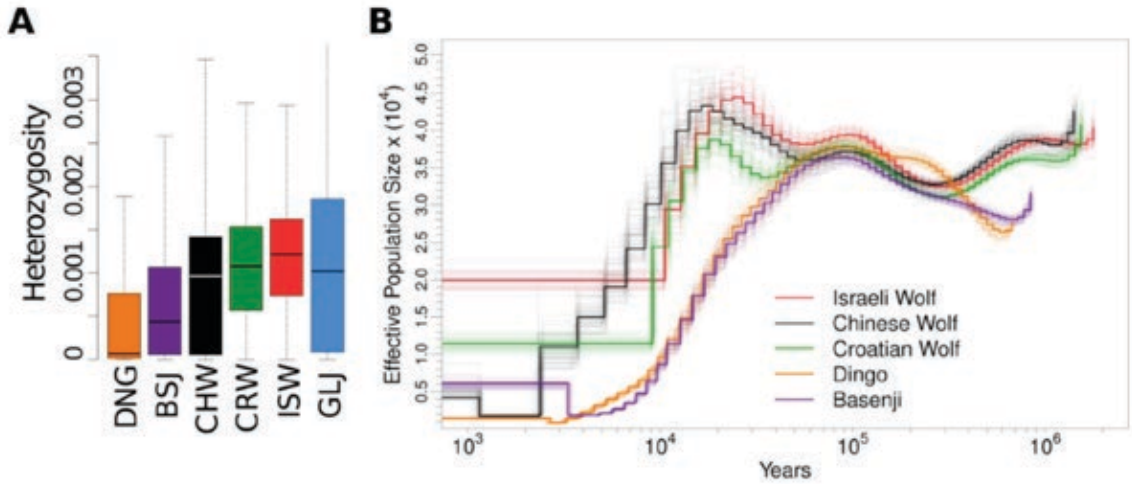

Fig. 1: *(from Freedman et al. 2014. Genome Sequencing Highlights the Dynamic Early History of Dogs.* PLoS Genetics *10 (1): e1004016). Heterozigosity values and PSMC (evolution of effective population sizes) in dogs and wolves. Notice the reduction of diversity in dogs and the corresponding stronger decline in the effective population size in the last 40.000 years.*

González and colleagues showed that a previously identified putatively adaptive mutation, the insertion of the transposable element *FBti0019627*, mediates resistance to both natural and synthetic xenobiotics in *Drosophila melanogaster*.

Mapping genotype to phenotype is a challenging task: many phenotypes are affected by a large number of genes and many individual genes affect multiple traits. Therefore, scientists at the IBE had to combine experimental and computational approaches in order to further elucidated the molecular and the biochemical mechanisms underlying this natural adaptive mutation. These results should be relevant for other organisms as well since there are many similarities between species in the way cells respond to stress.

Reference Article
Mateo, L., Ullastes, A., and González, J. 2014. A transposable element insertion confers xenobiotic resistance in Drosophila. *PLoS Genetics* 10 (8): e1004560.

Earliest holozoan expansion of phosphotyrosine signaling

One of the most important cell-to-cell communication pathways in multicellular animals or metazoans is phosphotyrosine (pTyr) signaling. Two of the main components of the pathway are tyrosine kinases and tyrosine phosphatases. These were considered for a long time specific to animals, since they appear to be absent from plants, fungi and other unicellular and multicellular eukaryotes. Analyses of the genomes of choanoflagellates and filastereans, two close relatives of animals, already showed that pTyr signaling was present before the origin of Metazoa. In Suga et al. (2014) new genomic and transcriptomic data from several animals and fungal relatives (Ichthyosporea, Nuclearia, Fonticula, Corallochytrea) were analysed to unravel the evolution of this pathway in the opisthokonts.

It was found that the genomes of both Icthyosporea and Corallochytrea, close relatives of animals, encode a large variety of receptor and cytoplasmic tyrosine kinases, as well as other components of the pTyr pathway. In contrast, neither Nucleariа nor Fonticula have tyrosine kinases. This means that metazoan-type tyrosine kinases and a complex pTyr signaling evolved in Holozoa (animals and their closest relatives). Interestingly, the evolution of both receptor and cytoplasmic tyrosine kinases is contrasting. The repertoires of cytoplasmic tyrosine kinases are similar between metazoans and the rest of holozoans (choanoflagellates, filastereans, ichthyosporeans, corallochytreans). However, the set of receptor tyrosine kinases are different in each of those lineages, demostrating a high extracellular plasticity in extracellular signal reception until the system was co-opted to work as cell-to-cell communication by metazoans. Overall, this analysis details the evolution of one of the most important signaling pathways from protists to multicellular animals.

Reference Article
Suga, H., Torruella, G., Burger, G., Brown, M.W., and Ruiz-Trillo, I. 2014. Earliest holozoan expansion of phosphotyrosine signaling. *Molecular Biology and Evolution*, 31(3), 517–528. doi:10.1093/molbev/mst241

IBE COLLECTIONS

The IBE holds extensive research collections of specimens, tissue samples and DNA extractions, resulting from the intense biodiversity surveys from around the Globe of some of the researchers and their numerous collaborators. 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 other Orders) and reptiles (more than 11,000 tissue samples), with additional important holdings of Amphibia (ca. 2,500 tissue samples) and small mammals (ca. 1,500 DNA samples). 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, be either in the form of DNA aliquotes, tissue samples or whole specimens, especially beetles (more than 70 species) but also some reptiles (five species) and other groups (ants, butterflies). It is important to emphasize that these collections are truly global, as can be seen in Fig. 1, with samples from 164 countries from all continents except Antarctica.

The IBE collections are not merely a storage of biological samples, but they represent both a repository of vouchers used in published research and a dynamic resource for ongoing and future studies. Although they have so far been actively curated by each research group, we expect to set up a common collection management and curation unit, due the increasing importance of our holdings and the growing demands from international agreements on biodiversity conservation and use of genetic resources (as, for example, the Nagoya Protocol).

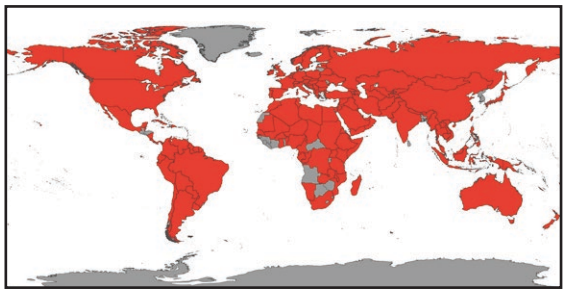

Fig. 1: *Truly global collections: in red, countries that are represented by samples at the IBE collections.*

Part of the material deposited in the IBE collections was donated by researchers and institutions worldwide, but most of it was obtained in expeditions carried out by IBE members (Fig. 2). The main collecting expeditions that took place in 2014 are:

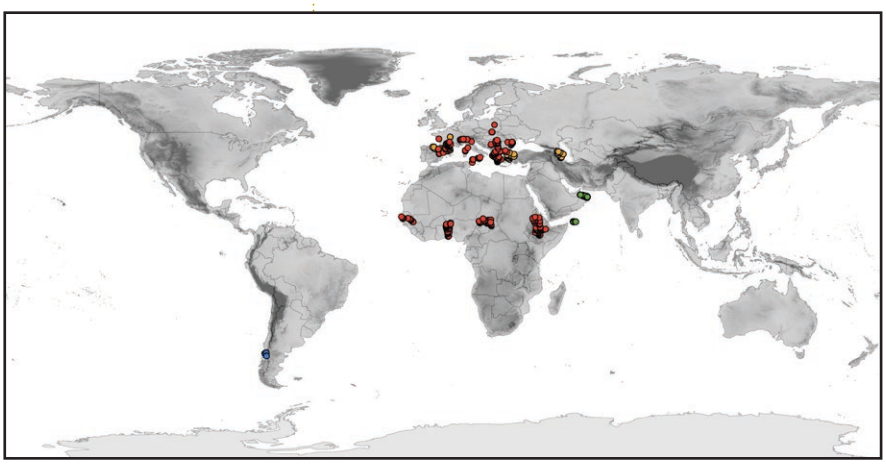

Fig. 2: *Sampling locations for the new collection specimens obtained by IBE members during 2014. Main targeted groups: red, butterflies; yellow, beetles; green, reptiles; blue, beetles and butterflies.*

Socotra and Oman: These are target areas for comparative studies on the diversification, biogeography and evolution of mainland and island arid reptile faunas. Expeditions were funded by MINECO and the Mohammed Bin Zayed Species Conservation fund.

Central Africa and Sahel: A National Geographic Society Exploration Grant financed expeditions to Ethiopia, Chad, Benin and Senegal to collect butterflies.

Europe: Different teams performed multiple collecting trips to localities in the Iberian Peninsula, Central Europe, the Balkans, etc.

Turkey and Azerbaijan: These are key regions for understanding the origin of the Mediterranean biota, but the knowledge of their faunas is still very incomplete.

Chilean Patagonia: A trip in December to the Huinay Biological Station was funded by Endesa to perform an entomological survey.

The IBE researchers perform a relentless taxonomical task strongly related to the collection material. The number of taxa described so far by IBE researchers, besides many new taxonomic combinations and status proposed, are:

Reptiles: 17 species, 3 subspecies
Amphibians: 1 genus, 1 subspecies
Acari (Trombiculidae): 1 genus, 1 species
Beetles: 1 tribe, 1 genus, 2 subgenera, 43 species
Ants: 1 species
Butterflies: 1 genus
Thrips: 2 species

Taxa described at IBE during 2014:

Reptilia

Gekkonidae

Hemidactylus minutus Vasconcelos and Carranza 2014

Coleoptera

Chrysomelidae

Taophila gaea Gómez-Zurita 2014
Taophila aphrodita Gómez-Zurita 2014
Taophila subgen. *Lapita* Gómez-Zurita and Cardoso 2014
Taophila subgen. *Jolivetiana* Gómez-Zurita and Cardoso 2014

Fig. 3: Taophila aphrodita *Gómez-Zurita 2014*

Limnichidae

Caccothryptus nepalensis Hernando and Ribera 2014
Caccothryptus jendeki Hernando and Ribera 2014
Caccothryptus fujianensis Hernando and Ribera 2014
Caccothryptus sinensis Hernando and Ribera 2014
Caccothryptus auratus Hernando and Ribera 2014
Caccothryptus malickyi Hernando and Ribera 2014
Caccothryptus luzonensis Hernando and Ribera 2014
Caccothryptus nanus Hernando and Ribera 2014

Caccothryptus ticaoensis Hernando and Ribera 2014
Caccothryptus zetteli Hernando and Ribera 2014
Caccothryptus schuhi Hernando and Ribera 2014
Caccothryptus jaechi Hernando and Ribera 2014
Caccothryptus sulawesianus Hernando and Ribera 2014
Caccothryptus wooldridgei Hernando and Ribera 2014
Pelochares sinbad Hernando and Ribera 2014
Pelochares sabaeanus Hernando and Ribera 2014
Byrrhinus socotrensis Hernando and Ribera 2014
Byrrhinus helicophallus Hernando and Ribera 2014
Limnichus arabicus Hernando and Ribera 2014

Fig. 4: *A species of the genus* Caccothryptus. *In 2014, Hernando and Ribera published a revision of this genus of aquatic beetles and described 14 species.*

Fig. 5: Pelochares sinbad, Byrrhinus helicophallus, Pelochares sabaeanus, Limnichus arabicus, Byrrhinus socotrensis *(clockwise, all Hernando and Ribera 2014). All these are new species of Limnichidae beetles of the Arabian Peninsula and the Island of Socotra described at IBE.*

Dytiscidae
Desmopachria andreae Mega and Sánchez-Fernández 2014

Thysanoptera
Heterothripidae
Aulacothrips levinotus Cavalleri and Kaminski 2014
Aulacothrips tenuis Cavalleri and Kaminski 2014

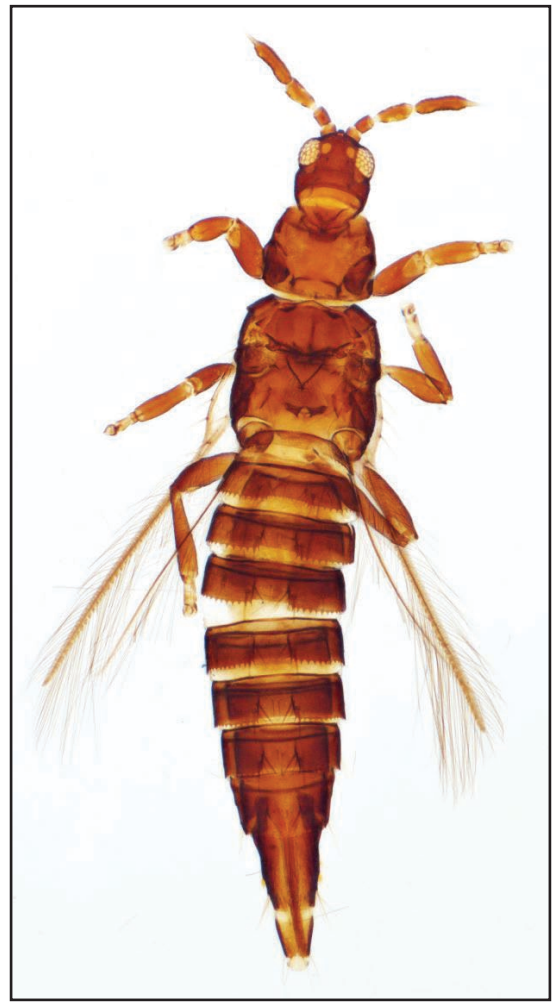

Fig. 6: Aulacothrips tenuis *Cavalleri and Kaminski 2014 (Thysanoptera) is a new South American ectoparasitic thrips that feeds on gregarious ant-tended hemipterans.*

References

Cavalleri, A. and Kaminski, L.A. 2014. Two new ectoparasitic species of Aulacothrips Hood, 1952 (Thysanoptera: Heterothripidae) associated with ant-tended treehoppers (Hemiptera). *Systematic Parasitology* 89: 271-278.

Gómez-Zurita, J. and Cardoso, A. 2014. Systematics of the New Caledonian endemic genus *Taophila* Heller (Coleoptera: Chrysomelidae, Eumolpinae) combining morphological, molecular and ecological data, with description of two new species. *Systematic Entomology* 39: 111-126.

Hernando, C. and Ribera, I. 2014. Taxonomic revision of the genus *Caccothryptus* Sharp (Coleoptera: Limnchidae). *Koleopterologische Rundschau* 84: 281-304.

Hernando, C. and Ribera, I. 2014. The Limnichidae of the Arabian Peninsula and the Island of Socotra (Coleoptera). *Acta Entomologica Musei Nationalis Pragae* 54(supp): 173-189.

Mega, Y.S. and Sánchez-Fernández, D. 2014. A new species of *Desmopachria* Babington (Coleoptera: Dytiscidae) from Cuba with a prediction of its geographic distribution and notes on other Cuban species of the genus. *Zootaxa* 3753: 585-596.

Vasconcelos, R. and Carranza, S. 2014. Systematics and biogeography of *Hemidactylus homoeolepis* Blanford, 1881 (Squamata: Gekkonidae), with the description of a new species from Arabia. *Zootaxa* 3835(4): 501-527.

Highlighted species

Hemidactylus minutus: A nearly endemic species of gecko described from Oman

A new species of gecko with the scientific name *Hemidactylus minutus* has been described from Oman and extreme eastern Yemen. It lives in rocky environments close to the Arabian Sea coast and is characterized morphologically by its very small size, and that is why is scientific name is *H. minutus* as it is the smallest *Hemidactylus* in mainland Arabia. The description of this new species is the result of more than 10 years of work of the group led by Dr. Carranza that is based at the Institute of Evolutionary Biology in Barcelona, Spain. Dr. Carranza has been carrying out research on reptile fauna of the arid areas of Arabia since 2005 and has already resulted in the description of 15 new species of reptiles, 14 of them endemic to Arabia. As this work is still ongoing, the description of new species for the country and production of important information for conservation management should follow. As a result of the detailed taxonomic knowledge on the reptile fauna of this biogeographically interesting area, IBE members can now try to understand how biodiversity is originated and maintained in one of the harshest environments in the world.

Reference

Vasconcelos, R. and Carranza, S. 2014. Systematics and biogeography of *Hemidactylus homoeolepis* Blanford, 1881 (Squamata: Gekkonidae), with the description of a new species from Arabia. *Zootaxa* 3835(4): 501-527.

Fig. 7: Hemidactylus minutus *Vasconcelos and Carranza 2014 is a new species of gecko described from Oman.*

Fig. 8: *Most of this year's new samples in the reptile collection have been obtained in an expedition to Oman.*

THESES. COURSES AND SEMINARS

Doctoral Thesis presented during 2014

- **PhD Student:** Alexandre Mendoza de Soler
  Title: Genòmica comparada a l'Origen dels Metazous
  Thesis Director: Iñaki Ruiz-Trillo
  Institution and Date: Universitat de Barcelona. January 15 2014

- **PhD Student:** Margarita Metallinou
  Title: Systematics biogeography and evolution of selected widespread reptile genera from the arid areas of North Africa and Arabia
  Thesis Director: Salvador Carranza
  Institution and Date: Universitat de Barcelona. 17th July 2014

- **PhD Student:** Joan García-Porta
  Title: Evolution and diversification of the geckos of the Arabian Peninsula and Socotra
  Thesis Director: Salvador Carranza
  Institution and Date: Universitat de Barcelona. 10th Oct 2014

- **PhD Student:** Pierre Luisi
  Title: Positive selection in humans: from single genes to interaction maps
  Thesis Director: Jaume Bertranpetit/Hafid Laayouni
  Institution and Date: Universitat Pompeu Fabra. 31st October 2014

- **PhD Student:** Federico Sánchez
  Title: Addressing Neandertal evolutionary genetics at three different resolution levels: admixture with modern humans, demography and social structure.
  Thesis Director: Carles Lalueza
  Institution and Date: Universitat Pompeu Fabra. 28st November 2014

- **PhD Student:** Jesús Lozano
  Title: Mecanisme d'acció de l'Hormona Juvenil en la metamorfosi dels insectes
  Thesis Director: Xavier Bellés
  Institution and Date: Universitat de Barcelona. December 4

- **PhD Student:** Elisenda López Panadés
  Title: Caracterització del cicle de vida dels retrotransposons telomèrics HeT-A i TART de Drosophila melanogaster
  Thesis Director: Elena Casacuberta
  Institution and Date: 12th December 2014

- **PhD Student:** Amparo Galiana
  Title: Evolution of thermal tolerance and size of the geographic range in closely related species of water beetles
  Thesis Director: Ignacio Ribera
  Institution and Date: 19th December 2014

- **PhD Student:** Guifré Torruella
  Title: Phylogeny and evolutionary perspective of Opisthokonta protists
  Thesis Director: Iñaki Ruiz-Trillo
  Institution and Date: 19th December 2014

- **PhD Student:** Javier Prado
  Title: Great ape genomics: Diversity and evolution
  Thesis Director: Tomàs Marqués-Bonet
  Institution and Date: 22nd December 2014

Teaching

IBE Scientists belonging to the Universitat Pompeu Fabra are also academic staff at this University (Experimental Sciences and Health Department; Evolutionary Biology and Complex Systems Program) and 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 (Universitat Pompeu Fabra)

- 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 (Universitat Pompeu Fabra)

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

Bachelor's Degree in Biomedical Engineering (Universitat Pompeu Fabra)

- 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) (Universitat Pompeu Fabra)

- Genomes and Systems (5 ECTS). Coordinator: Tomás 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 2014 IBE has hosted a total of 35 students. In particular:

- 5 High school juniors from "Programa Joves i Ciència" (4)- financed by Fundació La Caixa-la Pedrera-, Institut la Guineueta (1)
- 16 undergraduate students (practicums) from: Universitat de Barcelona (8), Universitat Pompeu Fabra (5), Universitat Autònoma de Barcelona (2), Universitat de Vic (1)
- 10 master students from: Universitat Pompeu Fabra (6), Universitat de Barcelona (3), Universitat Autònoma de Barcelona (1).

Seminars

Speaker	Talk	Institution	Date
Anna Ferrer	Influenza virus drug resistance: a time-sampled population-genetics approach	School of Life Sciences and Institute of Bioengineering, EPFL Department of Biology and Biochemistry, University of Fribourg Swiss Institute of Bioinformatics (SIB), Switzerland	24/02/2014
Sergio Castellano	Patterns of coding variation in the complete exomes of three Neandertals	Department of Evolutionary Genetics. Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany.	22/04/2014
Mario Cáceres	Population distribution, evolutionary history, and functional effects of inversions in the human genome	ICREA-Institut de Biotecnologia i de Biomedicina (IBB), Universitat Autónoma de Barcelona, Barcelona, Spain.	29/05/2014
Iñaki Comas	Evolution of Mycobacterium tuberculosis: from millennia to minutes	FISABIO-Salud Pública, Universitat de València, Spain.	17/06/2014
Eörs Szathmáry	The Major Transitions Revisited	Center for the Conceptual Foundations of Science, Parmenides Foundation, Pullach/Munich, Germany.	15/07/2014
Oscar Lao	New Callenges for detecting population substructure and the fingerprint of directional on standing variation in the genome	Departament of Forensic Molecular Biology, Erasmus University Medical Centre. Rotterdam, The Netherlands	17/07/2014
David Posada	Phylogenomics and species trees	Universidad de Vigo, Vigo, Spain	18/07/2014

Speaker	Talk	Institution	Date
Frédéric Thomas	Ecological and Evolutionary Perspectives on Cancer	CREEC, MIVEGEC—Centre IRD de Montpellier, France	18/09/2014
José Gómez-Skarmeta	Gene regulation dynamics and chromatin architecture during development and evolution	Centro Andaluz de Biología del Desarrollo. Sevilla, Spain	22/09/2014
Andrés Moreno Estrada	Human population genomics in the Americas: new approaches to address long-standing evolutionary riddles	Department of Genetics, School of Medicine, Stanford University, US	26/06/2013
Peter Elias	Basis of for the Development and Subsequent Loss of Pigmentation during Human Evolution	University of California, San Francisco, California, US	15/10/2014
Mark Kirkpactrick	Evolution of the genome by natural and sexual selection	University of Texas, Texas, US	04/11/2014

IBE RETREAT CHRONICLE

The IBE Scientific Retreat 2014 took place on March 24th-25th at the Eden Roc Hotel in Sant Feliu de Guíxols (Girona). Along the two days, IBE researchers shared research goals and experiences. The scientific program included an external invited lecture, two lectures by two IBE PIs and 22 presentations by postdocs and PhD students on their research and that of their groups. These 10-minute presentations were given to small rotating audiences in a variety of formats including laptops, posters, slides, specimens, pictures, and even a video. Ferran Casals (from the Evolutionary Systems Biology Lab) and Salvador Carranza (from the Systematics, Biogeography and Evolution of Reptiles Lab), who had already organized such group sessions in the previous retreat edition, improved the format and succeeded again in creating a quite dynamic and friendly atmosphere that promoted the exchange of ideas and discussion (see photos and groups below).

Group Session 1 included the presentations of the "Evolution of Insect Metamorphosis and Nutritional signals in Insects Lab (Bellés, X.; Maestro, J.L.)", "Systematics, Biogeography and Evolution of Reptiles Lab (Carranza, S.)", "Drosophila Telomeres Lab (Casacuberta, E.)", "Phylogeny and Phylogeography of Mammals Lab (Castresana, J.)", "Insect Reproduction Lab (Piulachs, M.D.)", "Nuclear Hormone Receptors in Insect Development Lab (Martín, D.)", "Morphology and Signalling Lab (Franch-Marro, X.)" and the "Multicell Genome Lab (Ruiz-Trillo, I.)".

Group Session 2 included the presentations of the "Evolutionary Systems Biology Lab (Bertranpetit, J.)", "Evolutionary Population Genetics Lab (Bosch, E.)", "Genomics of Individuality Lab (Calafell, F.)", "Human Genome Diversity Lab (Comas, D.)", "microRNAs in human adaptation and disease Lab (Espinosa-Parrilla, Y.)", "Herbivore Beetle Evolution Lab (Gómez-Zurita, J.)", and the "Evolutionary and Functional Genomics Lab (Gonzales, J.)".

Group Session 3 included the presentations of the "Paleogenomics Lab (Lalueza-Fox, C.)", "Primate Genomics Lab (Marquès-Bonet, T.)", "Evolutionary Genomics Lab (Navarro, A.)", "Water and Cave Beetle Evolution Lab (Ribera, I.)", "Complex Systems Lab (Sole, R.)", the "Language evolution Lab (Steels, L.)" and a quick overview of the services and type of projects that the Genomics Service Unit in the UPF can provide to the IBE groups.

On the first day, Tomàs Marquès-Bonet (ICREA Research Professor, Comparative Genomics Lab, IBE) unveiled his research career in his "Scientific Striptease". He took the audience from his early days as a bat ecologist, through his PhD work with Arcadi Navarro on gene expression and chromosome rearrangements, to his postdoc in Evan Eichler lab (Seatle) on segmental duplications, and back to Barcelona as a principal investigator leading work on primate population genomics.

After the dinner, IBE members were divided into 24 mixed groups, who battled for a prize in a four-part general culture quiz organized by Francesc Calafell. The winners were the "tryptophan" team, formed by Àlex Mas, Josep Sardanyés, Lourdes Riquelme, Marc Simó and Adriano Bonforti. After that, the youngest (and some of the elder) IBE members walked to town for additional social networking.

On the second day, Luc Steels (ICREA Research Professor Language evolution lab, IBE) in his talk "Darwin among the Robots" illustrated us on the robotic world and gave a tour from his

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early experiences using robots in ecosystem dynamics and behaviour experiments, to some details about the use of robot devices to simulate evolutionary processes to more complex adventures on how robots integrate and connect the real word with language.

David Comas briefly outlined the objectives and novelties of the IBE PhD Training and Outreach Program 2014.

And finally, Marc A. Martí-Renom (ICREA Research Professor, Genome Biology Group, Centre Nacional d'Anàlisi Genòmica and CRG) during his talk "Structure determination of genomes and genomic domains by satisfaction of spatial restraints" presented the latest advances on the field of three-dimensional genomics and explained how the structure of our genome in the nuclei is important for gene expression and regulation. Within the context of his recent ERC collaborative project, he gave an overview of his latest findings on gene expression differences, and differential distribution of ortholog genes and duplications in the Topological Associated Domains.

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 Institut de Biologia Evolutiva (IBE). The IBE Executive Board appointed David Comas, UPF Associate Professor, and Josefa González, Ramón y Cajal Researcher, 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 2014, IBE organized and participated in several outreach activities.

La Ciència Al Teu Món
(Science is part of your world).
Several PIs and students at the IBE are collaborating on *La Ciència Al Teu Món* (*LCATM*) outreach project lead by Josefa González (*Ramón y Cajal* Researcher at IBE). 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/el-mediterrani-recorregut-per-cel-mar-i-terra-per-entendre-la-diversitat-a-traves-de-les-papallones/
- http://lacienciaalteumon.cat/els-cims-de-mallorca-illes-encara-inexplorades-dins-duna-illa/
- http://lacienciaalteumon.cat/la-primera-vegada-dun-jove-cientific/

has been funded by the *Secretaria d'Universitats i Recerca*, the *Departament d'Economia i Coneixement*, the *Generalitat de Catalunya*, and the *Fundación Española para la Ciencia Y la Tecnologia (FECYT)*, and can be found on the web www.lacienciaalteumon.cat, on twitter, @LCATMon, and on Facebook, www.facebook.com/LCATMon.

Saló de l'Ensenyament
(teaching fair). 12th to 16th March 2014.
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). 21st and 28th May and 5th and 12th November 2014.
Organized by: Fundació Catalunya-La Pedrera.

IBE participated in the Professores i Ciència program by offering two courses to high-school teachers in collaboration with *LCATM*:
The conservation of biodiversity: the case of primates.

Evolutionary Genomics: Mechanisms, causes and consequences of the current genomic diversity of human populations.

PRBB Open Day
October 4th, 2014. Organized by: Parc de Recerca Biomèdica de Barcelona (PRBB)

The IBE participated with several activities, including the scientific conference "Biodiversity: make describe and conserve species using DNA" by Salvador Carranza, the Science Café "What do we need to imitate life?" with the participation of Ricard Solé, and the scientific workshop "Discover routes of human populations" directed by David Comas and organized by LCATM.
The workshop consisted of a small interactive conference by young researchers explaining concepts of evolutionary biology as "genomic variability", the "founder effect", the "bottleneck" or "adaptations to the environment", among others.

(Re)volució: Conquereix amb nosaltres les noves fronteres del coneixement
(R(e)volution: Conquer with us the new frontiers of knowledge")
The main event took place on the 5th of November 2013.

Researchers at the IBE discussed diverse topics such as predicting the behavior 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. During 2014, videos and educational material were created and disseminated.

Setmana de la Ciència 2014
(Science Week Activities). 18th and 19th November 2014. Organized by: Institut de Ciències del Mar and Institut de Biologia Evolutiva.

IBE participated in the science week activities by offering both schools and the general public a hands-on activity based on a research project that is currently being pursued at IBE.

Discover the routes of human populations. Participants competed to discover the routes of human migration, from their common origin in Africa until populating the entire world and surviving as a species. They had the chance to test their intuition, observation and strategic capacity in order to be part of the surviving population.

Joves i Ciència

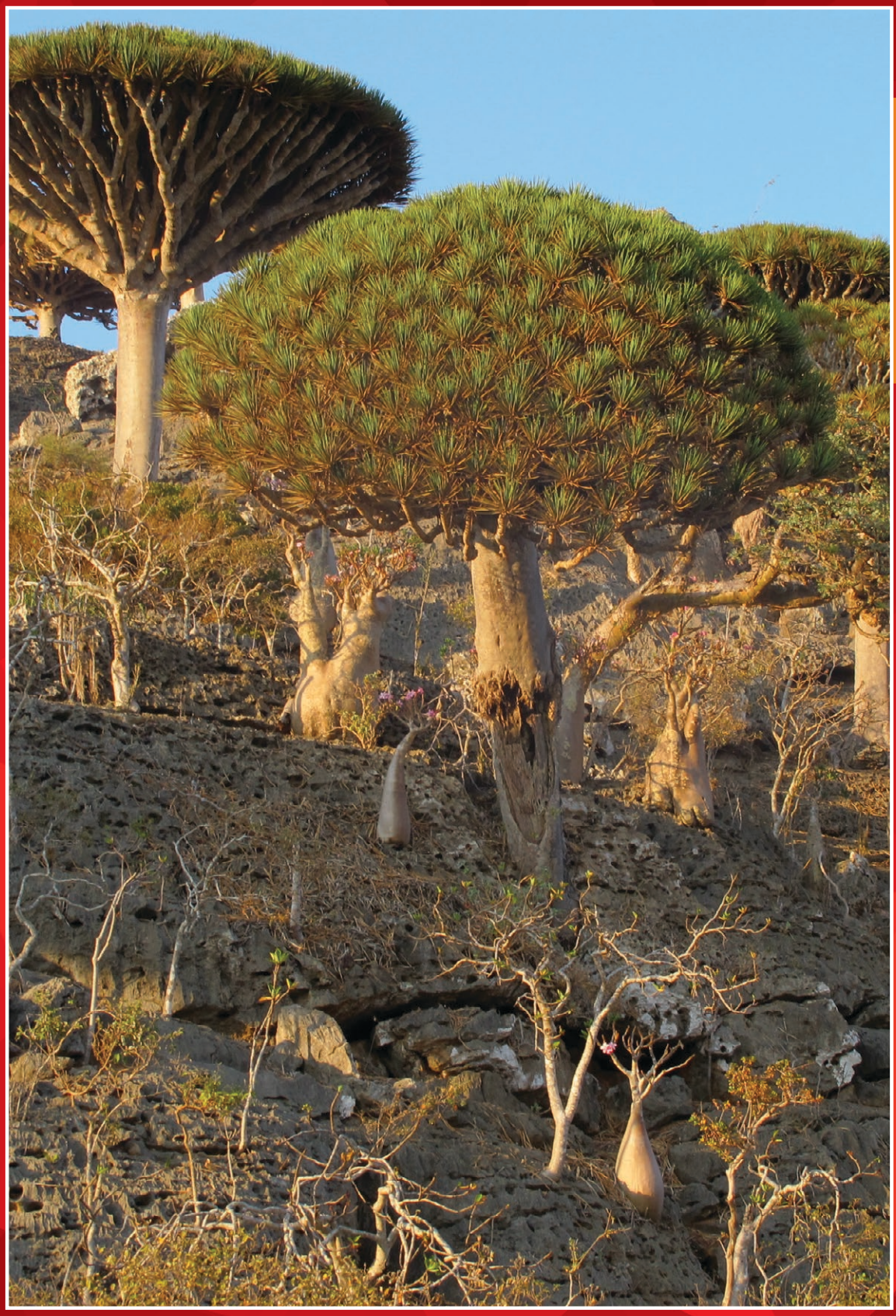
This is a program of short-term (1-2 months) internships for pre-selected secondary school students interested in science, organized and supported by Fundació Catalunya-La Pedrera. The students engage directly in scientific research guided by and collaborating with senior researchers who are at least at the PhD student level. In 2014, four 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

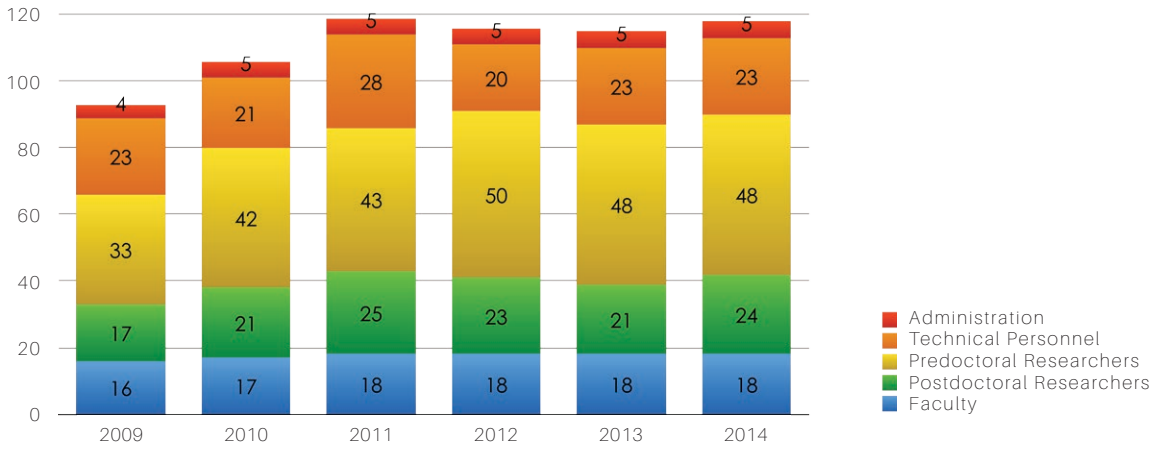


Fig. 1: Evolution of personnel distribution per categories

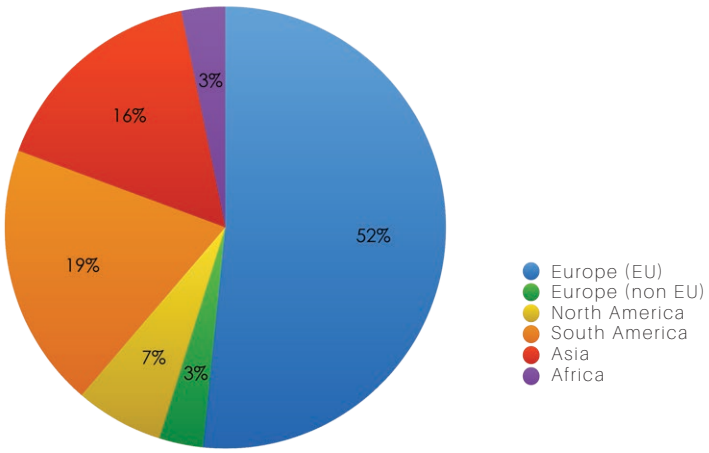


Fig. 2: Internationalisation. Foreign personnel represents 25 % of the total of IBE members (visitors not included). A part from Spain, we have researchers from 17 different countries from Europe, America, Asia and Africa.

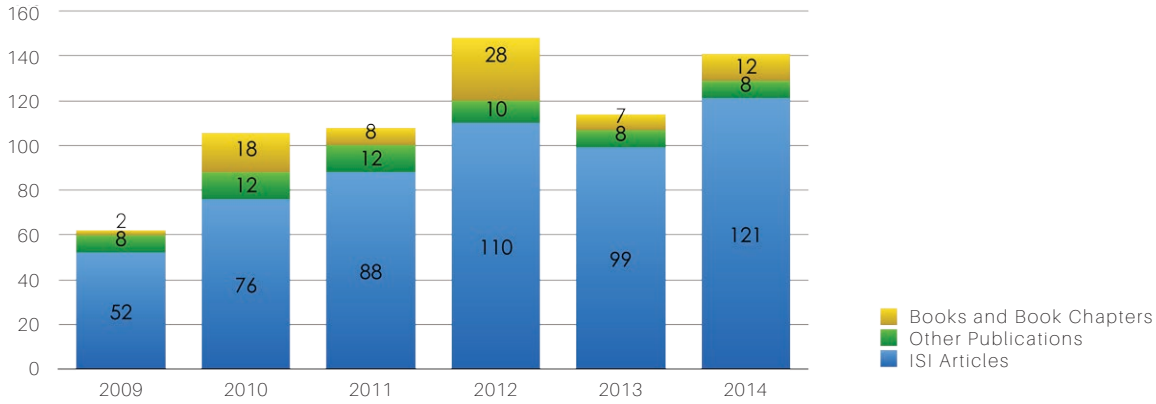


Fig. 3: Evolution of publications distribution per kind of publication

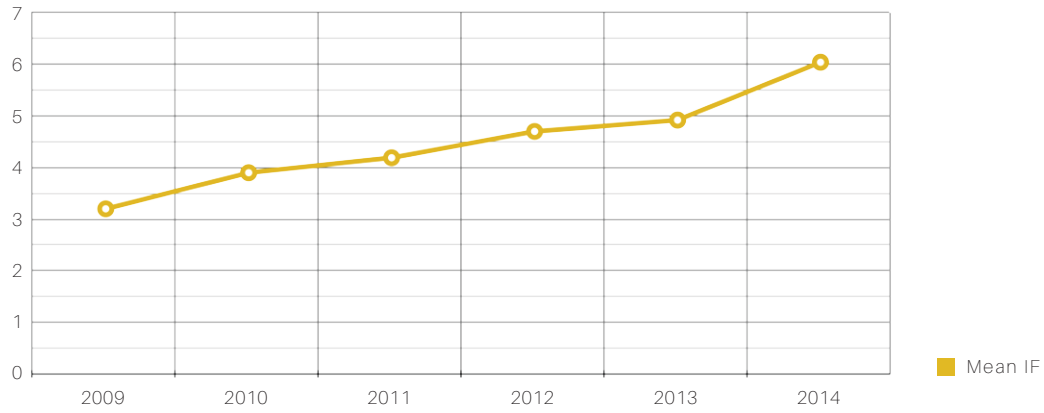


Fig. 4: Evolution of mean impact factor for ISI publications

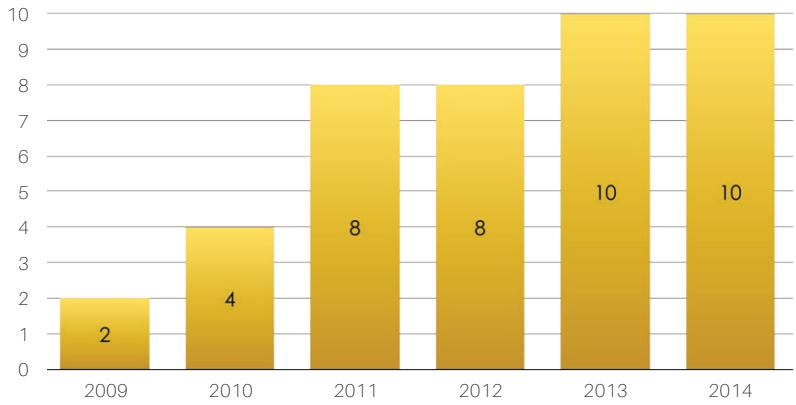


Fig. 5: Evolution in nº of theses defended

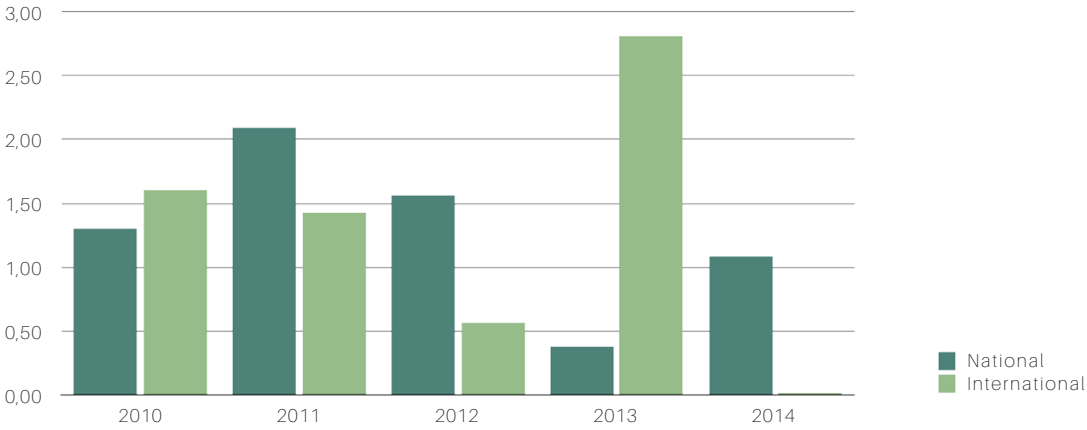


Fig. 6: Competitive new funds raised (in M€)

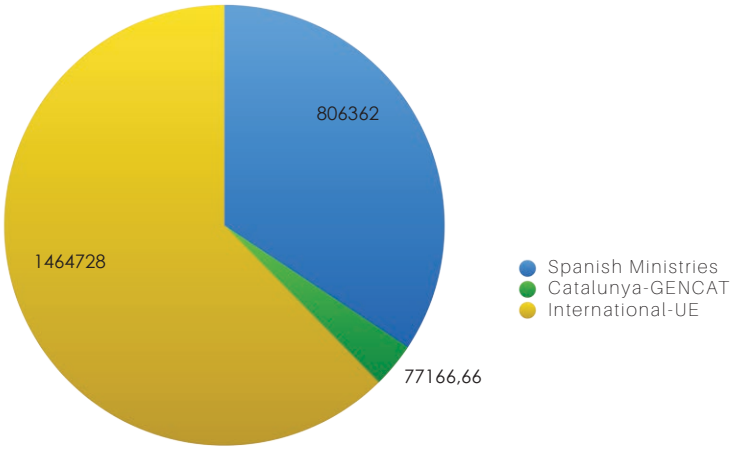


Fig. 7: Distribution of competitive funds of ongoing projects in 2014 acording to the origin of funds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