ANNUAL REPORT

2016

IBE
CSIC upf.

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2016

Produced by: Institut de Biologia Evolutiva (CSIC-UPF)
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Photo Cover Image: *The Pearly Heath* (Coenonympha arcania)*, photographed in southern Sweden on June 15, 2016. Available genetic data indicate that this widespread species displays three main mitochondrial DNA lineages in Europe. Iberia is exclusively populated by one of these lineages, which, interestingly, seems to lack from most Italian Peninsula and the Balkans, but has reached the northern limit of the species´ range in areas such as southern Sweden and Estonia.* Author: *Vlad Dincă.*

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FOREWORD

By Xavier Bellés, Director of the IBE

"What's past is prologue"

Shakespeare, *The Tempest* (II.i)

"Cridem qui som i que tothom ho escolti.
I, en acabat, que cadascú es vesteixi
com bonament li plagui, i via fora,
que tot està per fer i tot és possible."

Miquel Martí i Pol (*Ara mateix*,
del poemari *L'àmbit de tots els àmbits*)

The IBE turns 8 years old. At the level of intelligence, the 8-year-old child reaches the stage of the so-called "concrete operations", which means that it starts to practice the reflection and the logical understanding of things. Eight-year-olds demonstrate more highly-developed thinking skills as well as the ability to solve problems with creative strategies. Conversely, the magical thought diminishes. Physically, this is the age when the amount of practice and play done in the earlier years begins to manifest itself in skillfulness and in what might be called "athleticism". It is the time when children begin to identify themselves as "athletic" or "unathletic", thereby influencing their future endeavors and achievements.

Using a sport and quite acrobatic metaphor, in 2016 the IBE attained what we could call our Grand Slam, i.e. the accomplishment of a CNS: a paper in *Cell*, another in *Nature Genetics* and a third in *Science*, the three led by respective PIs that belong to the IBE. To these we can add other three *Nature* papers performed in collaboration with international teams. As for publications, the number continued to increase very slightly (from 130 in 2015 to 134 in 2016). It also slightly increased the average impact factor (from 6.21 in 2015 to 6.34 in 2016) and the percentage of papers published in the first quartile (72.8% in 2015 to 75.4% in 2016). Tentatively, and without thereby lower our guard, we might consider ourselves as "athletic."

Two events occurred in 2016 that deserve our comment. One is that Jaume Bertranpetit was awarded the Narcís Monturiol Medal for scientific and technological merit. The award ceremony took place on February 11 th at the Palau de la Generalitat, and was chaired by Jordi Baiget, Catalan Minister

of Business and Knowledge. The other event is the appointment of Arcadi Navarro as Secretary of Universities and Research of the Generalitat de Catalunya in January 2016. Arcadi Navarro was the first deputy director of the IBE during 2008-2013, and we are very proud that he has been appointed to such high responsibility.

One last new of 2016 refers to the IBE External Scientific Committee (CCE). On the one hand, a partial renovation of its components took place. Thus, Carlos Bustamante, Luis Serrano and Eske Willerslev were replaced by Anna di Rienzo (University of Chicago), Puri López-García (Université Paris-Sud) and Susanna Manrubia (Spanish National Center for Biotechnology, CSIC). We warmly thank the outgoing members for the valuable advice received while they have been serving in the CCE, and the incoming members for accepting our invitation. Moreover, and very important in 2016, from 12 to 14 December took place the second quadrennial Evaluation of the IBE by the CCE in the CMIMA building in Barcelona, where the seven CCE members carried out intense working sessions with IBE personnel at different levels, from the Director and the Executive Board to individual IBE fellows. Among other topics, the CCE discussed the change of director of the IBE. The current director had already expressed his intention to leave that responsibility after 8 years of being in exercise, and the Executive Board proposed Tomàs Marquès to replace him. The proposal was very favorably received by the CCE, and it only remains to comply with the Board of Trustees procedures to formalize the change.

After eight years of directing the IBE, since its foundation in 2008, I think it was the right time to make the change. After these eight founding years, where everything was to be done and everything was possible, I am happy to return to my natural status as a current researcher. I'm happy because my personal impression is that we are leaving an established Institute that has a splendid future. Also because I have the deep feeling that promoting and pushing the IBE from the very beginning has been the most important thing done in my scientific career. I like to recognize that serving as director of the Institute during their first eight years has been a great honor. Thanks a lot again to all of you that have been providing help and involvement with the IBE project. After all, the IBE people are the IBE project. Before leaving the director's duties, let me ask you one last request: please keep giving all your support to the IBE and, in particular, to the new director, Tomàs Marquès. He deserves it, and he will need it because there are still many things to be done and everything is still possible.

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 2016:

Antoni Bosch, Emeritus Professor at the UPF Department of Economy
Luis Calvo, CSIC Institutional Coordinator in Catalonia
Francesc Posas, UPF Vice chancellor for Scientific Policy
José Ramón Urquijo, 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 first External Scientific Committee was approved by the Board of Trustees in 2011. Subsequently, it was partially renovated in 2016, in which three replacements were made.
The last meeting and in situ evaluation of IBE activity by this commission took place on 12th, 13h and 14th December 2016.

The composition of the CCE is as follows.

Chairman:

Andrés Moya
Universitat de València
València, Spain

Members:

Brian Charlesworth
University of Edinburgh
Edinburg, UK

Anna di Rienzo
University of Chicago,
Chicago, IL, US

Gonzalo Giribet
Harvard University,
Cambridge MA, US

Puri López-García
Université Paris-Sud/Paris-Saclay,
Paris, France

Susanna Manrubia
Spanish National Centre
for Biotechnology – CSIC,
Madrid, Spain

Stuart Reynolds
University of Bath
Bath, UK

Executive Board

The IBE Executive Board is composed by 8 members:

IBE Director, Xavier Bellés
IBE Vice director, Tomàs Marquès-Bonet
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

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
Tomàs Marquès-Bonet

EXTERNAL SCIENTIFIC COMMITTEE

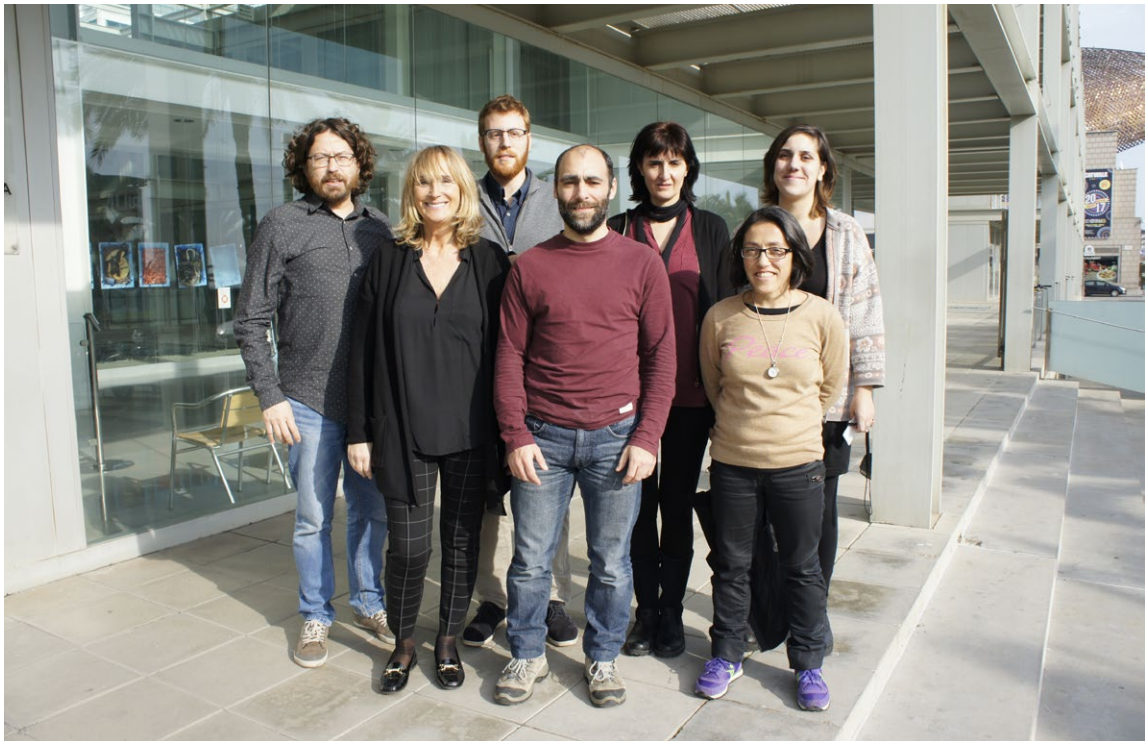
EXECUTIVE BOARD

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 and Arcadi Navarro *Group Leaders*	**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*	**Paleogenomics** Carles Lalueza-Fox *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*			**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 8 people and covers at a micro scale level all basic institute running processes: purchasing and accounting, human resources, logistics and safety, support to projects, communication and outreach.



From left to right: Vicente Vives, Isabel García, Jordi Lanuza, Pablo Álvarez, Anna Pérez, Judit Sainz and Mayte Cantero

group members

General Manager:
- Anna Pérez-Lezaun (UPF)

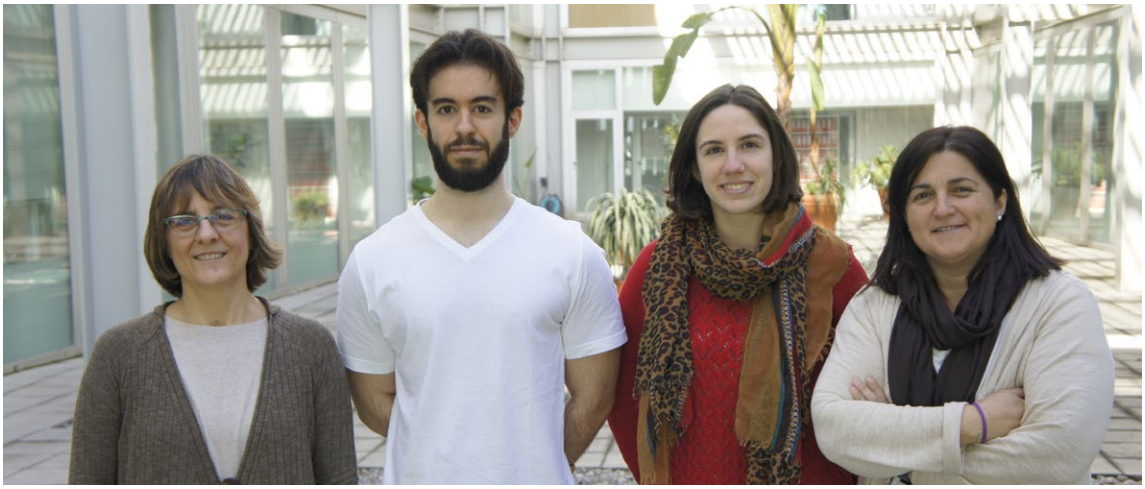
Vice Manager and Accountant:
- Vicente Vives (CSIC)

Administrative Support:
- Blanca Álvarez (CSIC)
- Pablo Álvarez (CSIC)
- Mayte Cantero (CSIC)
- Isabel García (CSIC)
- Judit Sainz (UPF)

Communications Manager:
- Jordi Lanuza (UPF)

Experimental Techniques Unit

There are some long-term and temporary laboratory technicians that give key scientific support to different IBE programs. These include the coordination and maintenance of the insect colonies and the specialized technical instrumentation and facilities. It is planned that the personnel and functions of this unit should be enlarged in the near future to give support to other programs and technological needs.



From left to right: Cristina Olivella, Eduard Hernández, Elena Plana and Mònica Vallès.

group members

Eduard Hernández, Technical staff (CSIC), Common Equipment Maintenance and user support
Cristina Olivella, Technical staff (CSIC), Supporting the Functional Genomics and Evolution Program
Elena Plana, Technical staff (CSIC), Supporting the Animal Biodiversity and Evolution Program
Mònica Vallés, Technical staff (UPF), Supporting the Population Genetics & the Comparative and Computational Genetics Programs

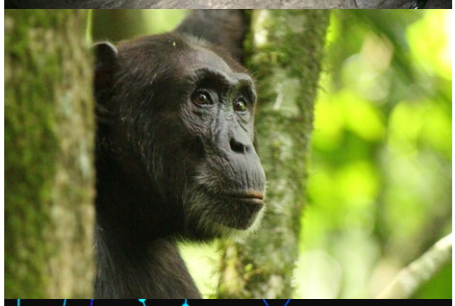
Localisation

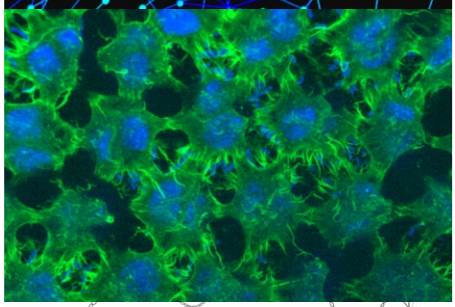
While it does not have a specific building, the IBE has two different headquarters:

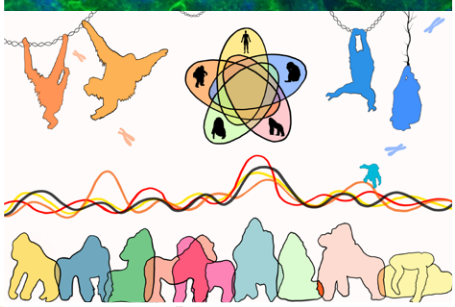
- **IBE at the PRBB building:**
  C/ Dr. Aiguader, 88.
  08003 Barcelona, Spain.

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

IBE
RESEARCH PROGRAMS







PROGRAM

ANIMAL BIODIVERSITY AND EVOLUTION

Collecting cave beetles in a muddy hole in Asturias (Cueva Porro Covanona).
Photo: *I. Ribera*

Research Groups

Butterfly Diversity and Evolution
Roger Vila, *Group Leader*

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

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

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

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

Members of this research program carry out research on animal biodiversity from a phylogenetic perspective with the aim of gaining further insight into the tree of life. The program's specific research interests include the origin and distribution of biodiversity (whether morphological, genetic, ecological or functional), systematics, speciation, hybridization, diversification, biogeography, evolutionary ecology, genomics, proteomics, bioinformatics, morphometry and phylogenetic methodology. Program members work on the systematics and phylogenetic relationships among certain groups of organisms, but also on the evolutionary processes that gave rise to current biodiversity patterns. The main groups studied are mammals, reptiles, amphibians, butterflies and beetles, thus including a broad variety of animal taxa. An important activity of the program members consists in the maintenance of extensive research collections of specimens, tissue samples and DNA extractions of these groups. A wide range of techniques is covered, from fieldwork and morphological analysis to genetic studies, genomic data mining and software development. The use of genomic data and large-scale phylogenetic analyses (both in terms of species considered and sequenced data) is helping to obtain more robust phylogenies and evolutionary conclusions. Phylogenetic trees are a common framework for many evolutionary studies and therefore this research program provides many points of contact with other programs at the IBE.

group BUTTERFLY DIVERSITY AND EVOLUTION

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

group members

Roger Vila, *Group Leader*
Tenured Scientist, CSIC

Vlad Dincă, Postdoctoral Researcher, Marie Curie Fellowship
Sämi Schär, Postdoctoral Researcher, Early Postdoc Mobility
Gerard Talavera, Postdoctoral Researcher, Marie Curie Fellowship
Leonardo Dapporto, Visiting Postdoctoral Researcher, Santander Research Scholarship
Raluca Vodă, PhD Student, FPU Scholarship, MEC
Joan Carles Hinojosa, MSc Student
Mattia Menchetti, MSc Student (Erasmus+ Traineeship)
Leonardo Platania, Postgraduate Student (Erasmus+ Traineeship)
Andrei Deulofeu, Undergraduate Student (Practicum TFG)
Patricia Giménez, Undergraduate Student (Practicum TFG)
Kiyriaki Vasileiou, Undergraduate Student (Erasmus Mundus Programme)
Cecília Corbella, Laboratory Technician
Camille Pitteloud, Laboratory Technician

Research Outline

We study butterfly diversity patterns in time and space, as well as their evolutionary causes. Our final goal is to answer longstanding questions regarding the limits between species, chromosomal evolution, and the link between phylogeography and ecology. When did a group of tiny butterflies colonize the New World and what route did they follow? How did parasitism evolve from a friendly association between species? Is a given population a new species worth protecting? These are a few 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 European butterflies, including DNA barcoding in Romania (which was the first country with all butterfly species barcoded), the Iberian Peninsula and Italy. We are working on the challenging project of obtaining a library of DNA barcodes for all the species of butterflies in Europe. Our main goals are to test the efficiency of the method on a large scale, and develop tools based on barcoding technology in order to characterize diversity.

2. Uncovering of cryptic butterfly biodiversity in Europe

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

3. Ecological factors determining butterfly biogeography

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

4. Chromosomal evolution in *Polyommatus* and *Leptidea*

Some butterfly groups have remarkably unstable chromosomes and display unusual patterns in their karyotypes. They constitute an ideal group to study chromosomal evolution in action. We are trying to understand the origin and evolutionary consequences of karyotype instability in *Polyommatus* and *Leptidea*.

Publications 2016

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Dapporto, L.; Stefanini, I.; Rivero, D.; Polsinelli, M.; Capretti, P.; De Marchi, P.; Viola, R.; Turillazzi, S.; Cavalieri, D. 2016. Social wasp intestines host the local phenotypic variability of Saccharomyces cerevisiae strains. *Yeast* 33(7):277-287.

Fig. 1: *Sámi Schar is studying ants with a Holarctic distribution, for which Beringia is a potential area of dispersal across continents. He travelled to Kamchatka in easternmost Asia, where ant populations represented the last piece of evidence needed for completing his project.*

Photo: *Mutnovski vulcano, Kamchatka, Russia*

Dincă, V. 2016. El 'DNA barcoding' de les papallones ibèriques ofereix una visió prèvia de la diversitat críptica potencial del grup a escala continental. / DNA barcodes of Iberian butterfly species enabled a continental-scale preview of potential cryptic diversity. *Cynthia* 13: 5-6, 16-17.

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Hernández-Roldán, J.L.; Dapporto, L.; Dincă, V.; Vicente, J.C.; Hornett, E.A.; Šíchová, J.; Lukhtanov, V.; Talavera, G. and Vila, R. 2016. Integrative analyses unveil speciation linked to host plant shift in Spialia butterflies. *Molecular Ecology* 25: 4267-4284.

Kaminski, L.A.; Iserhard, C.A.; Freitas, A.V.L. 2016. Thisbe silvestre sp. nov. (Lepidoptera: Riodinidae): A new myrmecophilous butterfly from the Brazilian Atlantic Forest. *Austral Entomology* 55(2):138-146.

Monasterio, Y.; de Freina, J.J.; Antonietty, C.A. and Vila R. 2016. Descrita una nueva especie de mariposa nocturna. *Quercus* 361: 45-47.

Mutanen, M.; Kivelä, S.M.; Vos, R.A.; [7 authors]; Vila, R.; [9 authors]; Tarmann, G.; Zahiri, R. and Godfray, H.C. 2016. Species-Level Para- and Polyphyly in DNA Barcode Gene Trees: Strong Operational Bias in European Lepidoptera. *Systematic Biology* 65: 1024-1040.

Pierce, N.E.; Eastwood, R.; Vila, R, Berry, A. and Dai, T. 2016. *Nabokov's notes and labels from the Museum of Comparative Zoology. Boon for a recondite biographer or data for a serious systematist?* In: Blackwell, S.H. & Johnson, K. (Eds.) *Fine lines. Vladimir Nabokov's scientific art*, New Haven & London, Yale University Press.

Shtinkov, N.; Kolev, Z.; Vila, R. and Dincă, V. 2016. The sibling species *Leptidea juvernica* and *L. sinapis* (Lepidoptera, Pieridae) in the Balkan Peninsula: Ecology, genetic structure, and morphological variation. *Zoology* 119: 1-20.

Síchová, J.; Ohno, M.; Dincă, V.; Watanabe, M.; Sahara, K. & Marec, F. 2016. Fissions, fusions, and translocations shaped the karyotype and multiple sex chromosome constitution of the northeast-Asian wood white butterfly, *Leptidea amurensis*. *Biological Journal of the Linnean Society* 118: 457-471.

Stefanescu, C.; Soto, D.X.; Talavera, G.; Vila, R. and Hobson, K.A. 2016. Long-distance autumn migration across the Sahara by painted lady butterflies: exploiting resource pulses in the tropical savannah. *Biology Letters* 12: 20160561.

Fig. 2-3: *The 2016 Butterfly Week took place in the Aeolian Islands. We spent a week exploring the fauna of these islands and sharing knowledge and projects with our Italian colleagues. The official group picture for the workshop was taken at the crater on top of Vulcano Island, where views of all the surrounding islands were breathtaking.*

Photos: *Vlad Dincă*

Fig. 4: *After gathering evidence during many years of work, we described a new species of butterfly: the Iberian endemic* Spialia rosae *Hernández-Roldán, Dapporto, Dincă, Vicente & Vila, 2016. It is morphologically undistinguishable from the sibling species* S. sertorius*, but their ecology, genetics and chemical profiles differ in sympatry.*

Photo: *Juan Carlos Vicente*

Stefanini, I.; Dapporto, L.; Berná, L.; Polsinelli, M.; Turillazzi, S; and Cavalieri, D. 2016. Social wasps are a Saccharomyces mating nest. *Proceedings of the National Academy of Sciences USA* 113(8):2247-2251.

Talavera, G.; Kaminski, L.A.; Freitas, A.V.L.; Vila, R. 2016. One-note samba: the biogeographical history of the relict Brazilian butterfly Elkalyce cogina. *Journal of Biogeography* 43(4):727-737.

Vicente, J.C.; Dincă, V.; Vila, R. and Parra, B. 2016. Leptidea reali Reissinger, 1990, nueva especie para Castilla y León (España) (Lepidoptera: Pieridae). *Arquivos Entomolóxicos* 16: 311-316.

Vila, R. 2016. Boon for a Recondite Biographer or Data for a serious systematist?. In: Blackwell, S.H. & Johnson, K. (Eds.) Fine lines. Vladimir Nabokov's scientific art, New Haven & London, Yale University Press.

Vodă, R.; Dapporto, L.; Dincă, V.; Shreeve, T.G.; Khaldi, M.; Barech, G.; Rebbas, K.; Sammut, P.; Scalercio, S.; Hebert, P.D.N. and Vila, R. 2016. Historical and contemporary factors generate unique butterfly communities on islands. *Scientific Reports* 6: 28828.

Fig. 5-6: *We have been busy developing the EUGENMAP project (European Genetic Map of Butterflies). Some of the last and most difficult species inhabit exclusively the extreme north of Europe. Raluca Vodă and Vlad Dincă, with the invaluable help of our collaborator Sylvain Cuvelier, drove more than 10 thousand kilometres throughout Scandinavia in order to find these butterflies.*

Photo: *Vlad Dincă.*

The butterfly in the picture is Boloria improba*, which in Europe is extremely local, well above the Polar Circle*

Photo: *Raluca Vodă*

Funded Projects

- **Project Title:** Speciation genomics in non-model organisms: exploring the diversification continuum in European butterflies (RADMAR)
  Financed by: Spanish Ministerio de Economía y Competitividad (CGL2016-76322-P)
  Years: 2016-2019
- **Project Title:** Eco-PhyloGeo - Linking phylogeography to ecology: extracting rules for butterfly biodiversity at large spatial scale.
  Financed by: Marie Curie Actions - European Fellowships (EF). (H2020-MSCA-IF-2014-EF_658844)
  Years: 2015-2017
  Scientist in Charge/Coordinator: Roger Vila. Research Fellow: Leonardo Dapporto.
- **Project Title:** Dynamics of Mediterranean butterflies in a phylogeographic framework: mapping genetic diversity across time and space (DynaGen)
  Financed by: Spanish Ministerio de Economía y Competitividad (CGL2013-48277-P)
  Years: 2014-2017

Fig. 7: *Joan Carles Hinojosa, in the picture, performed a long expedition to collect butterflies in Central Europe. He was helped by our collaborator Paula Escuer and together they crossed Poland, Slovakia, Czech Republic and Germany.*
Photo: *Paula Escuer, Tatra Mountains, Poland*

- **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 Dinca
- **Project Title:** MIGRATION— The most cosmopolitan animal migration: phylogeography and population genomics of the butterfly *Vanessa cardui*
  Financed by: Marie Curie Actions— International Outgoing Fellowships (IOF) (FP7-PEOPLE-2013-IOF_622716)
  Years: 2015-2018
  Coordinator: Roger Vila. Research Fellow: Gerard Talavera
- **Project title:** PENINSULA— Peninsular patterns for species richness and genetic diversity in Mediterranean butterflies
  Financed by: the European Union's Seventh Framework programme for research and innovation under the Marie Skłodowska-Curie grant agreement No 609402 – 2020 researchers: Train To Move (T2M)
  Years: 2016-2018
  Scientist in Charge/Coordinator: Simona Bonelli. Research Fellow: Raluca Voda.
- **Project Title:** ButterflyNet—an integrative framework for comparative biology
  Financed by: GoLife Program. National Science Foundation (USA)
  Years: 2016-2020
  PI: David J. Lohman
- **Project Title:** El largo viaje de *Vanessa cardui*
  Financed by: Spanish Foundation for Science and Technology (FECYT) (FCT-15-10115)
  Year: 2016
  PI: Roger Vila
- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014-2016
  PI: Salvador Carranza

group HERBIVORE BEETLE EVOLUTION

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

group members

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

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Josep Roca, Research Assistant, MINECO
Gissela De la Cadena, PhD Student, SENESCYT Scholarship (Ecuador)
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Nguyen Thi Dinh, PhD Student, CSIC Scholarship (International Cooperation)
Helena Vizán, PhD Student, MINECO Scholarship
Nikolaos Vlachopoulos, ERASMUS+ Practical Training

Research Outline

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

Fig. 1: *Most North American species of* Calligrapha *feed on riparian plants, and it is common to find them in places like this thicket of willows by the placid current of a river in eastern Oregon.*
Photo: *T. Montelongo*

Research Lines

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

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

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

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

5. Beetle systematics: The work being undertaken in ongoing and previous projects always results in interesting samples, some representing new species for science. We use molecular phylogenetics to investigate species relationships and whenever it is possible we describe the unknown diversity.

Publications 2016

Gómez-Zurita, J. 2016. Systematic revision of *Calligrapha* Chevrolat (Coleoptera: Chrysomelidae) with pale spots on dark elytra and description of two new species. *Zootaxa* 4072: 61-89.

Gómez-Zurita, J.; Cardoso, A.; Coronado, I.; De la Cadena, G.; Jurado-Rivera, J.A.; Maes, J.-M.; Montelongo, T.; Nguyen, D.T. and Papadopoulou, A. 2016. High-throughput biodiversity analysis: rapid assessment of species richness and ecological interactions of Chrysomelidae (Coleoptera) in the tropics. *ZooKeys, Research on Chrysomelidae vol. 6*, 597: 3-26.

Maes, J.M. and Gómez-Zurita, J. 2016. Chrysomelidae (Coleoptera) de Nicaragua, Parte IV, Chrysomelinae. *Revista Nicaragüense de Entomología* 76(4): 3-94.

Maes, J.M.; Gómez-Zurita, J.; Riley, E.G.; Windsor, D.; Borowiec, L. and Chaboo, C.S. 2016. Chrysomelidae

Fig. 2: Calligrapha alni, *as its name clearly suggests, is one of the few species in the genus that specialized in the use of Alnus as food. It can be easily recognized by the brown color occupying most of the surface of elytra.*

Photo: *T. Montelongo*

de Nicaragua, Parte VIII, Cassidinae *sensu stricto* (tortoise beetles). *Revista Nicaragüense de Entomología* 76(8): 3-189.

Maes, J.M.; Gómez-Zurita, J. and Staines, C.L. 2016. Chrysomelidae (Coleoptera) de Nicaragua, Parte IX, Cassidinae Hispinos. *Revista Nicaragüense de Entomología* 76(9): 3-201.

Nguyen, D.T. and Gómez-Zurita, J. 2016. Subtle ecological gradient in the tropics triggers high species-turnover in a local geographical scale. *PLoS ONE* 11(6): e0156840.

Tuset, V.M.; Otero-Ferrer, J.L.; Gómez-Zurita, J.; Venerus, L.A.; Stransky, C.; Imondi, R.; Orlov, A.M.; Ye, Z.; Santschi, L.; Afanasiev, P.K.; Zhuang, L.; Farré, M.; Love, M.S. and Lombarte, A. 2016. Otolith shape lends support to the sensory drive hypothesis in rockfishes. *Journal of Evolutionary Biology* 29: 2083-2097.

Funded Projects

- **Project Title:** Community changes associated to biome shifts and their importance for conservation
  Financed by: Consejo Superior de Investigaciones Científicas (2012VN0004).
  Years: 2012-2016
  PI: Jesús Gómez-Zurita
- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014-2016
  PI: Salvador Carranza
- **Project Title:** ¿Tienen los endosimbiontes de herencia materna algún papel en el origen y mantenimiento de la unisexualidad en *Calligrapha* (Coleoptera: Chrysomelidae)?
  Financed by: Ministerio de Economía (CGL2014-52937-P)
  Years: 2015-2017
  PI: Jesús Gómez-Zurita
- **Project Title:** Phylogeny and biogeography of Polyrhaphidini and their placement among the Lamiinae (Coleoptera: Cerambycidae).
  Financed by: «Ciência sem Fronteiras» Programme (CNPq, Brasil)
  Year: 2016
  PI: Jesús Gómez-Zurita

Fig. 3: *Beautiful and diverse* Platycorynus *in the Núi Chúa National Park (Vietnam). The diversity of leaf beetles in tropical forests is stunning. Our modest survey in some 10 sq. km of dry and broadleaf and evergreen forest in Núi Chúa yielded an estimate of more than 300 species in the lower stratum of plants alone.*

Photo: *A. Cardoso*

group PHYLOGENY AND PHYLOGEOGRAPHY OF MAMMALS

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

group members

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Research Scientist, CSIC

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Marina Querejeta, Predoctoral Researcher, FPI Contract, MINECO
Karla García, Visiting Researcher from Universitat de Barcelona

Research Outline

Our main goal is the application of phylogenetic and genomic analyses to the study of animal biodiversity and evolution, with specific interest in mammals. Using next-generation sequencing techniques and advanced bioinformatic tools, we are analyzing the population divergence and speciation process in different species complexes in order to obtain a better description of our biological diversity. We also use these modern methodologies to understand the evolutionary history of some species of great conservation importance.

Research Lines

1. Population genomics and speciation

The reconstruction of species trees of closely related species based on multiple genomic markers and coalescent theory can help to estimate speciation times, study gene flow, delimit species and, in general, better understand the speciation process. To be able to effectively use these techniques in mammals, we have developed a large set of intronic markers. In addition, we are generating massive genomic information using next-generation sequencing techniques. We are sequencing these markers in several groups of small mammals such as *Neomys*, *Sorex* and *Arvicola*, which we use as models to understand population divergence and speciation in a comparative perspective, with the Iberian Peninsula as common geographical scenario. To obtain material for these studies we are making extensive use of noninvasive samples such as skulls obtained from owl pellets. The rigorous characterization of speciation in these species complexes is expected to lead to a better understanding of our biological diversity.

2. Conservation genomics

The Pyrenean desman (*Galemys pyrenaicus*) is a small semi-aquatic mammal endemic to the northern half of the Iberian Peninsula and is endangered in a large part of its distribution range. We are currently studying several aspects of the evolutionary history of this unique species using large amounts of sequence data and SNPs obtained by next-generation sequencing techniques. We are also analyzing postglacial and contemporary dispersal patterns, as well as connectivity problems between populations, using highly innovative approaches. Much of the material we use for genetic analysis comes from the small faeces that desmans deposit on emerged rocks in the rivers, whose use for genetic studies was pioneered by our group. To get additional samples and carry out this research we are collaborating with different scientists and administrations involved in the conservation of the Pyrenean desman. The results we are obtaining are of high scientific relevance at the same time that have crucial implications for the conservation of this species.

Publications 2016

Hawlitschek, O.; Morinière, J.; Dunz, A.; Franzen, M.; Rödder, D.; Glaw, F.; Haszprunar, G. 2016. Comprehensive DNA barcoding of the herpetofauna of Germany. *Molecular Ecology Resources* 16(1):242-

Hawlitschek, O.; Scherz, M.D.; Straube, N.; Glaw, F. 2016. Resurrection of the Comoran fish scale gecko Geckolepis humbloti Vaillant, 1887 reveals a disjunct distribution caused by natural overseas dispersal. *Organisms Diversity and Evolution* 16(1):289-298.

Hawlitschek, O.; Wang-Claypool, C.Y.; Scherz, M.D.; Montfort, L.; Soumille, O.; Glaw, F. 2016. New size record of the snake genus Liophidium by the island endemic L. Mayottensis (Squamata, lamprophiidae). *Spixiana* 39(2):287-288.

Querejeta, M.; González-Esteban, J.; Gómez, A.; Fernández-González, A.; Aymerich, P.; Gosálbez, J.; Escoda, L.; Igea, J. and Castresana, J. 2016. Genomic diversity and geographical structure of the Pyrenean desman. *Conservation Genetics* 17, 1333-1344.

Funded Projects

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

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

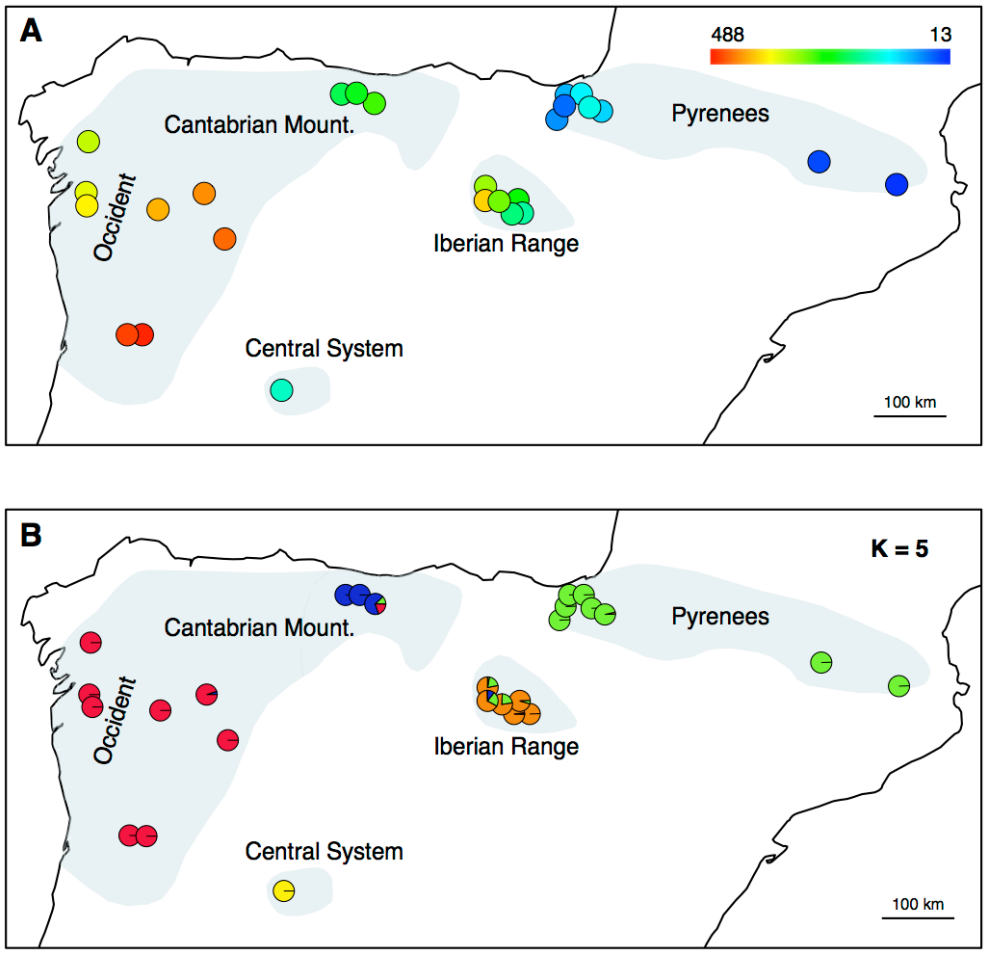

Fig. 1: *Analysis of ddRAD sequences from the Pyrenean desman* (Galemys pyrenaicus)*, a small semi-aquatic mammal endemic to the Iberian Peninsula. The total amount of sequence information analyzed was 45,000 loci and 1185 single nucleotide polymorphisms. (A) Map plotting color-coded heterozygosity rates in different specimens of the Pyrenean desman. The color scale is in number of heterozygous positions per million bases. The shadowed area approximately represents the current species distribution according to different sources. Interestingly, specimens from the southeastern Pyrenees had some of the lowest proportions of heterozygous positions inferred from genome-wide data in mammals so far. (B) Map plotting color-coded admixture proportions of each specimen as determined with Structure and K = 5. This analysis supported the existence of five distinct genomic clusters largely coincident with the main mountain ranges where the species occurs, with few specimens presenting relevant admixture levels.*

group SYSTEMATICS, BIOGEOGRAPHY AND EVOLUTION OF REPTILES AND AMPHIBIANS

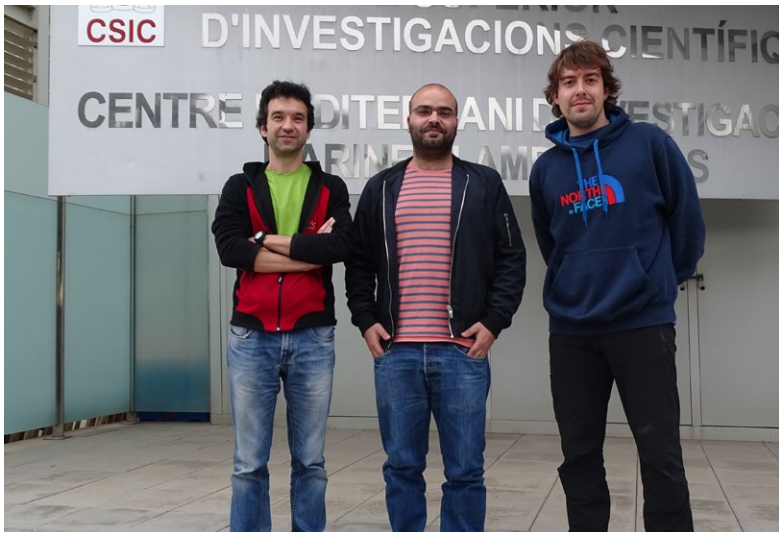

Photo group, from left to right: Salvador Carranza, Luis Machado and Marc Simó
Right from top to down: Raquel Vasconcelos and Joao Campos
Down from left to right: Joana Mendes, Duarte Gonçalves, Pedro Tarroso and Meritxell Xipell

group members

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Tenured Scientist, CSIC

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Raquel Vasconcelos, Postdoctoral Researcher, FCT Scholarship, Portugal
Marc Simó, PhD Student, FPI Scholarship, MEC
Joao Campos, PhD Student co-supervised with Dr. José Carlos Brito, CIBIO, Portugal, FCT Scholarship, Portugal
Duarte Gonçalves, PhD Student co-supervised with Dr. J.C. Brito, CIBIO, Portugal, FCT Scholarship, Portugal
Luis Machado, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Joana Mendes, PhD Student co-supervised with Dr. D.J. Harris, CIBIO, Portugal, FCT Scholarship, Portugal
Meritxell Xipell, MSc in Terrestrial Ecology and Biodiversity Management

Research Outline

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

Research Lines

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

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

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

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

3. Island biogeography and evolution

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

Publications 2016

Carranza, S. and Bauer, A. 2016. Margarita Metallinou (1985-2015). *Zootaxa* 4132: 598-600.

Carranza, S.; Simó-Riudalbas, M.; Jayasinghe, S.; Wilms, T. and Els, J. 2016. Microendemicity in the northern Hajar Mountains of Oman and the United Arab Emirates with the description of two new species of geckos of the genus *Asaccus* (Squamata: Phyllodactylidae). *PeerJ* 4: e2371.

de Pous, P., Simó-Riudalbas, M., Els, J., Jayasinghe, S., Amat, F. and Carranza, S. 2016. Phylogeny and biogeography of Arabian populations of the Persian Horned Viper *Pseudocerastes persicus* (Duméril, Bibron & Duméril, 1854). *Zoology in the Middle East* 62: 231-238.

de Pous, P., Machado, L., Metallinou, M., Cervenka, J., Kratochvil, L., Paschou, N., Mazuch, T., Smid, J., Simó-Riudalbas, M., Sanuy, D. and Carranza, S. 2016. Taxonomy and Biogeography of *Bunopus spatalurus* (Reptilia: Gekkonidae) from the Arabian Peninsula. *Journal of Zoological Systematics and Evolutionary Research* 54: 67-81.

Froufe, E.; Prié, V.; Faria, J.; Ghamizi, M.; Gonçalves, D.V.; Gürlek, M.E.; Karaouzas, I.; Kebapçi, Ü.; Şereflişank, H.; Sobral, C.; Sousa, R.; Teixeira, A.; Varandas, S.; Zogaris, S.; Lopes-Lima, M. 2016. Phylogeny, phylogeography, and evolution in the Mediterranean

Fig. 1: *Milking Echis omananeis for venomic analyses*

region: News from a freshwater mussel (Potomida, Unionida). *Molecular Phylogenetics and Evolution* 100: 322-332.

Froufe, E.; Gonçalves, D.V.; Teixeira, A.; Sousa, R.; Varandas, S.; Ghamizi, M.; Zieritz, A.; Lopes-Lima, M. 2016. Who lives where? Molecular and morphometric analyses clarify which Unio species (Unionida, Mollusca) inhabit the southwestern Palearctic. *Organisms Diversity and Evolution* 16(3): 597-611.

Garcia-Porta, J.; Šmíd, J.; Sol, D.; Fasola, M. and Carranza, S. 2016. Testing the island effect on phenotypic diversification: insights from the *Hemidactylus* geckos of the Socotra Archipelago *Scientific Reports* 6: 23729.

Garcia-Porta, J.; Morales, H.E.; Gómez-Díaz, E.; Sindaco, R. and Carranza, S. 2016. Patterns of diversification in islands: A comparative study across three gecko genera in the Socotra Archipelago *Molecular Phylogenetics and Evolution* 98: 288-299.

Gonçalves, D.V.; Pereira, P.; Godinho, R.; Lopes, S.; Velo-Antón, G.; Brito, J.C. 2016. Development of 23 microsatellite loci for Boulenger's agama (*Agama boulengeri*) with partial cross-amplification in other Agama species. *Amphibia - Reptilia* 2(27): 246-52.

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Maia, J.P., Harris, D.J. and Carranza, S. 2016. Reconstruction of the evolutionary history of Haemosporida (Apicomplexa) based on the cyt *b* gene with characterization of *Haemocystidium* in geckos (Squamata: Gekkota) from Oman *Parasitology International* 65: 5-11.

Maia, J.P., Harris, D.J., Carranza, S. and Gómez-Díaz, E. 2016. Assessing the diversity, host-specificity and infection patterns of apicomplexan parasites in reptiles from Oman, Arabia. *Parasitology* 143: 1730-1747.

Mendes, J., Harris, D.J., Carranza, S. and Salvi, D. 2016. Evaluating the phylogenetic signal limit from mitogenomes, slow evolving nuclear genes, and the concatenation approach. New insights into the Lacertini radiation using fast evolving nuclear genes and species trees *Molecular Phylogenetics and Evolution* 100: 254-267.

Rato, C., Harris, J., Carranza, S., Machado, L., Perera, A. 2016. The taxonomy of the *Tarentola mauritanica* species complex (Gekkota: Phyllodactylidae): Bayesian species delimitation supports six candidate species. *Molecular Phylogenetics and Evolution* 94: 271-278.

Smid, J.; Shobrak, M.; Wilms, T.; Joger, U.; Carranza, S. 2016. Endemic diversification in the mountains: genetic, morphological, and geographical differentiation of the *Hemidactylus* geckos in southwestern Arabia. *Organisms Diversity & Evolution*:1-21.

Tamar, K.; Carranza, S.; Sindaco, R.; Moravec, J.; Trape, J.F. and Meiri, S. 2016. Out of Africa: phylogeny and biogeography of the widespread genus *Acanthodactylus* (Reptilia: Lacertide). *Molecular Phylogenetics and Evolution* 103: 6-18.

Tamar, K.; Scholz, S.; Crochet, P.A.; Geniez, P.; Meiri, S.; Schmitz, A.; Wilms, T. and Carranza S. 2016. Evolution around the Red Sea: Systematics and biogeography of the agamid genus *Pseudotrapelus* (Squamata: Agamidae) from North Africa and Arabia *Molecular Phylogenetics and Evolution* 97: 55-68.

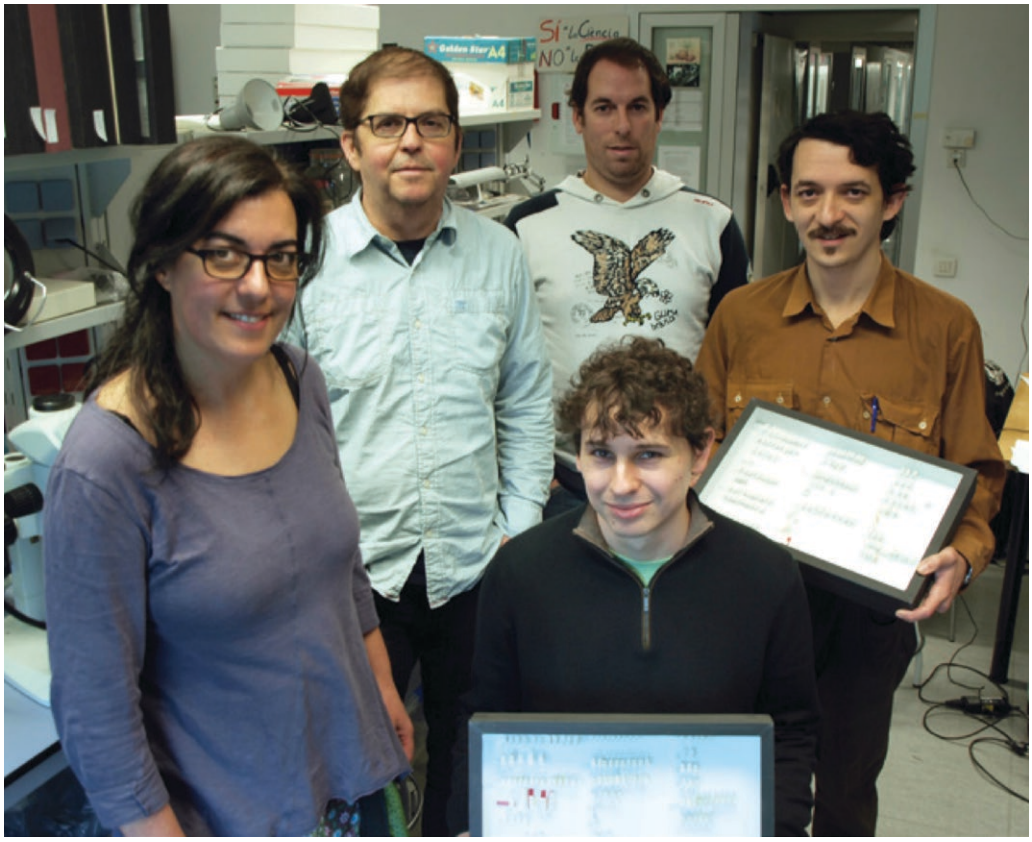
Tamar, K.; Smid, J.; Göçmen, B.; Meiri. S. and Carranza, S. 2016. An integrative systematic revision and biogeography of *Rhynchocalamus* snakes (Reptilia, Colubridae) with a description of a new species from Israel. *PeerJ* 4: e2769.

Vasconcelos, R.; Montero-Mendieta, S.; Simó-Riudalbas, M.; Sindaco, R.; Santos, X.; Fasola, M.; Llorente, G.; Razzetti, E. and Carranza, S. 2016. Unexpectedly high levels of cryptic diversity uncovered by a complete DNA barcoding of reptiles of the Socotra Archipelago *PLoS ONE* 11(3): e0149985.

Funded Projects

- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014-2017
  PI: Salvador Carranza
- **Project Title:** Arabian reptiles as a model to investigate how biodiversity is generated and maintained in arid areas
  Financed by: Ministerio de Economía y Competitividad MINECO (CGL2015-70390-P)
  Years: 2016-2018
  PI: Salvador Carranza
- **Project Title:** Dragon's blood tree's gecko – a flagship for Socotra fauna
  Financed by: Mohamed bin Zayed Species Conservation Fund (Ref: 14259910)
  Years: 2015-2016
  PI: Raquel Vasconcelos

group WATER AND CAVE BEETLE EVOLUTION



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

group members

Ignacio Ribera, *Group Leader*
Research Scientist, CSIC

Anabela Cardoso, Lab Manager, MICINN Contract
David García-Vázquez, PhD Student, MICINN Scholarship
Andrey Rudoy, PhD Student, JAE Scholarship, CSIC
Adrián Villastrigo Carbajo, PhD Student, MICINN Scholarship

Research Outline

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

Research Lines

1. Origin of widespread species of European lotic water beetles

Most species have narrow geographic ranges, but many groups also include some widespread species. In most cases why and how these widespread species have reached their current ranges is unknown. A particularly intriguing case is that of species with continental-scale distributions despite belonging to lineages with generally poor dispersal abilities. We investigate the origin of these species, to understand how they have reached their current distributions.

2. Evolution of the complex male genitalia in Hydraenidae

The extraordinary complexity of the male genitalia of some arthropods has always intrigued evolutionary biologists. Using a comparative phylogenetic and morphometric approach we study the selective forces shaping the evolution of male genitalia in different groups of beetles.

3. Evolution of the tolerance to salinity

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

Fig. 1: Aphaobius haraldi *Faille, Fresneda & Ribera 2016, a new subterranean species of Leptodirini from Austria.*

Photo: *J. Fresneda.*

Fig. 2: *Antennae of different species of the genus* Aphaobius. *Most species of the genus are inhabitants of the deep part of caves, but some are also found in shallow subterranean environments. However, to which degree differences in the elongation of the antennae are related to the type of habitat is still unknown.*

Photo: *J. Fresneda.*

4. Evolution of subterranean beetles

Cave animals have fascinated evolutionary biologists since their discovery in the early XIX Century. The origin of the morphological modifications of subterranean species - loss of pigments and eyes, elongation of body and appendages, modifications of the life cycle and physiology among others - is still controversial, specially in that many of these changes have independently evolved in many unrelated lineages, sometimes to an astonishing degree of similarity. We study the evolution of troglomorphy in different lineages of beetles in the Mediterranean area.

Publications 2016

ISI Articles

Andújar, C.; Faille, A.; Pérez-González, S.; Zaballos, J.P.; Vogler, A.P. and Ribera, I. 2016. Gondwanian relicts and oceanic dispersal in a cosmopolitan radiation of euedaphic ground beetles. *Molecular Phylogenetics and Evolution* 99: 235-246.

Beutel, R.G. and Ribera, I. 2016. 7. Adephaga Schellenberg, 1806. In: Beutel, R.G. & Leschen, R.A.B. (eds.): Handbook of Zoology, Arthropoda: Insecta. Coleoptera, Beetles. Vol. 1: Morphology and

Systematics (Archostemata, Adephaga, Myxophaga, Polyphaga partim). 2nd Edition. Walter de Gruyter, Berlin. pp. 77-79.

Beutel, R.G.; Balke, M. and Ribera, I. 2016. 7.7. Aspidytidae Ribera,Beutel, Balke and Vogler, 2002. In: Beutel, R.G. & Leschen, R.A.B. (eds.): Handbook of Zoology, Arthropoda: Insecta. Coleoptera, Beetles. Vol. 1: Morphology and Systematics (Archostemata, Adephaga, Myxophaga, Polyphaga partim). 2nd Edition. Walter de Gruyter, Berlin. pp. 141-149.

Bruno, D.; Gutiérrez-Cánovas, C.; Sánchez-Fernández, D.; Velasco, J. and Nilsson, C. 2016. Impacts of environmental filters on functional redundancy in riparian vegetation. *Journal of Applied Ecology* 53: 846-855.

Faille, A.; Ribera, I. and Fresneda, J. 2016. On the genus *Aphaobius* Abeille de Perrin, 1878, with description of a new species from the mesovoid shallow substratum (MSS) of Austria (Coleoptera: Leiodidae: Cholevinae: Leptodirini). *Zootaxa* 4169: 44-56.

García-Vázquez, D.; Bilton, D.T.; Alonso, R.; Benetti, C.J.; Garrido, J.; Valladares, L.F. and Ribera, I. 2016. Reconstructing ancient Mediterranean crossroads in *Deronectes* diving beetles. *Journal of Biogeography* 43: 1533-1545.

García-Vázquez, D. and Ribera, I. 2016. The origin of widespread species in a poor dispersing lineage (diving beetle genus Deronectes). *PeerJ* 4:e2514.

Hernando, C. and Ribera, I. 2016. 19.5. Limnichidae Erichson, 1846. In: Beutel, R.G. & Leschen, R.A.B. (eds.): Handbook of Zoology, Arthropoda: Insecta. Coleoptera, Beetles. Vol. 1: Morphology and Systematics (Archostemata, Adephaga, Myxophaga, Polyphaga partim). 2nd Edition. Walter de Gruyter, Berlin. pp. 605-612.

Hernando, C. and Ribera, I. 2016. Family Limnichidae. In: Löbl, I. & Löbl, D. (eds) Catalogue of Palaearctic Coleoptera: Volume 3. Scarabaeoidea Scirtoidea Dascilloidea Buprestoidea - Byrrhoidea. Revised and Updated Edition. Brill, Leiden, pp. 607-610.

Hidalgo-Galiana, A.; Monge, M.; Biron, D.G.; Canals, F.; Ribera, I. and Cieslak, A. 2016. Protein expression parallels thermal tolerance and ecologic changes in the diversification of a diving beetle species complex. *Heredity* 116: 114-123.

Morinière, J.; Van Dam, M.H.; Hawlitschek, O.; Bergsten, J.; Michat, M.C.; Hendrich, L.; Ribera, I.; Toussaint, E.F.A. and Balke, M. 2016. Phylogenetic niche conservatism explains an inverse latitudinal diversity gradient in freshwater arthropods. *Scientific Reports* 6: 26340.

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Rudoy, A. and Ribera, I. 2016. The macroevolution of size and complexity in insect male genitalia. *Peerj*, 4:e1882.

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Toussaint, E.F.A.; Beutel, R.G.; Morinière, J.; Jia, F.; Xu, S.; Michat, M.C.; Zhou, X, Bilton, D.T.; Ribera, I.; Hájek, J. and Balke, M. 2016. Molecular phylogeny of the highly disjunct cliff water beetles from South Africa and China (Coleoptera: Aspidytidae). *Zoological Journal of the Linnean Society* 176: 537-546.

Funded Projects

- **Project Title:** Evolution of habitat transitions in aquatic Coleoptera.
  Financed by: Ministerio de Ciencia e Innovación.
  Years: 2014-2017
  PI: Ignacio Ribera
- **Project Title:** Biodiversitat Animal i Evolució
  Financed by: Generalitat de Catalunya (2014 SGR 1532)
  Years: 2014-2016
  PI: Salvador Carranza

PROGRAM

COMPARATIVE AND COMPUTATIONAL GENOMICS

Research Groups

Comparative Genomics
Tomàs Marquès -Bonet and Arcadi Navarro, *Group Leaders*

Evolutionary and Functional Genomics
Josefa González, *Group Leader*

Paleogenomics
Carles Lalueza-Fox, *Group Leader*

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

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

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

group COMPARATIVE GENOMICS

From left to right and top to down: Diego Hartasánchez, Gerard Muntané, Rajendra Mandaje, Marc de Manuel Montero, Arcadi Navarro, Inna Povolotskaya, Tomàs Marquès-Bonet, Aitor Serres, Lukas Kuderna, Marco Telford, Luis Ferrández, Txema Heredia, Juan Antonio Rodríguez-Pérez, Jessica Hernández, David de Juan, Irene Lobón, Manuel Solís, Laura Batlle and Marina Brasó

group members

Tomàs Marquès-Bonet,
Group Leader
Professor , UPF •
Research Professor, ICREA

Arcad*i Navarro,*
Group Leader
Professor , UPF •
Research Professor, ICREA

David A. Hughes, Postdoctoral Researcher
David de Juan, Postdoctoral Researcher
Esther Lizano, Postdoctoral Researcher
Gerard Muntané, Postdoctoral Researcher
Inna Povolotskaya, Postdoctoral Researcher
Josephine Daub, Postdoctoral Researcher
Martin Kuhlwilm, Postdoctoral Researcher
Aitor Serres, PhD Student
Claudia Fontsere, PhD Student
Diego Hartasánchez, PhD Student
Irene Lobon, PhD Student
Jessica Hernadez, PhD Student
Juan Antonio Rodríguez-Pérez, PhD Student
Luis Ferrández, PhD Student
Lukas Kuderna, PhD Student
Manuel Solís, PhD Student
Marc de Manuel, PhD Student
Marco Telford, PhD Student
Marina Brasó, PhD Student
Rajendra Mandaje, PhD Student
Raquel Garcia, PhD Student
Sojung Han, PhD Student
Txema Heredia, PhD Student
Xavier Ferré, IT Technician

Research Outline

The main line of research in our labs is centered in study of the many different biological processes, particularly natural selection, during millions of years. Specifically, we focus on the discovery of the extent of all kinds of genome variation within different phenotypically genomes. 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. But also, interrogating these patterns of genome diversity we can infer what the forces affect living organisms, how and when they act and how they affect such various things as biodiversity or the differential susceptibility of different persons to certain diseases.

Research Lines

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

2. Epigenetics and transcriptomics of non-human primates
DNA methylation is an epigenetic modification involved in regulatory processes. However, the dynamics of DNA methylation changes between human and their closest relatives is still poorly understood. We evaluate methylation patterns in recent human evolution.

3. ELIXIR - the European life science Infrastructure for Biological Information - is a distributed organisation comprising national bioinformatics research infrastructures and the European Bioinformatics Institute (EMBL-EBI). This coordinated infrastructure includes data standards, exchange, interoperability, storage, security and training.

Publications 2016

Abascal, F.; Corvelo, A.; Cruz, F.; [39 authors]; Marques-Bonet, T.; [4 authors]; Gabaldón, T.; Alioto, T. and Godoy, J.A. 2016. Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. *Genome Biol.* 17 (1):251.

Buzdugan, L.; Kalisch, M.; Navarro, A.; Schunk, D.; Fehr, E. and Bühlmann, P. 2016. Assessing statistical significance in multivariable genome wide association analysis. *Bioinformatics* 32: 1990-2000.

Cagan, A.; Theunert, C.; Laayouni, H.; Santpere, G.; Pybus, M.; Casals, F.; Prüfer, K.; Navarro, A.; Marques-Bonet, T.; Bertranpetit, J. and Andrés, A.M. 2016. Natural Selection in the Great Apes. *Molecular Biology and Evolution* 33 (12): 3268-3283.

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Corrales-Acuña, E.; Navarro, A.; Cuenca, P.; Albertazzi, F. and Campos, D. 2016. Candidate gene study reveals DRD1 and DRD2 as putative interacting risk factors for youth depression. *Psychiatry Research* 244: 71-77.

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de Valles-Ibáñez, G.; Hernandez-Rodriguez, J.; Prado-Martinez, J.; Luisi, P.; Marquès-Bonet, T. and Casals, F. 2016. Genetic load of loss-of-function polymorphic variants in great apes. *Genome Biol Evol.* 8 (3): 871-877.

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exomes reveal population-specific differences in disease-related genetic variation. *Molecular Biology and Evolution* 33: 1205-1218.

Fan, Z.; Silva, P.; Gronau, I.; Wang, S.; Armero, AS.; Schweizer, RM.; Ramire,z O.; Pollinger, J.; Galaverni, M.; Ortega Del-Vecchyo, D.; Du, L.; Zhang, W.; Zhang, Z.; Xing, J.; Vilá, C.; Marques-Bonet, T.; Godinho, R.; Yue, B. and Wayne, RK. 2016. Worldwide patterns of genomic variation and admixture in gray wolves. *Genome Res.* 26(2): 163-73.

Freedman , A.H; Schweizer, R.M.; Ortega-Del Vecchyo, D.; [23 authors]; Marques-Bonet, T.; Ostrander, L.A.; Wayne, R.K. and Novembre, J. 2016. Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. *Plos Genetics* 12(3): e1005851.

Gallego, A.; Melé, M.; Balcells, I.; García-Ramallo, E.; Torruella-Loran, I.; Abelló, T.; Hvilsom, C.; Navarro, A.; Marquès-Bonet, T. and Espinosa-Parrilla, Y. 2016. Functional Implications of Human-Specific Changes in Great Ape microRNAs. *PLoS ONE* 11 (4): e0154194.

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Koblmüller, S.; Vilà, C.; Lorente-Galdos, B.; Dabad, M.; Ramirez, O.; Marques-Bonet, T.; Wayne, R.K. and Leonard, J.A. 2016. Whole mitochondrial genomes illuminate ancient intercontinental dispersals of grey wolves (Canis lupus*). Journal of Biogeography* 43: 1728-1738.

Kuhlwilm, M.; de Manuel, M.; Nater, A.; Greminger, M.P.; Krützen, M. and Marques-Bonet, t. 2016. Evolution and demography of the great apes. *Current Opinion in Genetics & Development* 41: 124-129.

Kuhlwilm, M.; Gronau, I.; Hubisz, M.J.; [12 authors]; Marques-Bonet, T.; Andrés, A.M.; Viola, B.; Pääbo, S.; Meyer, M.; Siepel, A. and Castellano, S. 2016. Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature* 530(7591): 429-33.

Lobon, I., Tucci S.; de Manuel, M.; Ghirotto, S.; Benazzo, A.; Prado-Martinez, J.; Lorente-Galdos, B.; Nam, K.; Dabad, M.; Hernandez-Rodriguez, J.; Comas, D.; Navarro, A.; Schierup, M.H.; Andres, A.M.; Barbujani, G.; Hvilsom, C. and Marques-Bonet, T. 2016. Demographic history of the genus Pan inferred fromwhole mitochondrial genome reconstructions. *Genome Biology and Evolution* 8: 2020-2030.

Marigorta, U.M.; Rodriguez J.A. and Navarro, A. 2016. GWAS: a milestone in the road from genotypes to phenotypes. In: Genome-Wide Association Studies: From Polymorphism to Personalized Medicine. Ed: K.Appasani. ISBN: 9781107042766. Cambridge University Press (Cambridge).

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Marsden, C.D.; Ortega-Del Vecchyo, D.; O'Brien, D.P.; Taylor, J.F.; Ramirez, O.; Vilà, C.; Marques-Bonet, T.; Schnabel, R.D.; Wayne, R.K. and Lohmueller, K.E. 2016. Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. *Proc Natl Acad Sci* U S A 113(1): 152-7.

Mieth, B.; Kloft M.; Rodríguez, J.A.; Sonnenburg, S.; Vobruba R.; Morcillo-Suárez, C.; Farré, X.; Marigorta, U.M.; Fehr, E.; Dickhaus, T.; Blanchard, G.; Schunk, D.; Navarro ,A. and Müller, K.R. 2016. Combining Multiple Hypothesis Testing with Machine Learning Increases the Statistical Power of Genome-wide Association Studies. *Scientific Reports* 6: 36671.

Sanchez-Delgado, M.; Court, F.; Vidal, E.; Medrano, J.; Monteagudo-Sánchez, A.; Martin-Trujillo, A.; Tayama, C.; Iglesias-Platas, I.; Kondova, I.; Bontrop, R.; Poo-Llanillo, M.E.; Marques-Bonet, T.; Nakabayashi, K.; Simón, C. and Monk D. 2016. Human Oocyte-Derived Methylation Differences Persist in the Placenta Revealing Widespread Transient Imprinting. *PLoS Genetics* 12(11): e1006427.

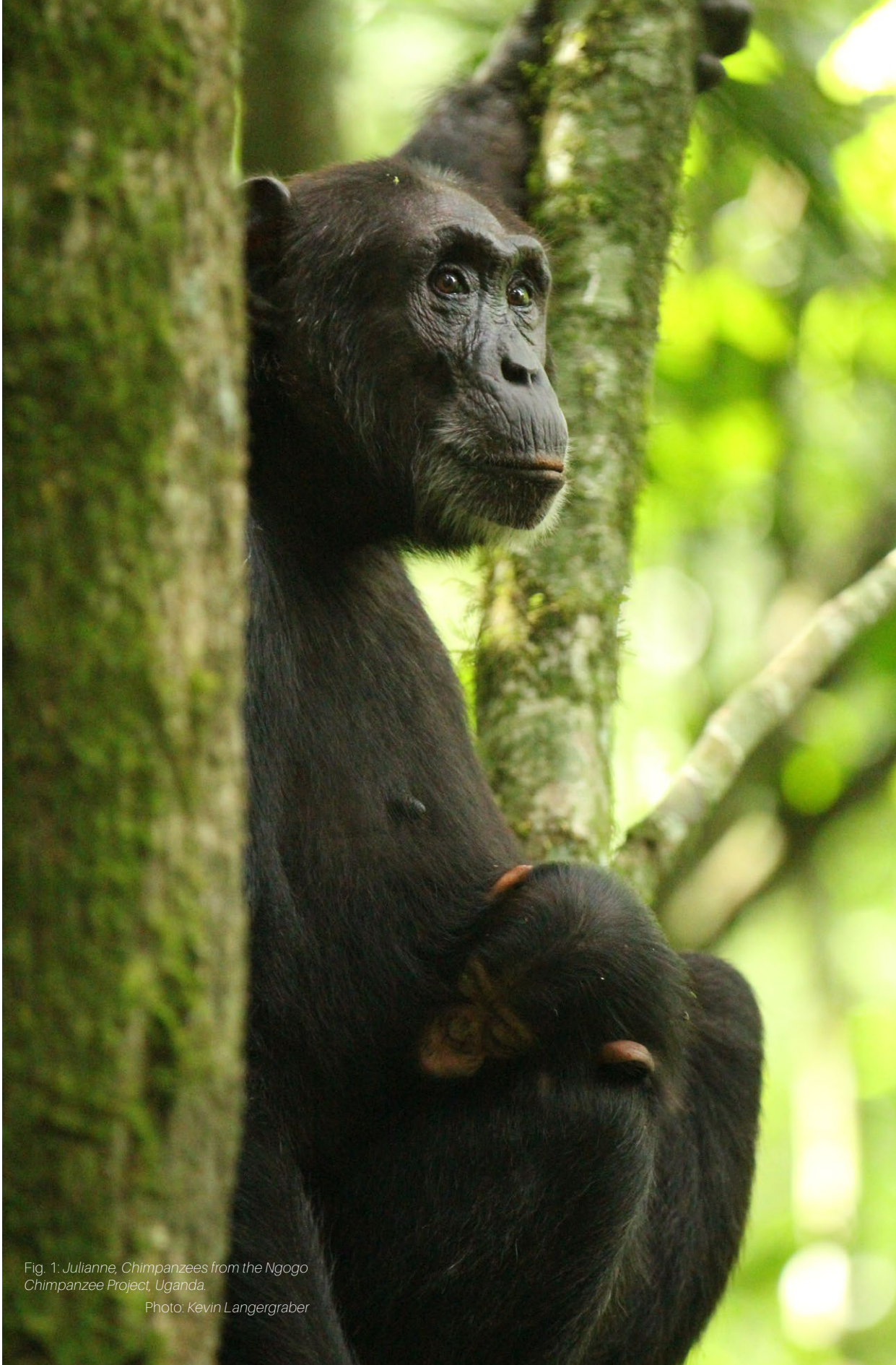


Fig. 1: *Julianne, Chimpanzees from the Ngogo Chimpanzee Project, Uganda.*
Photo: *Kevin Langergraber*

Santpere, G.; Lopez-Valenzuela, M.; Petit-Marty, N.; Navarro, A. and Espinosa-Parrilla, Y. 2016. Differences in molecular evolutionary rates among microRNAs in the human and chimpanzee genomes. *BMC Genomics* 17: 528.

Stange, J.; Dickhaus, T.; Navarro, A. and Schunk, D. 2016. Multiplicity- and dependency-adjusted p-values for control of the family-wise error rate. *Statistics and Probability Letters* 111: 32-40.

Stevison, L.S.; Woerner, A.E.; Kidd, J.M.; Kelley, J.L.; Veeramah, K.R.; McManus, K.F.; Great Ape Genome Project; Bustamante, C.D.; Hammer, M.F.; Wall, J.D. 2016. The Time Scale of Recombination Rate Evolution in Great Apes. *Molecular Biology and Evolution* 33(4):928-45

Funded Projects

- **Project Title:** Somatic mutations in autism spectrum disorders (ASD): single neuron analysis
  Financed by: NIH
  Years: 2015-2020
  PI: Nenad Sestan / Christopher Walsh
- **Project Title:** Evolución de la diversidad estructural del cromosoma y humano (BFU2014-55090-P)
  Financed by: MICINN (Spain)
  Years: 2015-2017
  PI: Tomàs Marquès-Bonet / Oscar Fornas
- **Project Title:** Structural variation and impact on gene expression of the human y chromosome (BFU2015-7116-ERC)
  Financed by: MICINN (Spain)
  Years: 2016
  PI: Tomàs Marquès-Bonet
- **Project Title:** Ebola genetics in gorilla (PRIC)
  Financed by: Fundacio Zoo Barcelona
  Year: 2016
  PI: Tomàs Marquès-Bonet
- **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: 2014-2017
  PI: Arcadi Navarro (Coordinator: Ana Conesa)
- **Project Title:** Fast-track ELIXIR implementation and drive early user exploitation across the life-sciences (Excellerate)
  Financed by: European Commission (INFRADEV-3-2015-676559)
  Years: 2015-2018
  PI: Arcadi Navarro
- **Project Title:** Creating medically-driven integrative bioinformatics applications focused on oncology, CNS disorders and their comorbidities (MedBioinformatics)
  Financed by: European Commission (H2020-PHC-32-2013 Call; Grant # 634143-2))
  Years: 2015-2018
  PI: Arcadi Navarro
- **Project Title:** ELIXIR-EXCELERATE: Fast-track ELIXIR implementation and drive early user exploitation across the life-sciences.
  Financed by: The Comission of the European Community.
  Years: 2015-2019
  PI: Arcadi Navarro
- **Project Title:** MEDBIOINFORMATICS Creating medically-driven integrative bioinformatics applications focused on oncology, CNS disorders and their comorbidities
  Financed by: The Comission of the European Community
  Years: 2015-2018
  PI: Arcadi Navarro
- **Project Title:** National Institute of Bioinformatics. Telematic nets of cooperative investigation in the field of health
  Financed by: Instituto de Salud Carlos III-Ministerio de Economía y Competitividad
  Years: 2014-2017
  PI: Arcadi Navarro

group EVOLUTIONARY AND FUNCTIONAL GENOMICS

From left to right: Nicolás N. Moreyra, Lain Guio, Josefa González, José Luis Villanueva-Cañas, Maite G. Barrón, Miriam Merenciano, Anna Ullastres, Vivien Horváth and Gabriel Rech

group members

Josefa González, *Group Leader*
Ramón y Cajal Researcher

Maite G. Barrón, Postdoctoral Researcher, CSIC Contract
Lain Guio, Postdoctoral Researcher, CSIC Contract
Gabriel E. Rech, Postdoctoral Researcher, CSIC Contract
José Luis Villanueva-Cañas, Postdoctoral Researcher, CSIC Contract
Miriam Merenciano , PhD Student, CSIC Contract
Anna Ullastres, PhD Student, FPI Fellowship
Nicolás N Moreyra, PhD visiting Student
Vivien Horváth, Master Student, Erasmus Fellowship
Lorena Espinar, Laboratory Technician

Research Outline

The key question in genomics is how genomes vary and evolve at both large and fine scales. In our lab, we are particularly interested in understanding the molecular processes underlying adaptive evolution and the functional consequences of adaptive mutations. Towards this end, we combine -omics strategies with detailed molecular and functional analyses of the candidate adaptive mutations in order to arrive at a comprehensive picture of adaptation. We study both transposable element (TE)-induced adaptations and point mutations in the model organism Drosophila melanogaster.
We are also interested in the population dynamics of TEs. TEs are the most active, diverse, and ancient components in a broad range of genomes. As such, a complete understanding of genome function and evolution cannot be achieved without a thorough understanding of TE impact and TE biology.

Research Lines

1. Deciphering the role of transposable elements in adaptive evolution
2. Spatial and temporal patterns of natural variation in European Drosophila melanogaster populations
3. Population dynamics of transposable element insertions

Publications 2016

Bergland, A.O.; Tobler, R.; González J.; Schmidt, P. and Petrov D.A. 2016. Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in *Drosophila melanogaster*. *Molecular Ecology* 25: 1157-1174.

Merenciano, M.; Ullastres, A.; Barrón, M.G; de Cara, M.A.R. and González, J. 2016. Functional analysis of a natural mutational hotspot in the proximal promoter of a stress-response gene in *Drosophila melanogaster*. *PLoS Genetics* 12(8):e1006249.

Ullastres, A.; Merenciano, M.; Guio, L.; and González, J. Transposable Elements: a toolkit for stress and environmental adaptation in bacteria. In: *Stress and Environmental Control of Gene Expression in Bacteria* (pp. 137) . Frans J. de Bruijn, Editor. Wiley-Blackwell Publishers, 2016.

Funded Projects

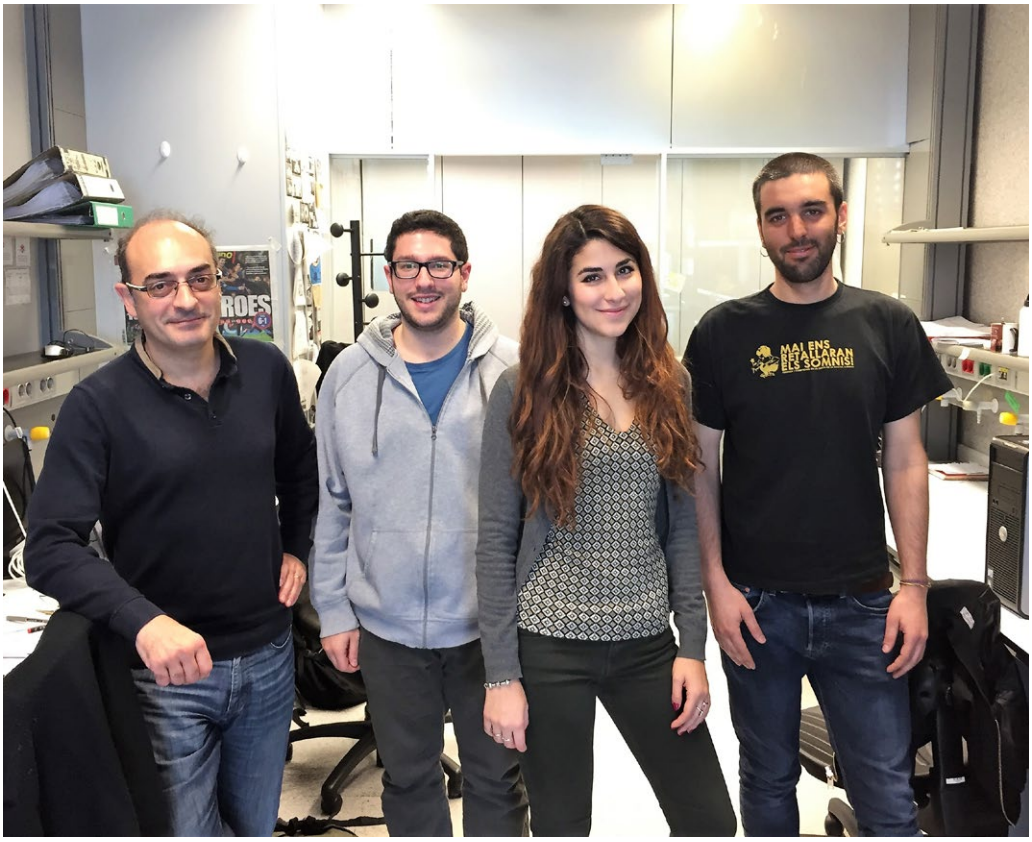
- **Project Title:** New approaches to long-standing questions: adaptation in Drosophila (H2020-ERC-2014-CoG-647900)
  Financed by: European Commission
  Years: 2016-2020
  PI: Josefa González
- **Project Title:** Origin, diversification and diversity of metazoans, fungi and their unicellular relatives; an ecological and evolutionary approach (BFU2014-57779-P).
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2015-2017
  co-PI: Josefa González and Iñaki Ruiz-Trillo
- **Project Title:** Drosophila population genomics network.
  Financed by: European Society for Evolutionary Biology
  Years: 2016-2020
  co-PI: Josefa González
- **Project Title:** Origin and evolution of sylvatic populations of *Anopheles gambiae*.
  Financed by: International Program for Scientific Cooperation (CNRS-CSIC).
  Years: 2016-2018
  co-PI: Josefa González
- **Project Title:** AdaptNET. Genomics of adaptation network (CGL2015-71726-REDT).
  Financed by: Ministerio de Ciencia e Innovación. Spain.
  Years: 2015-2017
  co-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: 2011-2016
  co-PI: Josefa González

Outreach Projects

- **Project Title:** Ciència i convivència: compendre el nostre entorn per sobreviure en una societat canviant (16S00307-006).
  Financed by: Ajuntament de Barcelona
  Year: 2016
  PI: Josefa González
- **Project Title:** Melanogaster Catch The Fly
  Financed by: Fundación Española para la Ciencia y la Tecnologia
  Year: 2016
  PI: Josefa González
- **Project Title:** Com els organismes s'adapten a l'ambient
  Financed by: Joves i Ciència. Fundació Catalunya-La Pedrera
  Year: 2016
  PI: Josefa González

Fig. 1-2: *Collection sites of natural populations of Drosophila melanogaster. A. Tomelloso Ciudad Real (Spain). B. Baza, Granada (Spain).*

group PALEOGENOMICS



From left to right: Carles Lalueza-Fox, Toni de-Dios, Benedetta Mattorre and Pere Gelabert

group members

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

Pere Gelabert, PhD Student
Toni de-Dios, Master Student
Benedetta Mattorre, Master Student

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 on Neanderthal remains from the site of El Sidrón in Asturias (Spain). We are also investigating the evolutionary dynamics of the prehistory of Europe through the analysis of Mesolithic, Neolithic, Copper and Bronze Age human genomes. We are also interested in the history of pathogens, and we are currently studying ancient malaria in Europe.

Research Lines

1. Neandertal genomic diversity

We are working on the remains from the El Sidrón site in Asturias, Spain. This is a family group of at least 13 Neandertal individuals that became accidentally accumulated in a single, synchronic event within a subterranean karstic system. El Sidrón offers the unique opportunity of launching for understanding the behaviour, diversity and kinship relationships within a contemporaneous Neandertal social group.

2. European prehistory

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

3. Ancient pathogens

We are reconstructing the adaptive effect of the eradicated malaria pathogens in Europe. We have retrieved *Plasmodium* DNA from antique microscopy slides from the Ebro Delta and we are planning to analyse also ancient human remains with potential signs of malaria.

Fig. 1: *Typical Bell Beaker ceramics.*

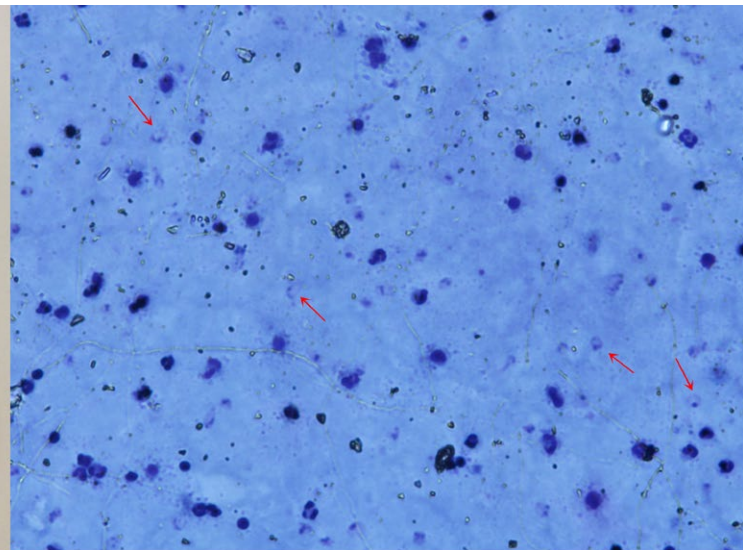


Fig. 2: *70 year-old blood drop slides from the Ebro Delta (left) from which DNA from the eradicated European malaria pathogens (right, arrows) have been retrieved.*

Publications 2016

Calafell, F.; Anglada, R.; Bonet, N.; González-Ruiz, M.; Prats-Muñoz, G.; Rasal, R.; Lalueza-Fox, C.; Bertranpetit, J.; Malgosa, A. and Casals, F. 2016. An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936-1939). *Electrophoresis* 37(21): 2841-2847.

Gelabert, P.; Sandoval-Velasco, M.; Olalde, I.; Fregel, R.; Rieux, A.; Escosa, R.; Aranda, C.; Paaijmans, K.; Mueller, I.; Gilbert, M.T.P. and Lalueza-Fox, C. 2016. Mitochondrial DNA from the eradicated European *Plasmodium vivax* and *P. falciparum* from 70-year-old slides from the Ebro Delta in Spain. *Proceedings of the National Academy of Sciences USA* 113(41):11495-11500.

Kuhlwilm, M.; Gronau, I.; Hubisz, M.; Prado-Martinez, J.; Kircher, M.; Fu, Q.; de Filippo, C.; Burbano, H.; Lalueza-Fox, C.; de la Rasilla, M.; Rosas, A.; Rudan, P.; Brajkovic, D.; Kucan, Z.; Gušic, I.; Marques-Bonet, T.; Andrés, A.; Viola, B.; Pääbo, S.; Meyer, M.; Siepel, A. and Castellano, S. 2016. Ancient gene flow from modern humans into Siberian Neandertals. *Nature* 530(7591):429-433.

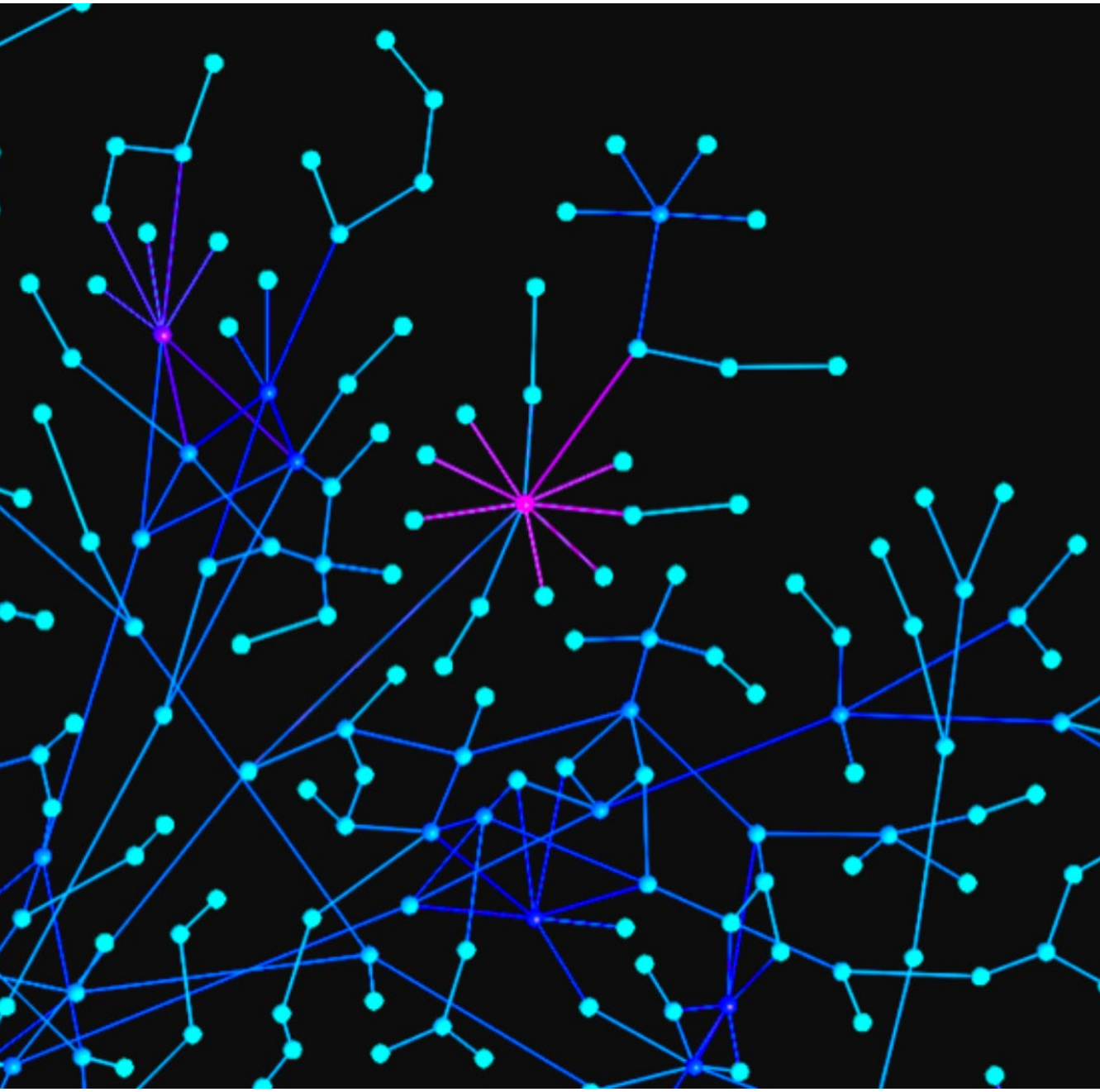
Lalueza-Fox, C. 2016. Genes, reyes e impostores. Una historia detectivesca tras los análisis genéticos de reyes europeos. Ed. Cálamo. ISBN: 978-84-16742-02-8.

Funded Projects

- **Project Title:** The genomic prehistory of the Iberian Peninsula (Ref: BFU2015-64699P)
  Financed by: Ministry of Economy and Competitivity, Spain
  Years: 2016-2018
  PI: Carles Lalueza-Fox
- **Project Title:** Grup de Recerca Consolidat en Biologia Evolutiva
  Financed by: Generalitat de Catalunya (2014SGR1311)
  Years: 2014-2016
  PI: Arcadi Navarro

PROGRAM

COMPLEX SYSTEMS



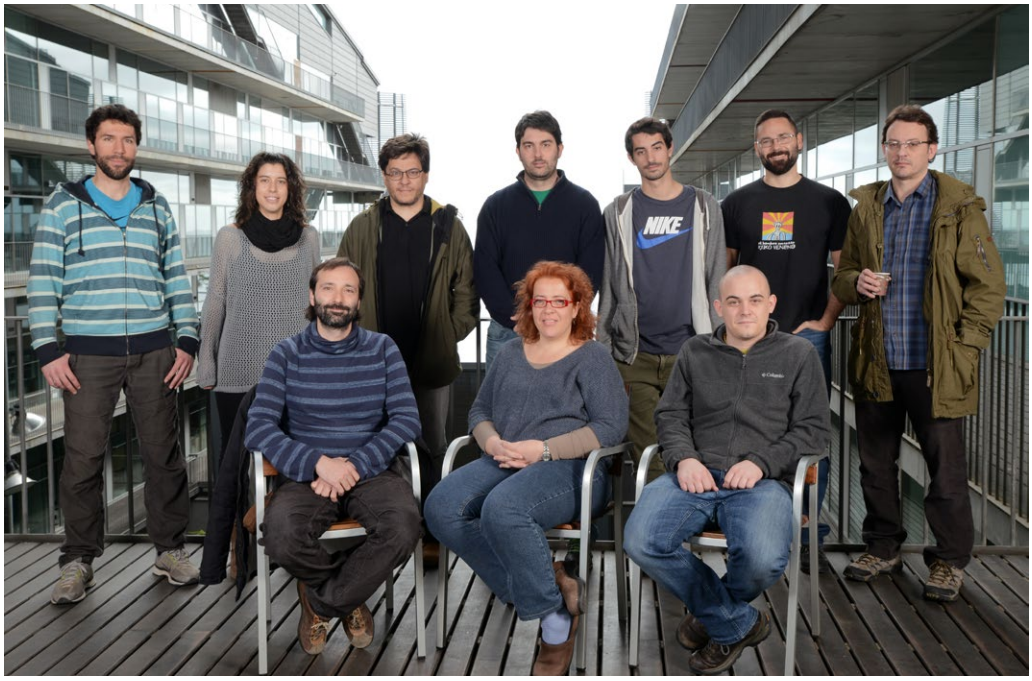
Research Groups

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

group members

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

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

Research Outline

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

Research Lines

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

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

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

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

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

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

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

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

Publications 2016

Bonforti; A.; Duran-Nebreda, S.; Montañez, R.; and Solé, R. 2016. Spatial self-organization in hybrid models of multicellular adhesion. *Chaos* 26, 103113.

Carbonell-Ballestero, M.; García-Ramallo, E.; Montañez, R.; Rodriguez-Caso, C.; Macía, J. 2016. Dealing with the genetic load in bacterial synthetic biology circuits: convergences with the Ohm's law. *Nucleic Acids Research* 44(1):496-507.

de Lorenzo, V.; Marlière, P. and Solé, R. 2016. Bioremediation at a global scale: from the test tube to planet Earth. *Microbial Biotechnology* 9, 618-625.

Duran-Nebreda, S.; Bonforti, A.; Montañez, R.; Valverde, S. and Solé, R. 2016. Emergence of proto-organisms from bistable stochastic differentiation and adhesion. *J. Royal Society Interface* 13, 20160108.

Duran-Nebreda, S. and Solé, R. 2016. Toward Synthetic Spatial Patterns in Engineered Cell Populations with Chemotaxis. *ACS Synth Biol.* 5, 654-661.

Macia, J.; Manzoni, R.; Conde, N.; Urrios, A.; de Nadal, E.; Solé, R. and Posas, F. 2016. Implementation

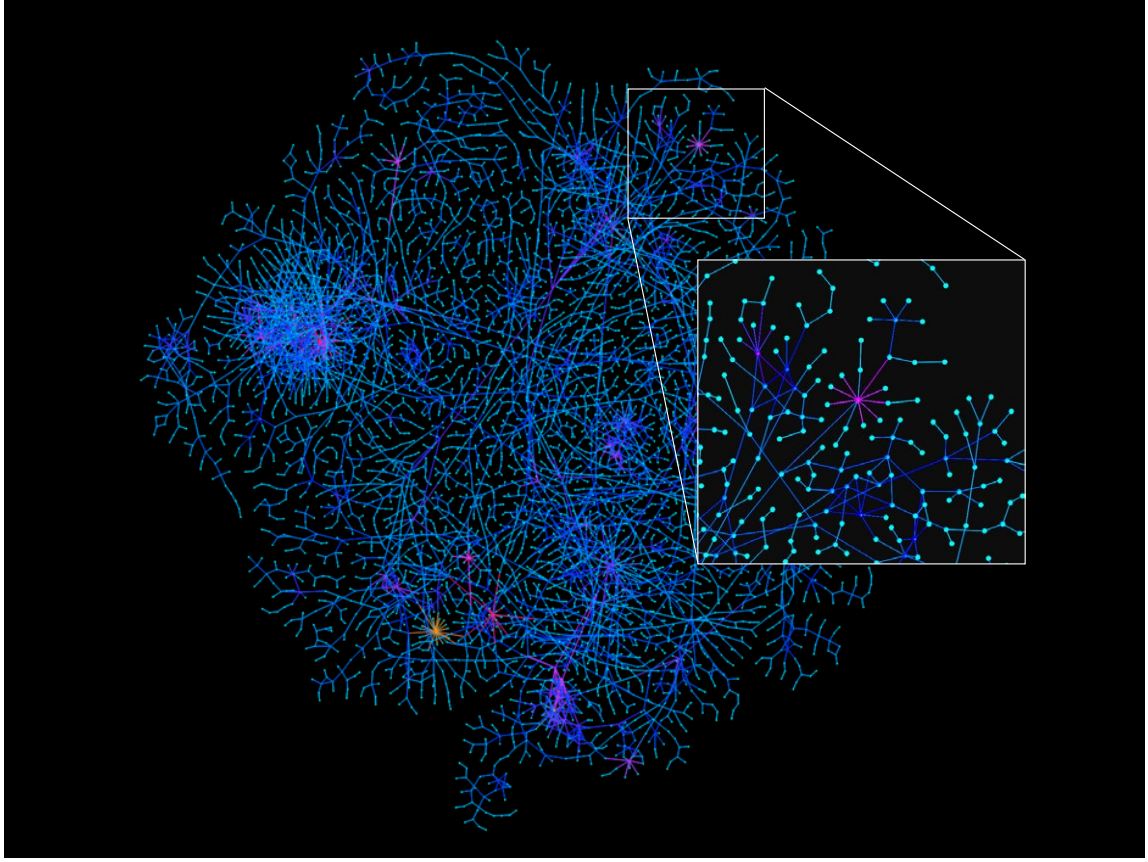


Fig. 1: *Network representation of US patent citations.*

of Complex Biological Logic Circuits Using Spatially Distributed Multicellular Consortia. *PLOS computational Biology* 12(2): e1004685.

Ollé-Vila, A.; Duran-Nebreda, S.; Conde-Pueyo, N.; Montañez, R. and Solé, R. 2016. A morphospace for synthetic organs and organoids: the possible and the actual. *Integr Biol (Camb)* 8: 485-503.

Seoane, L. and Solé, R. 2016. Multiobjective optimization and phase transitions, Chapter in Springer Proceedings in Complexity, pp 259-270. Ed. Battiston, De Pellegrini, Caldarelli, and Merelli.

Solé, R. 2016. Moldeados por la tecnología ¿Cuál será nuestro futuro como especie?. *Investigación y Ciencia* 482.

Solé, R. 2016. Back from the brink. *NewScientist*.

Solé, R. 2016. La lógica de los monstruos ¿Hay alternativas a la naturaleza tal como la conocemos?. Editorial Tusquets.

Solé, R. 2016. Synthetic transitions: towards a new synthesis. *Philos Trans R Soc Lond B Biol Sci.* 371(1701)

Solé, R. 2016. The major synthetic evolutionary transitions. *Philos Trans R Soc Lond B Biol Sci.* 371(1701)

Solé, R.; Amor D.R.; Duran-Nebreda, S.; Conde-Pueyo, N.; Carbonell-Ballestero, M. and Montañez, R. 2016. Synthetic collective intelligence. *Biosystems* 148, 47-61.

Solé, R.; Amor, R.D. and Valverde, S. 2016. On Singularities and Black Holes in Combination-Driven Models of Technological Innovation Networks. *PLoS ONE* 11(1):e0146180.

Solé, R.; and Elena, S. 2016. Viruses as Complex Adaptive Systems. As part of the collection SFI Primers in Complex Systems, Princeton U. Press.

Solé, R.; Montañez, R.; and Duran-Nebreda, S. 2016. Hacia una bioingeniería del planeta. *Investigación y Ciencia* 477.

Urrios, A.; Macia, J.; Manzoni, R.; Conde, N.; de Nadal, L.; Posas F. and Solé, R. 2016. A synthetic multicellular memory device. *ACS Synthetic Biology*, 5, 862-873.

Valverde, S. 2016. Major transitions in information technology. *Phil. Trans. Royal Soc.* B 371 (1701), 20150450.

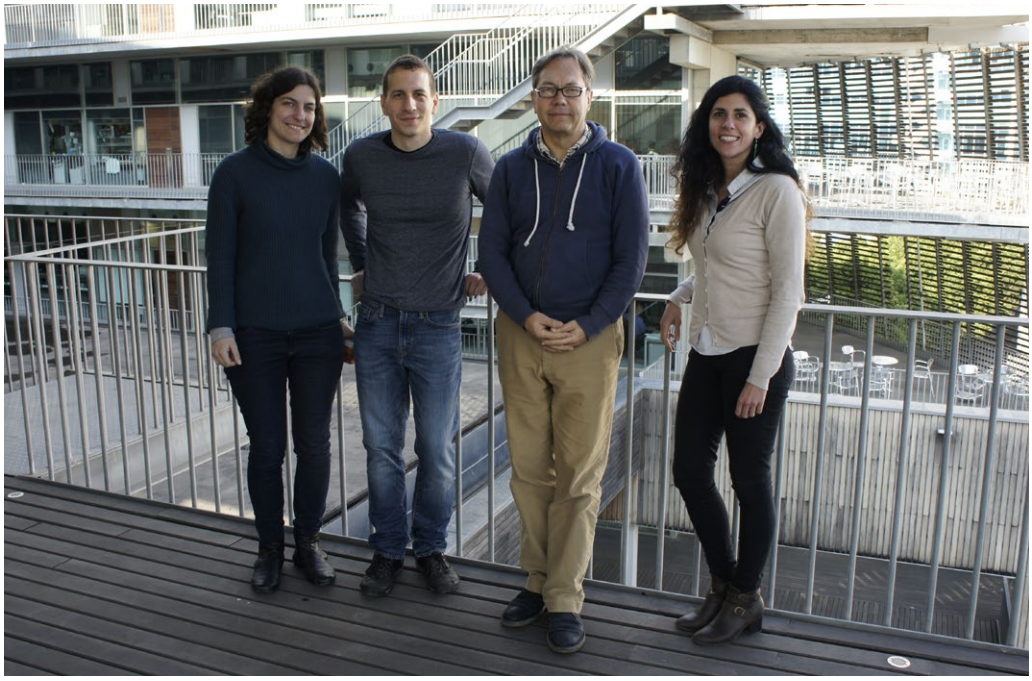
Valverde, S.; García-Ojalvo, J. 2016. Hacia una teoría unificada de la criticalidad biológica. *Investigación y Ciencia* 474.

Willemsen, A.; Zwart, M.P.; Higueras, P.; Sardanyés, J. and Elena S.F.2016. Predicting the Stability of Homologous Gene Duplications in a Plant RNA Virus. *Genome Biol Evol.*

Funded Projects

- **Project Title:** SYNCOM
  Financed by: European research Council (ERC)
  Years: 2012-2017
  PI: Ricard Solé
- **Project Title:** Cellular computation (Convenio de colaboración en materia de apoyo a la transferencia tecnológica en el campo de la biotecnología)
  Financed by: Fundación Marcelino Botín
  Years: 2010-2016
  PI: Ricard Solé
- **Project Title:** Evolució de Sistemes Complexes
  Financed by: Generalitat de Catalunya (SGR 497)
  Years: 2014-2016
  PI: Ricard Solé
- **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: 2015-2019
  PI: Ricard Solé
- **Project Title:** Aproximaciones desde la biología de sistemas y sistémica en el diseño de circuitos celulares para la homeostasis de la glucemia en diabéticos
  Financed by: Ministerio de economía y competitividad (MINECO)
  Years: 2015-2017
  PI: Javier Macía
- **Project Title:** Hacia una física de las grandes transiciones evolutivas
  Financed by: Ministerio de economía y competitividad (MINECO)
  Years: 2016-2018
  PI: Ricard Solé
- **Project Title:** Detección de tecnologias emergentes en redes de innovació (FIS2013-44674-P).
  Financed by: Ministerio de economía y competitividad (MINECO/FEDER).
  Years: 2013-2016
  PI: Sergi Valverde
- **Project Title:** Prediccion de innovacion tecnologica en redes de culturomica (FIS2016-77447-R)
  Financed by: Ministerio de economía y competitividad (MINECO/FEDER).
  Years: 2016-2020
  PI: Sergi Valverde

group LANGUAGE EVOLUTION



From left to right: Emilia García-Casademont, Miquel Cornudella, Luc Steels and Andrea Barquet

group members

Luc Steels, *Group Leader*
ICREA Researcher

Miquel Cornudella, Research Collaborator
Andrea Barquet, Research Assistant
Emília García Casademont, PhD Student

Research Outline

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

Research Lines

1. Origins and evolution of grammatical structures

Although there is a lot of data about the historical change in language, there is virtually no theory of the fundamental processes underlying this kind of evolution. We try to understand the cognitive mechanisms, interaction patterns, and collective dynamics that could explain how grammatical structures arise in human language by building agent-based models and using the hypothesis that self-organization and (linguistic) selection are the primary driving forces. We analyze the 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 grammatical patterns (such as noun phrases).

2. Fluid Construction Grammar (FCG)

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

3. Neural implementations of Fluid Construction Grammar

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

Publications 2016

Hannape, P.; Dunlop, R.; Duval, N.; Maes, A. and Steels, L. 2016. Agroecology: A Fertile Field for Human Computation. *Human Computation* 3: 1:225-233

Garcia-Casademont, E. and Steels, L. 2016. Insight Grammar Learning. *Journal of Cognitive Science* 17(1): 27-62.

Steels, L. 2016. De toekomst van de mensheid. In: Brockman, J. (ed.) Machines die denken. Invloedrijke denkers over de komst van kunstmatige intelligentie. Maven Publishing, Amsterdam. pp. 521-524

Steels, L. 2016. [monograph] The Talking Heads Experiment. The origins of words and meanings. Berlin: Language Science Press.

Steels, L. 2016. Agent-based models for the emergence and evolution of grammar. *Phil. Trans. Royal Society Journal* 371(1701).

Steels, L. 2016. Do languages evolve or merely change? *Journal of Neurolinguistics* 39: 1-5.

Steels, L. 2016. I'm gonna have to science the shit out of this: Comment on "Towards a Computational Comparative Neuroprimatology: Framing the language-ready brain" by Michael A. Arbib. *Phisics of life reviews* 16: 96-98.

Steels, L. 2016. Meaning and creativity in language. Creativity and Universality in Language 2016. Part of the series Lecture Notes in Morphogenesis pp. 197-208.

Steels, L.; Loetzsch, M. and Spranger, M. 2016. A Boy Named Sue. The Semiotic Dynamics of Naming and Identity. *Belgian Journal of Linguistics* 30(1): 147-152.

Steels, L. and Szathmary, E. 2016. Fluid Construction Grammar as a Biological System. *Linguistics Vanguard* 2(1): 20150022.

Funded Projects

- **Project Title:** INSIGHT - Darwinian Neurodynamics
  Financed by: FP7-EU
  Years: 2013-2016
- **Project Title:** ATLANTIS
  Financed by: CHIST-ERA (EU)
  Years: 2015-2018

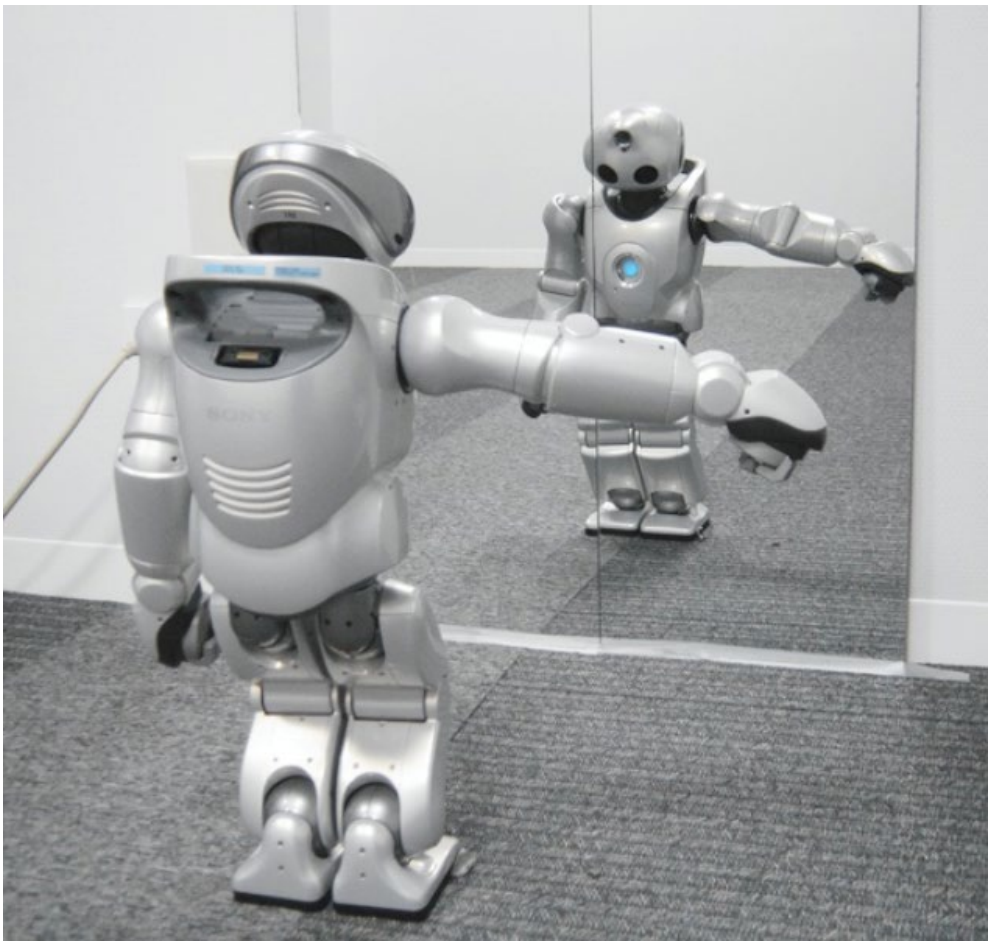
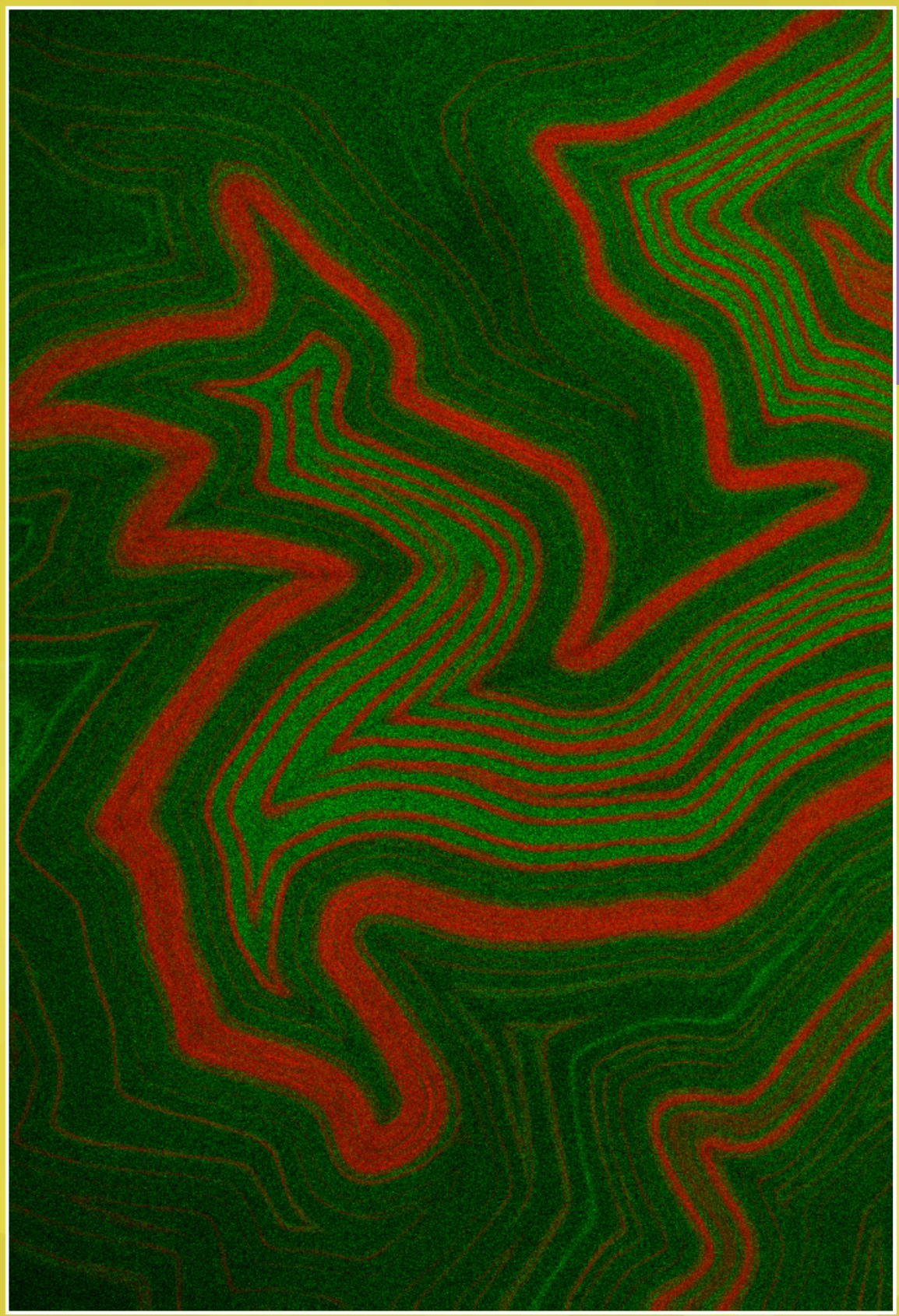
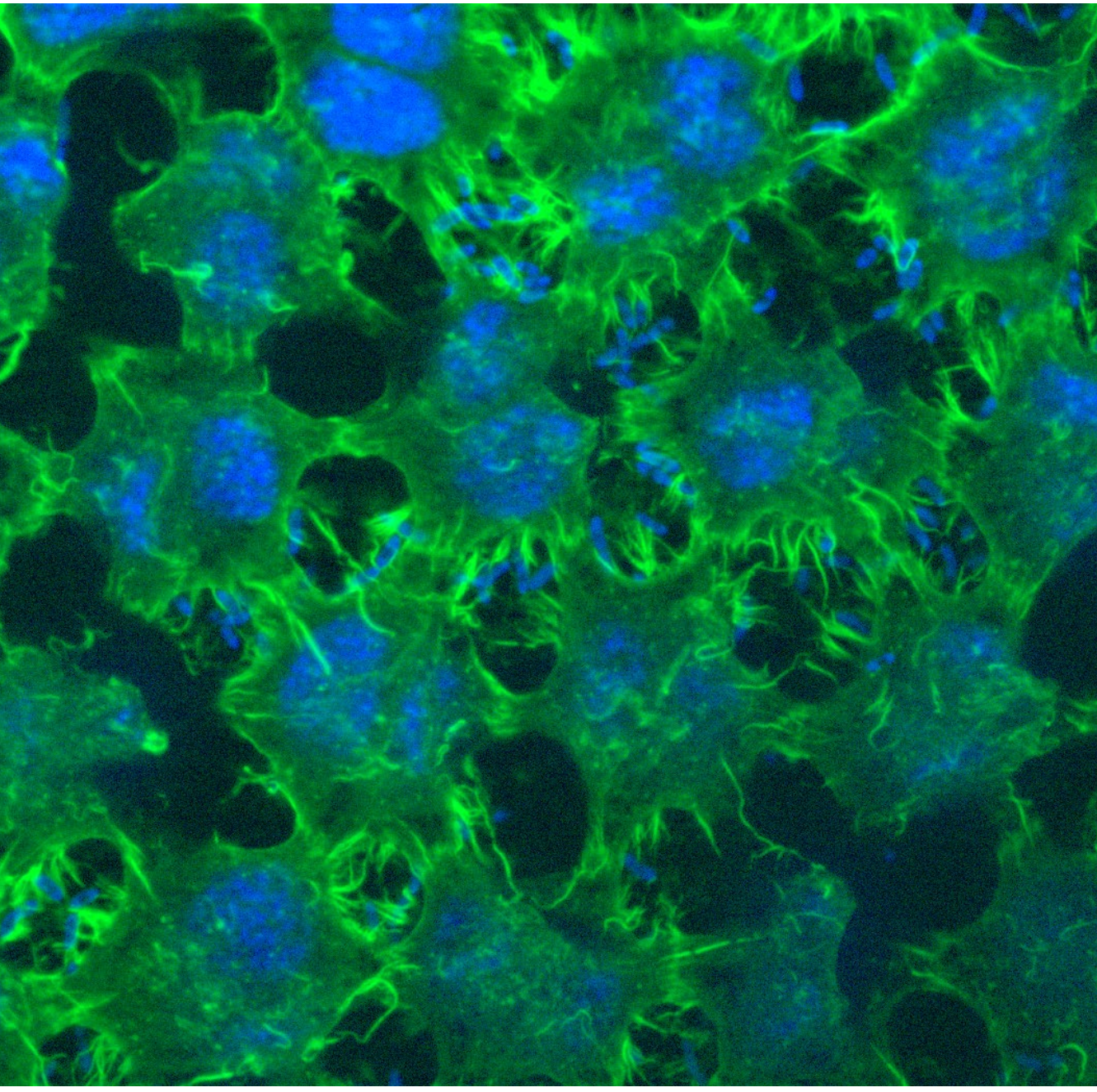


Fig. 1: *The QRIO humanoid robot stands before a mirror and performs various motor behaviours thus observing what visual body-images these behaviours generate.*



PROGRAM

FUNCTIONAL GENOMICS AND EVOLUTION



Research Groups

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

Other PIs in the group
Elena Casacuberta
David Martin

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 common goal of the different groups within the program is to study fundamental biological questions under a comparative perspective and combining evo-devo analyses with functional genomic approaches. Concerning the biological questions, the different research groups of the program address basic processes at different evolutionary levels, such as the evolution of multicellularity, development, growth, metamorphosis and oogenesis.

Most evolutionary research has been restricted to few 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. By further studying new 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 with respect to the others since it combines both comparative data generation on a diversity of taxa, and at the application of a number of different experimental techniques mostly related to cell and developmental biology and to comparative genomics.

group EVOLUTION AND DEVELOPMENTAL BIOLOGY

From left to right: Elena Casacuberta, David Martín, Silvia Chafino, Joan Valls, Xavier Franch-Barro, Josefa Cruz and Adrià Chorro

group members

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

David Martín, Principal Investigator, Tenured Scientist, CSIC
Elena Casacuberta, Principal Investigator, Tenured Scientist, CSIC
Josefa Cruz, Postdoctoral Researcher
Mohammed Rahman, Postdoctoral Researcher
Silvia Chafino, PhD Student, FPI Scholarship, MEC
Adrià Chorro, Master Student UB.
Nicola di Stasi, Master Student UB.
Joan Valls, Master Student, UB

Research Outline

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

Research Lines

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

Our group is characterizing the mechanistic and regulatory changes that underlie the evolution of Holometaboly, focusing, in particular, on the functional characterization of a conserved regulatory metamorphic toolkit formed by three critical genes, E93, Kr-h1 and Br-C.

2. Role of E93 in the regulation of insect metamorphosis

Our group identified E93 as the critical master gene of the metamorphic toolkit that promotes adult differentiation in hemimetabolous and holometabolous insects (Ureña et al., PNAS 2014). Currently we are trying to identify (1) the developmental signals that induce the stage-specific induction of E93; and (2) the mechanisms, at the molecular level, of the mode of action of E93 during insect metamorphosis.

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

Insects present different morphologies of the tracheal network depending on their habitat. We found that changes in the expression pattern of the mutually repressed spalt and cut transcription factors explain the formation of different tracheal structures. We aim thus to define a molecular mechanism underlying the evolution of independent but functionally related structures.

4. Evolution of SUMO protein functions in insect metamorphosis

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

5. In addition, we are developing molecular tools for new model organisms from marine holozoans (*Ministeria vibrans, Abeoforma whisleri, Pirum gemmata, Sphaeroforma arctica* and *Corallochytrium limacisporum)*. We are screening for antibiotic or selection agents, generating recombinant plasmids with endogenous promoters and fluorescent proteins. We are trying to optimize the methodology to genetically transform these organisms.

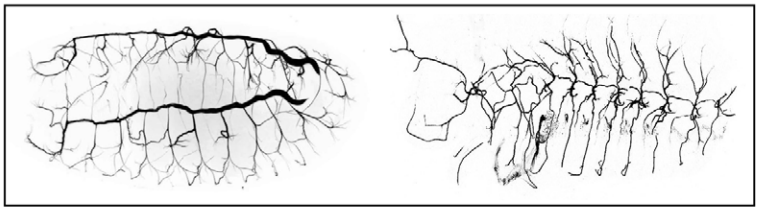


Fig. 1: *Tracheal systems of* Drosophila melanogaster *(left) and* Tribolium castaneum *(right).*

Publications 2016

de Miguel, C.; Linsler, F.; Casanova, J. and Franch-Marro, X. 2016. Genetic basis for the evolution of organ morphogenesis: the case of spaltand cutin the development of insect trachea. *Development*. 143(19): 3615-3622.

López-Panadès, E.; Casacuberta, E. (2016). NAP-1, Nucleosome assembly protein 1, a histone chaperone involved in Drosophila telomeres. *Insect Biochemistry and Molecular Biology* 70: 111-5

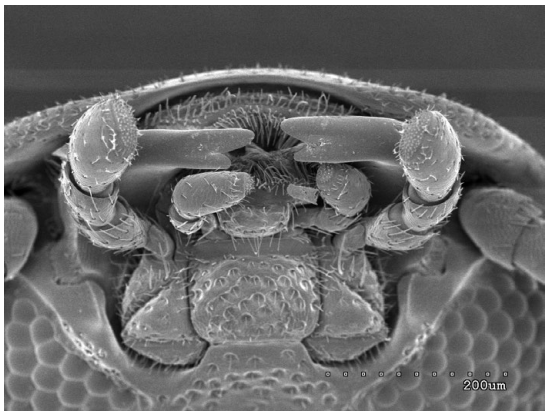


Fig. 2: *Scanning electron microscopy photograph of the head of the coleopteran* Tribolium castaneum.
Photo: *Enric Ureña.*

Mansilla, A.; Martín, F.A.; Martín, D. and Ferrús, A. 2016. Ligand-independent requirements of steroid receptors EcR and USP for cell survival. *Cell Death & Differentiation* 23: 405-416.

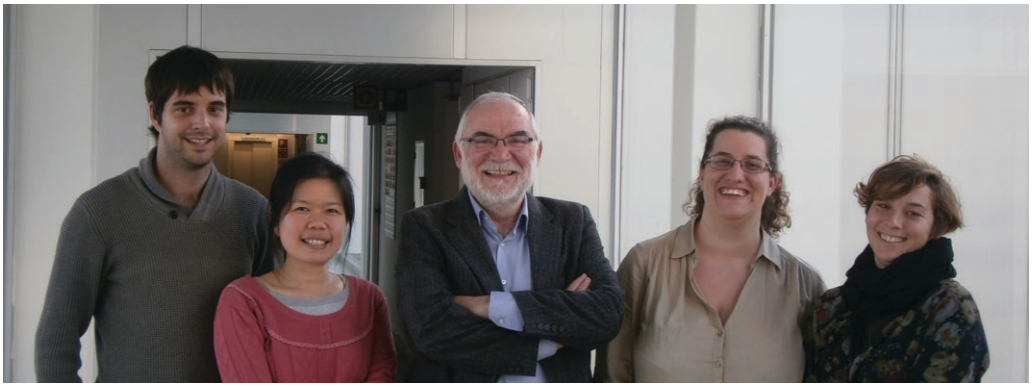
Ureña, E.; Chafino, S.; Manjón, C.; Franch-Marro, X. and Martín, D. 2016. The occurrence of the holometabolous pupal stage requires the interaction between E93, Krüppel-homolog 1 and Broad-Complex. *PLOS Genetics* 12(5): e1006020.

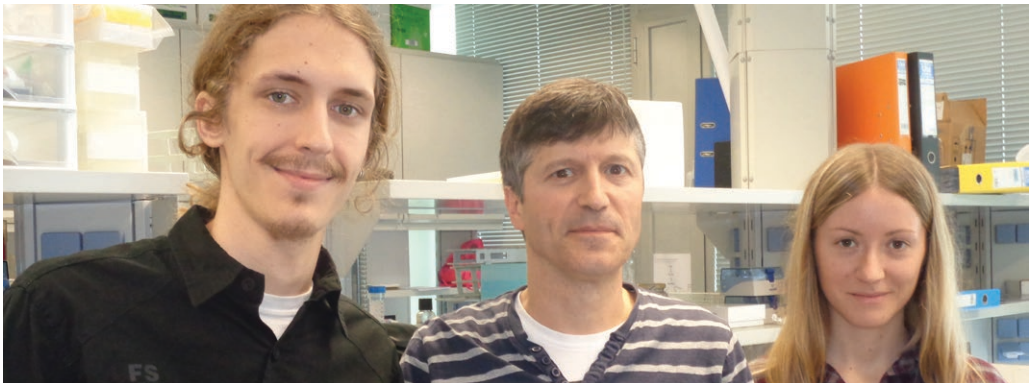
Ureña, E.; Pirone, L.; Chafino, S.; Pérez, C.; Sutherland, J.D.; Lang, V.; Rodriguez, M.S.; Lopitz-Otsoa, F.; Blanco, F.J.; Barrio, R. and Martín, D. 2016. Evolution of SUMO function and chain formation in insects. *Molecular Biology and Evolution* 33(2):568-584.

Funded Projects

- **Project Title:** Origin of insect metamorphosis: dissection and evolution of the metamorphic gene toolkit
  Financed by: Ministerio de Economía y Competitividad. CGL2014-55786-P.
  Years: 2015-2017
  PI: David Martín and Elena Casacuberta
- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2015 SGR 619)
  Years: 2014-2016
  PI: Xavier Bellés Ros
- **Project Title:** Screening Marine Holozoans, the closest relatives to Eukaryotes
  Financed by: Betty and Gordon Moore Foundation
  Years: 2015 -2016
  PI: Iñaki Ruíz-Trillo; Elena Casacuberta Suñer Co-IP

group INSECT PHYSIOLOGY AND MOLECULAR BIOLOGY





Top, from left to right: Guillem Ylla, Orathai Kamsoi, Xavier Belles, Alba Ventós and Ana Fernández
Bottom, from left to right: Lamil Ferrer, Josep Lluis Maestro and Júlia Castro

group members

Xavier Bellés, *Group Leader*
Research Professor, CSIC

Subgroups

Evolution of Insect Metamorphosis

Xavier Belles, Research Professor, CSIC
Ana Fernández Nicolás, PhD Student, MICINN Scholarship, Spain
Orathai Kamsoi, PhD Student, Royal Thai Government Scholarship, Thailand
Alba Ventós Alfonso, PhD Student, MICINN Scholarship, Spain
Guillem Ylla, Bioinformatitian and PhD Student, Project Contract.

Nutritional Signals in Insects

José Luis Maestro, Tenured Scientist, CSIC
Júlia Castro, Master Student, Universitat Pompeu Fabra
Lamil Ferrer, Undergraduate Student, Universitat de Barcelonaduate Student, Universitat de Barcelona

Research Outline

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

Subgroup: Evolution of Insect Metamorphosis (Xavier Belles)

Our goal is to elucidate the endocrine regulation of metamorphosis in *B. germanica* and then compare our results with data available in holometabolan species. The general idea is to describe the evolutionary history underlying the transition from hemimetaboly to holometaboly. We work at different levels, from comparative transcriptomics to functional genomics using RNAi, in pre-adult nymphal stages and in the embryo, where the essential differences between hemimetaboly and holometaboly are to be sought. In postembryonic development, analyses of tergal gland transcriptomes in metamorphic and non-metamorphic transitions led us to identify important genes involved in metamorphosis, like E93 (a transcription factor that triggers metamorphosis), Nejire (a CREB-binding protein), and Smad factors (from the TGFß signaling pathway). In the last nymphal stage we study the fine regulation of the MEKRE93 pathway: Methoprene-tolerant (Met), the juvenile hormone (JH) receptor, Krüppel homolog 1 (Kr-h1), the main transductor of the antimetamorphic signal of JH, and E93. In embryos we are studying the regulation of key developmental transitions, looking at hormonal influence and at the transcription factors and miRNAs. We are using transcriptomes and small RNA libraries of key embryo stages, whose study is revealing which transcripts and miRNAs operate in the regulation of each developmental transition. Subsequent functional validation is based on maternal RNAi targeting the key mRNAs and miRNAs identified in the transcriptomic analyses.

Subgroup: Nutritional Signals in Insects (José Luis Maestro)

We are working on two related research lines: 1) We continue our research on the nutritional regulation of reproduction and the role of Insulin-like Peptides (ILPs) in activating juvenile hormone (JH) production. We have demonstrated that this activation is not produced by a single ILP but that some redundancies exist, and that JH is able to regulate ILPs expression. 2) In collaboration with Dr. M. D. Piulachs group, we are studying how RNAi works in insects. This project involves the identification of the features of dsRNA that optimize the knock down effect, the contribution of RNAi enzymes to this effect, and the identification of which intermediary molecules are more prone to be produced. As a model molecule we use the Insulin Receptor.

Publications 2016

Elias-Neto, M. and Belles, X. 2016. Tergal and pleural structures contribute to the formation of ectopic prothoracic wings in cockroaches. *Royal Society Open Science* 3(8): 160347.

Fernandez-Nicolas, A. and Belles, X. 2016. CREB-binding protein contributes to the regulation of endocrine and developmental pathways in insect hemimetabolan pre-metamorphosis. *Biochimica et Biophysica Acta (General Subjects)* 1860 (3): 508-515.

Naghdi M, Maestro JL, Belles X, Bandani, A. 2016. Transduction of the vitellogenic signal of juvenile hormone by Methoprene-tolerant in the cockroach *Blattella germanica* (L.) (Dictyoptera, Blattellidae). *Arthropods* 5: 130-137.

Santos, C.G.; Fernandez-Nicolas, A. and Belles X. 2016. Smads and insect hemimetabolan metamorphosis. *Developmental Biology* 417(1): 104-113.

Ylla, G.; Fromm, B.; Piulachs, M.D. and Belles X. 2016. The microRNA toolkit of insects. *Scientific Reports* 6: 37736.

Other research results 2016

Belles, X. and Perkovsky, E.E. 2016. New data on the genus Sucinoptinus (Coleoptera, Ptinidae) from Rovno amber. *Vestnik zoologii* 50(1): 17-22, 2016.

Funded Projects

- **Project Title:** Key transitions in the embryogenesis of a hemimetabolan insect. Juvenile hormone, transcription factors and microRNAs.
  Finaced by: Ministry of Economy and Competitiveness, Spain. CGL2015-64727-P
  Years: 2016-2019
  PI: Xavier Belles
- **Project Title:** Functional Genomics and Evolution
  Finaced by: Generalitat de Catalunya (Ref: 2014 SGR 619)
  Years: 2014-2016
  PI: Xavier Belles
- **Project Title:** Modifying plants to produce interfering RNA (iPlant)
  Finaced by: COST Program (EU). OC-2015-2-20281
  Years: 2015-2019
  PI: Bruno Mezzetti, main proposer. Xavier Belles, Spain secondary proposer and Management Committee member.
- **Project Title:** Control of cockroaches with tailored RNAi
  Finaced by: Ministry of Economy and Competitiveness, Spain. CGL2016-76011-R
  Years: 2016-2019
  PI: José Luis Maestro and Maria Dolors Piulachs.

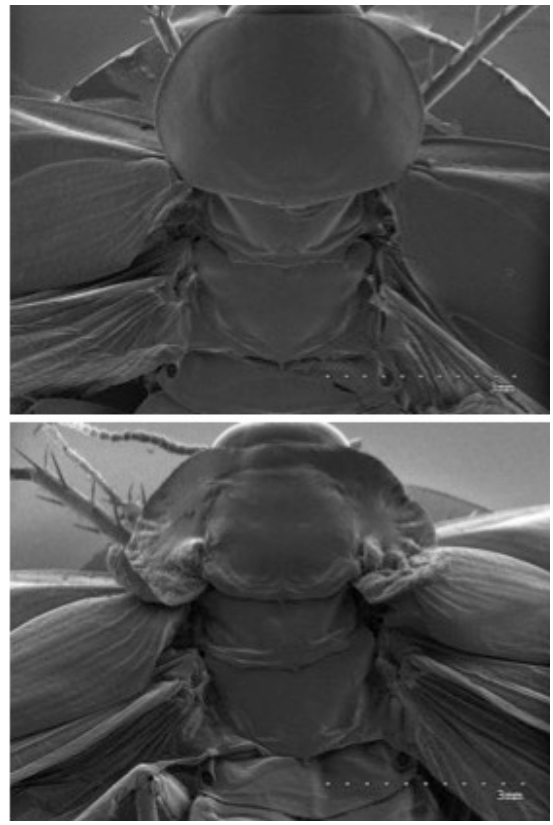


Fig. 1: *Ectopic winglets in the prothorax of the German cockroach triggered by depleting the expression of the gene Sex comb reduced (SCR). Control above, and SCR-depleted specimen below. From Elias-Neto M, Belles X. 2016.* Royal Society Open Science 3(8): 160347.

Photo: *Xavier Belles*

Fig. 2: *Defficient molt and adut marformations obtained in German cockroach after depleting the expression of the gene Nejire. From Fernandez-Nicolas A, Belles X. 2016.* Biochimica et Biophysica Acta (General Subjects) 1860 (3): 508-515.

Photo: *Ana Fernández*

group INSECT REPRODUCTION

From left to right: Natalia Llonga, Guillem Ylla, Maria-Dolors Piulachs, Patricia Toro and Ariadna Pedraza

group members

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

Guillem Ylla, Bioinformatician, Project Contract
Patricia Toro, Master Student, Universitat Autonoma de Barcelona
Natalia Llonga, Graduate Student, Universitat de Vic
Saray Ramos, Graduate Student, Universitat de Barcelona
Ariadna Pedraza, Undergraduate Student, Universitat de Barcelona
Jordi Velez, Undergraduate Student, Universitat de Vic

Research Outline

Our goal is to understand the mechanisms that regulate insect oogenesis. Through RNA interference (RNAi) methodologies we are unveiling the function of key genes in the oocyte development of *Blattella germanica,* an insect with a panoistic ovary type, the most primitive type among insects. The next step we are addressing is to study the hormonal regulation of these genes, and the role of small non coding RNA modulating its expression. The comparison of these results with those already described in other, more modified insect species, suggests that some functions are preserved in evolution, although the regulation of these functions could have changed.

Research Lines

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

The Notch pathway in oogenesis. We focused our attention on their function regulating the activity of Hippo pathway and oocyte polarity. We established a relationship between both, Hippo and Notch pathways and we demonstrated the importance of Notch in maintaining the correct cell number in ovarian follicle. Our next step will be to determine the regulatory role of juvenile hormone and ecdysone over these two.

Small noncoding RNAs. The miRNA have always kept our interest, and in the last year, we completed the identification of all the *B. germanica* miRNAs. A number of miRNAs appeared as common to all insect species, while there is a number of species-specific miRNA. Our next step will be to identify the function of this specific miRNA on oogenesis. In addition, we are also analyzing the piRNA present in the genome of *B. germanica*, since the identification of all these small noncoding RNA can help to understand the fine-tuning of some developmental steps in insects.

This last year we start a new research project in collaboration with Dr. Jose Luis Maestro, to know how RNAi works in insects and which characteristics should accomplish a dsRNA to be the most effective.

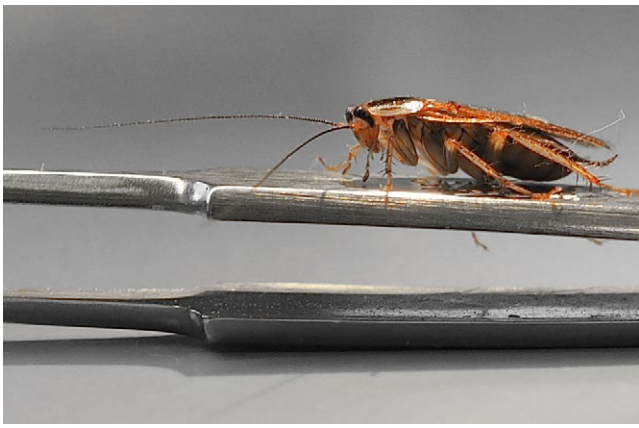


Fig. 1: *Adult female of Blattella germanica.*
Photo: *Cristina Olivella*

Publications 2016

Irles, P.; Elshaer, N. and Piulachs, M.D. 2016. The Notch Pathway regulates both the proliferation and differentiation of follicular cells in the panoistic ovary of *Blattella germanica*. *Open Biology* 6: 150197.

Macedo, L.M.F.; Nunes, F.M.F.; Freitas, F.C.P.; Pires, C.V.; Tanaka, E.D.; Martins, J.R.; Piulachs, M.D.; Cristino, A.S.; Pinheiro D.G. and Simões, Z.L.P. 2016. MicroRNA signatures characterizing caste-independent ovarian activity in queen and worker honeybees (Apis mellifera L.). *Insect Molecular Biology* 25(3):216-26.

Ylla, G.; Fromm, B.; Piulachs, M.D. and Belles, X. 2016. The microRNA toolkit of insects. *Scientific Reports* 6: 37736.

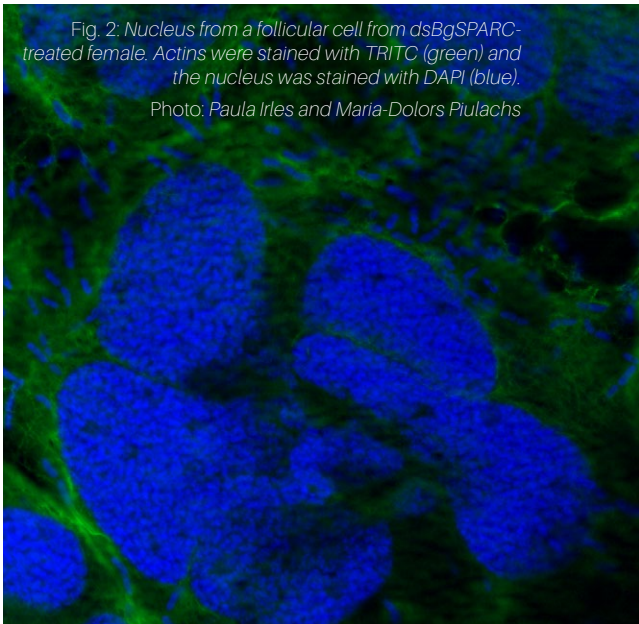


Fig. 2: *Nucleus from a follicular cell from dsBgSPARC-treated female. Actins were stained with TRITC (green) and the nucleus was stained with DAPI (blue).*
Photo: *Paula Irles and Maria-Dolors Piulachs*

Funded Projects

- **Project Title:** Global change and physiological diversity
  Financed by: International Laboratory of Global Change (LINCGlobal), CSIC (Spain)-PUC (Chile)
  Years: 2009-
  PIs: Xavier Bellés and Francisco Bozinovic
- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2014 SGR 619)
  Years: 2014-2016
  PI: Xavier Belles Ros
- **Project Title:** Modifying plants to produce interfering RNA (iPlant)
  Financed by: COST Program (EU). OC-2015-2-20281
  Years: 2015-2018
  PI: Bruno Mezzetti, main proposer. M.D. Piulachs, Spain Management Committee member.
- **Project Title:** RNAi "a la carta" para el control de cucarachas
  Financed by: MINECO (CGL2016-76011-R)
  Years: 2016-2019
  PI: M.Dolors Piulachs and Jose Luis Maestro.

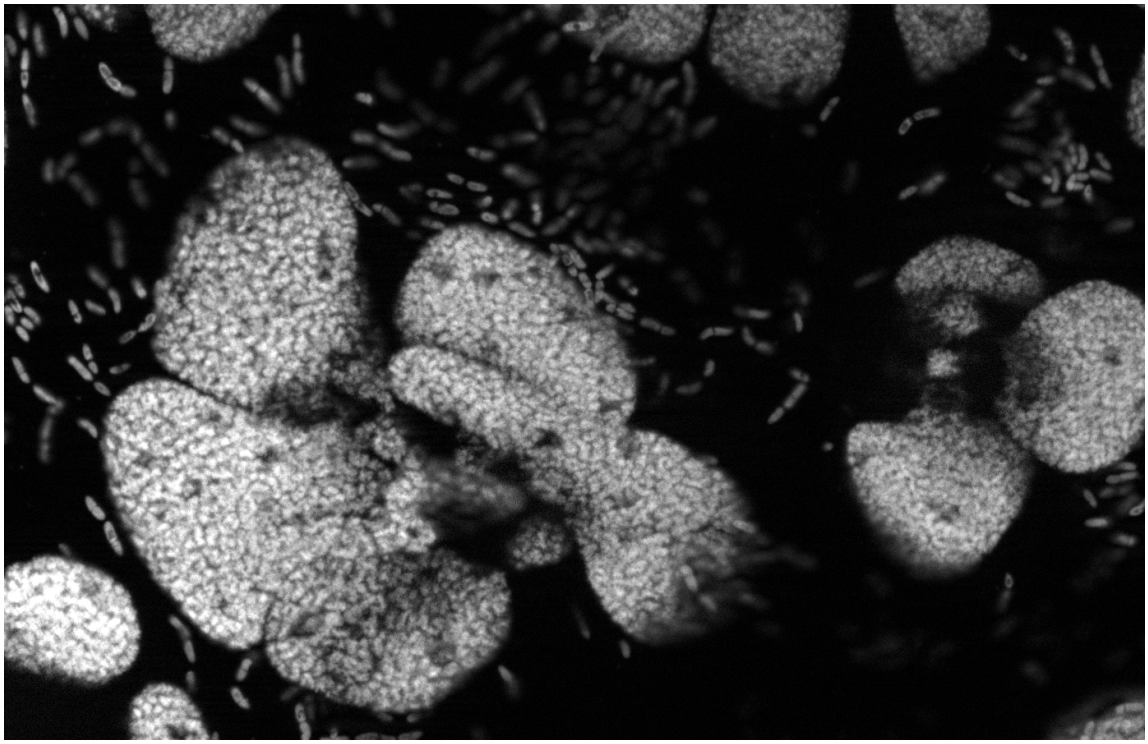


Fig. 3: *Nucleus from a follicular cell from dsBgSPARC-treated female. The nucleus was stained with DAPI (white).*

Photo: *Paula Irles and Maria-Dolors Piulachs*

group MULTICELL GENOME

From left to right: Matija Harcet, Alicia Sánchez, David López, Xavier Florenza, Eduard Ocaña, Alberto Pérez, Takaaki Kai, Xavier Grau-Bové, Sebastián Najle, Gema Blasco, María Rubio, Núria Ros, Iñaki Ruiz-Trillo, Meritxell Antó, Helena Parra, María Ferrer and Cristina Aresté

group members

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

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

Research Outline

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

Research Lines

1. Biodiversity and Molecular Ecology of Opisthokonts

As the real diversity of opisthokonts remains unknown, we are analyzing environmental data and molecular data from the Biomarks and Tara Oceans projects in order to expose its real diversity.

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

Our goal is to elucidate the evolution of genes that are key in animal multicellularity. We are part of the UNICORN (UNICellular Opisthokonts Research iNitiative) initiative: an international multi-taxon genome project recently funded by NHGRI which aims to understand how multicellularity first evolved in both animals and fungi. UNICORN, through the Broad Institute (BI), is obtaining the genome sequence from several of the closest unicellular relatives of animals and fungi (see the Multicellularity Project at BI). 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.

Recently, we analyzed the genome sequence of the filasterean amoeboid *Capsaspora owczarzaki*, a close unicellular relative of metazoa. In its genome, we found several genes that are required for metazoan development, such as the protein tyrosine kinases, integrins and several transcription factors. This implies that the unicellular ancestor of animals was much more complex than previously thought.

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

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

Besides identification, we want to understand the role of these genes in, and how these genes were later on co-opted to the new functions in metazoa. Thus, by elucidating the "ancestral function" of these genes, we will provide significant insights into the role that cell-signalling and cell-adhesion genes played in the onset of metazoa.

We are currently working on developing transgenesis protocols in *Capsaspora owczarzaki* and the ichthyosporean *Creolimax fragrantissima*.

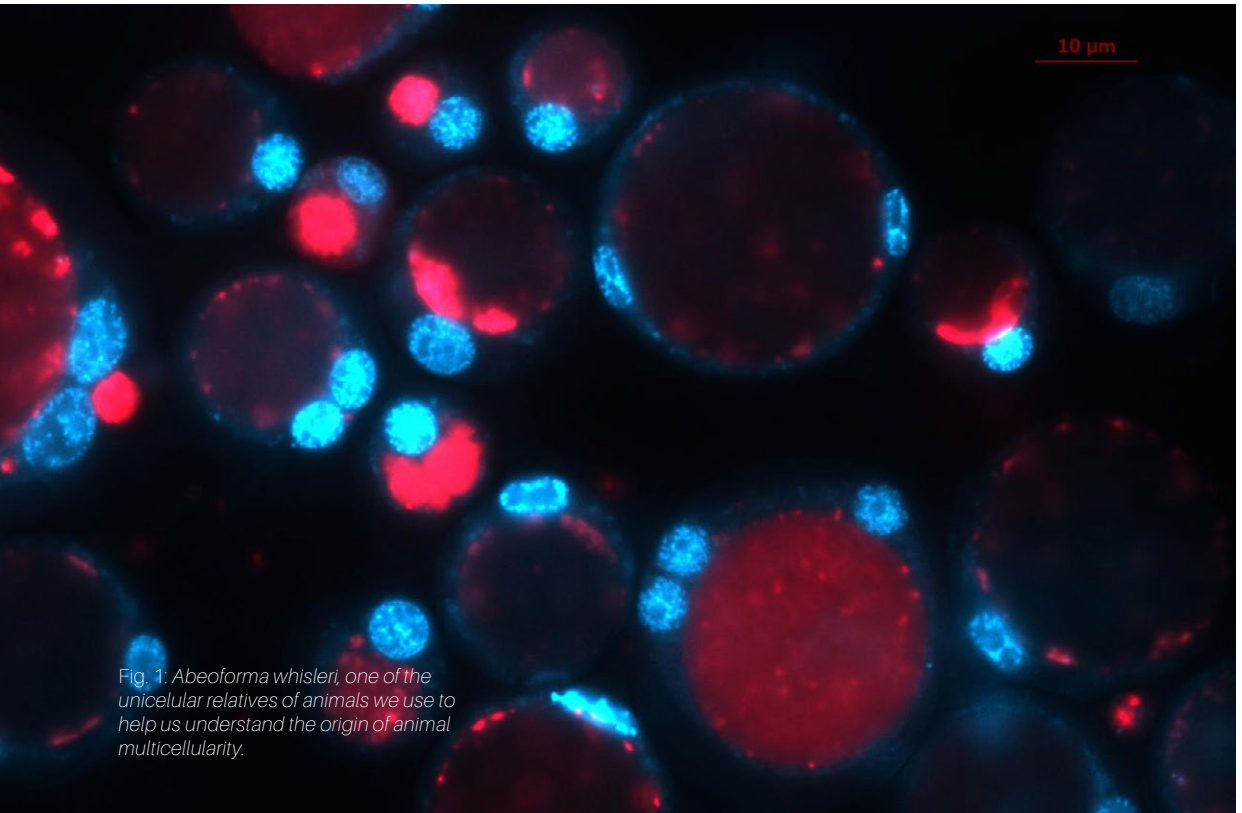


Fig. 1: *Abeoforma whisleri, one of the unicelular relatives of animals we use to help us understand the origin of animal multicellularity.*

4. Phylogenomics

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

Publications 2016

Arroyo, A.; López-Escardó, D.; de Vargas, C. and Ruiz-Trillo, I. 2016. Hidden diversity of Acoelomorpha revealed through metabarcoding. *Biology Letters* 12: 20160674.

Esquerdo, M.; Grau-Bové, X.; Garanto, A.; Toulis, V.; Garcia-Monclús, S.; Millo, E.; López-Iniesta, M.J.; Abad-Morales, V.; Ruiz-Trillo, I. and Marfany, G. 2016. Expression atlas of the deubiquitinating enzymes in the adult mouse retina, their evolutionary diversification and phenotypic roles. *PLoS ONE* 11(3): e0150364.

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O'Malley, M.A.; Wideman, J.G. and Ruiz-Trillo, I. 2016. Losing complexity: the role of simplification in macroevolution. *Trends in Ecology and Evolution* 31 (8): 608-621.

Ruiz-Trillo, I. 2016. "What are the genomes of the premetazoan lineages telling us about the origins of metazoa?" In *Multicellularity: Origins and Evolution*. ISBN: 9780262034159.

Ruiz-Trillo, I. and Paps, J. 2016. Acoelomorpha: earliest-branching bilaterians or deuterostomes? *Organisms Diversity and Evolution* 16: 391.

Sebé-Pedrós, A.; Ballaré, C.; Parra-Acero, H.; Chiva, C.; Tena, J.J.; Sabidó, E.; Gómez-Skarmeta, J.L.; Di Croce, L. and Ruiz-Trillo, I. 2016. The Dynamic Regulatory Genome of Capsaspora *and the Origin of Animal Multicellularity. Cell* 165 (5): 1224-1237.

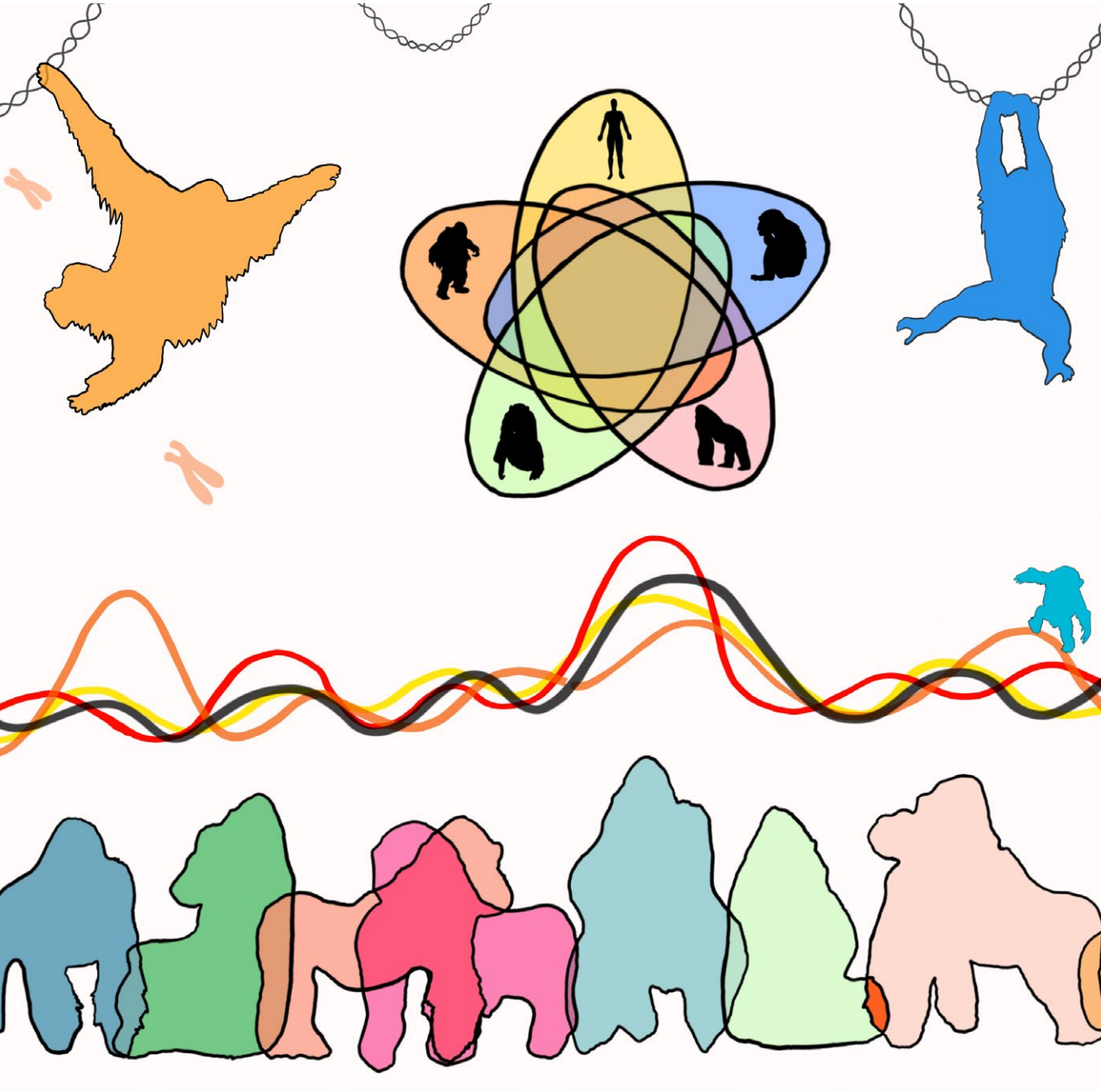
Sebé-Pedrós, A.; Peña, M.I.; Capella-Gutiérrez, S.; Antó, M.; Gabaldón, T.; Ruiz-Trillo, I. and Sabidó, E. 2016. High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. *Developmental Cell* 39 (2): 186-197.

Funded Projects

- **Project Title:** Unravelling the unicellular prehistory of metazoans by functional analyses and single-cell genomics
  Financed by: European Research Council (ERCCo-PREMETAZOANEVOLUTION-616960)
  Years: 2014-2019
  PI: I. Ruiz-Trillo
- **Project Title:** Functional Genomics and Evolution
  Financed by: Generalitat de Catalunya (Ref: 2014 SGR 619)
  Years: 2014-2016
  PI: Xavier Bellés
- **Project Title:** Origen, diversificación y diversidad de metazoos, hongos y sus parientes unicelulares.; una aproximación ecológica y evolutiva
  Financed by: Ministerio de Ciencia e Innovación
  Years: 2015-2017
  PI: I. Ruiz-Trillo and Josefa González
- **Project Title:** Screening marine holozoans, the closest unicellular relatives of animals
  Financed by: Gordon and Betty Moore Foundation
  Years: 2015-2016
  PI: I. Ruiz-Trillo and Elena Casacuberta
- **Project Title:** Promoting single cell genomics to explore the ecology and evolution of hidden microeukaryotes
  Financed by: European Comission
  Years: 2016-2019
  Coordinator: CSIC

PROGRAM

POPULATION GENETICS



Research Groups

Evolutionary Population Genetics
Elena Bosch, *Group Leader*

Evolutionary Systems Biology
Jaume Bertranpetit, *Group Leader*

Genomics of Individuallity
Francesc Calafell, *Group Leader*

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

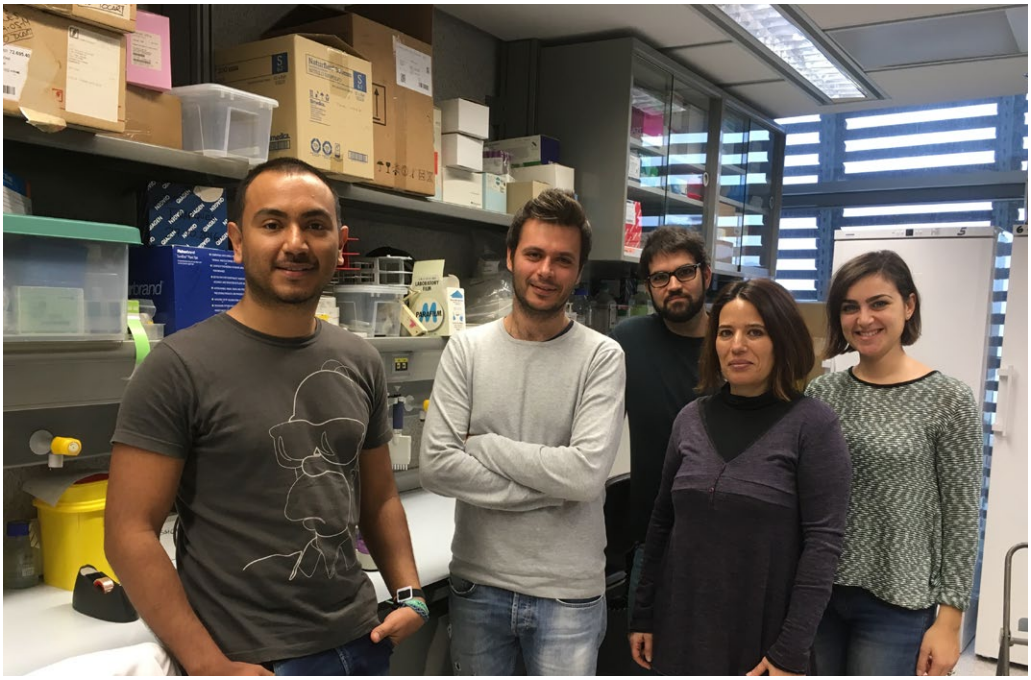
Subgroups

Human Genome Diversity
David Comas, *PI*

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

In the population genetics line, intraspecific diversity patterns within populations and comparative data are explored with the general aim of reconstructing the processes that have created such diversity. Genetic diversity is the result of the intricate interaction of different processes: some are embedded in the genome, such as mutation and recombination; others are absolutely independent from the genome and affect its entirety, such as demographic events; and finally, other processes result from the exposure of the genetic diversity to the environment, such as natural selection. Within this line, we are interested in all three types of processes mainly in humans. Namely, we investigate how recombination can be affected by genetic differences between populations; the demographic histories of particular populations or population groups; and the extent of the adaptation of humans to their pathogen exposure or to nutrient availability in their diets through the detection of selection footprints in the genome. In addition, the functional consequences of these processes in both the coding and non-coding parts of the human 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: Gabriel Felipe Rodríguez, Nino Spataro, Juan Antonio Rodríguez, Elena Bosch and Barbara Sinigaglia

group members

Elena Bosch, *Group Leader*
Associate Professor, UPF

Juan Antonio Rodríguez, PhD Student
Barbara Sinigaglia, PhD Student
Nino Spataro, PhD Student
Gabriel Felipe Rodríguez, Master Student

Research Outline

Our research focuses on investigating different aspects of human genetic diversity. In particular, we are interested in the architecture of the genetic predisposition to complex disease and in human adaptive traits that have undergone positive selection during human evolution. For that, we usually analyze full genome sequencing data from different control/case settings or geographically diverse human populations and apply state-of-the-art analytical methods for rare variant association and genome-wide detection of selection. Furthermore, by using *in silico* predictions, relevant molecular biology techniques and human phenotypic data, we aim to elucidate the genetic variants and molecular phenotypes underlying the functional genetic basis of different human adaptations presumably related to immunity and pathogen interaction, diet and micronutrient content.

Research Lines

1. Recent human adaptation and nutrition

Micronutrients play an important role in human health and their physiological and cellular concentrations are kept in homeostasis by a number of membrane transport proteins and metal-binding proteins. Besides identifying signatures of selection in genes related to the metabolism of micronutrients, we have described the interplay between genetic variation, mRNA and protein expression, together with trace element content in different human tissue samples in order to gain insight into possible adaptive responses to nutrient availability and past diet changes. In that case, we are also especially interested in the parallel interrogation of the functional effects of multiple putative adaptive genetic variants of small effect contributing to zinc homeostasis.

2. Role of natural selection in human disease genes

By analyzing different evolutionary and biological features we have characterized the selective pressures acting in genes associated to Mendelian and complex diseases to understand differences in penetrance, age of onset, and risk allele frequencies between genetic disorders. Also, in collaboration with Arcadi Navarro (Evolutionary Genomics Lab) we hope to provide genomic evidence for the evolutionary theories of senescence by identifying antagonistically pleiotropic variants and signatures of positive selection in pleiotropic genes associated to age-related traits.

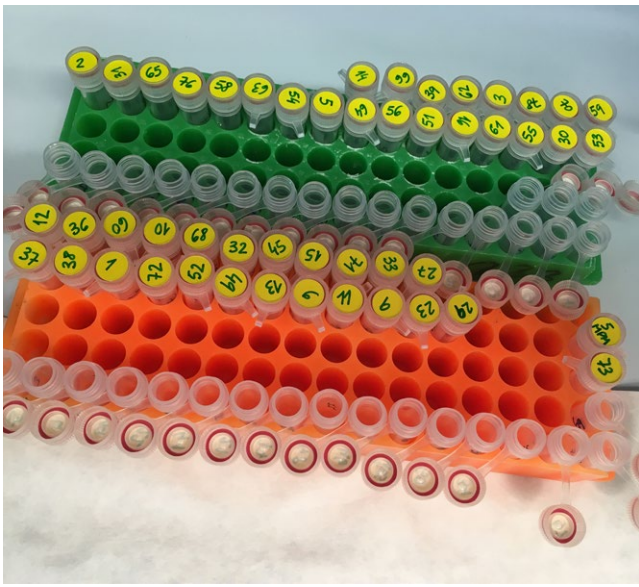


Fig. 1: *Tubes with human DNA samples.*

Publications 2016

Bosch E and Casals F. Chapter 15: *Next-generation sequencing for rare diseases* in book *Genome-Wide Association Studies: From Polymorphism to Personalized Medicine*, edited by Dr. Krishnarao Appasani, Cambridge University Press. 2016. ISBN: 978-1-107-04276-6.

Casals F and Bosch E. Chapter 16: *Next-generation sequencing for complex disorders* in book *Genome-Wide Association Studies: From Polymorphism to Personalized Medicine*, edited by Dr. Krishnarao Appasani, Cambridge University Press. 2016. ISBN: 978-1-107-04276-6.

Engelken, J.; Espadas, G.; Mancuso, FM.; Bonet, N.; Scherr, A.L.; Jímenez-Álvarez, V.; Codina-Solà, M.; Medina-Stacey, D.; Spataro, N.; Stoneking, M.; Calafell, F.; Sabidó, E. and Bosch, E. 2016. Signatures of evolutionary adaptation in quantitative trait loci influencing trace element homeostasis in liver. *Molecular Biology and Evolution* 33(3): 738-754.

Spataro, N.; Roca-Umbert, A.; Cervera-Carles, L.; Vallès, M.; Anglada, R.; Pagonabarraga, J.; Pascual-Sedano, B.; Campolongo, A.; Kulisevsky, J.; Casals, F.; Clarimón, J.; and Bosch, E. 2016. Detection of genomic rearrangements from targeted resequencing data in Parkinson's disease patients. *Mov Disord* 32 (1), 165-169.

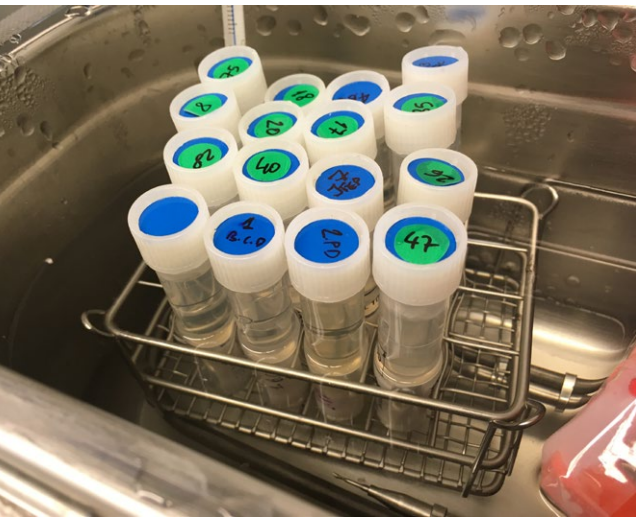


Fig. 2: *DNA extraction from human samples.*

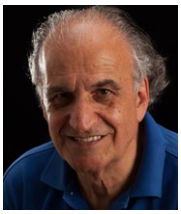
Funded Projects

- **Project Title:** Genètica de les Poblacions Humanes (2014 SGR-866)
  Financed by: Generalitat de Catalunya
  Years: 2014-2016
  PI: Jaume Bertranpetit
- **Project Title:** AdaptNET. Genomics of adaptation network (CGL2015-71726-REDT)
  Financed by: Ministerio de Ciencia e Innovación
  Years: 2015-2017
  PI: Julio Rozas
- **Project Title:** Icrea Academia Award- Life and Medical Sciences
  Financed by: Icrea Academia
  Years: 2015-2020
  PI: Elena Bosch
- **Project Title:** Seleccion adaptativa en las poblaciones humanas
  Financed by: MICINN (BFU2016-77961-P)
  Years: 2016-2019
  PIs: Jaume Bertranpetit and Elena Bosch

group EVOLUTIONARY SYSTEMS BIOLOGY

From left to right and top to bottom: Sandra Walsh, Pablo Villegas, Hafid Laayouni, Mayukh Mondal, Begoña Dobón, Jaume Bertranpetit, Jessica Nye and Apostolia Topaloudi

group members



Jaume Bertranpetit, *Group Leader*
Professor, UPF

Hafid Laayouni, Senior Scientist, ESCI-UPF
Begoña Dobón Berenguer, PhD Student , FPU Scholarship
Mayukh Mondal, PhD Student, FI Scholarship, Generalitat de Catalunya
Jessica Nye, PhD Student, FI Scholarship, Generalitat de Catalunya
Sandra Walsh, PhD Student, FPI Scholarship, MINECO
Pablo Villegas, Master Student
Apostolia Topaloudi, Erasmus Student

Research Outline

Presently, our main research focuses on the understanding of natural selection and adaptation in humans and primates through the comparative analysis of genomes. Our goal is to understand complex adaptations through genome-wide analyses of the footprints that natural selection leaves in genomes after their action, and not only by detecting single signals (in one specific gene or genome region) but trying to place selection in a functional molecular framework of molecular pathways.
The different forms of selection (purifying, balancing and positive) are analyzed at two levels: among human populations in order to detect population-specific adaptations, and among primates in order both to recognize species-specific adaptive selection and to measure the relative strength of purifying selection.
We also have an ongoing project reconstructing population history by studying human genetic diversity.

Research Lines

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

The action of natural selection is at the base of different amounts of gene dispensability or relative importance (in cases of negative or purifying selection) or of adaptation (in cases of positive selection and in the special case of balancing selection). The final goal is, on the one hand, to understand in specific pathways how evolution has taken place, where positive selection (and balancing selection) has taken place and where purifying selection has been shaping the genome, and on the other, to obtain possible general patterns of evolution in molecular pathways and networks. The study of the whole metabolome is of special interest.
Some special cases are being studied. For humans, Indian (including Andaman) and African populations are being studied, with a particular focus on the existence of admixture in these populations. Moreover, the study of apes, and especially chimpanzees, will shed light on their specific adaptations.

2. Human genetic diversity and population history

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

Publications 2016

Aterido, A.; Julià A.; Ferrándiz, C.; [18 authors]; Bertranpetit, J.; Absher, D.; Capon, F.; Myers, R.M.; Barker, J.N. and Marsal, S. 2016. Genome-wide pathway analysis identifies new genetic pathways associated with psoriasis. *J Invest Dermatol* 136(3):593-602.

Cagan, A.; Theunert, C.; Laayouni, H.; Santpere, G.; Pybus, M.; Casals, F.; Prüfer, K.; Navarro, A.; Marques-Bonet, T.; Bertranpetit, J. and Andrés, A.M. 2016. Natural Selection in the Great Apes. *Molecular Biology and Evolution* 33(12): 3268-3283.

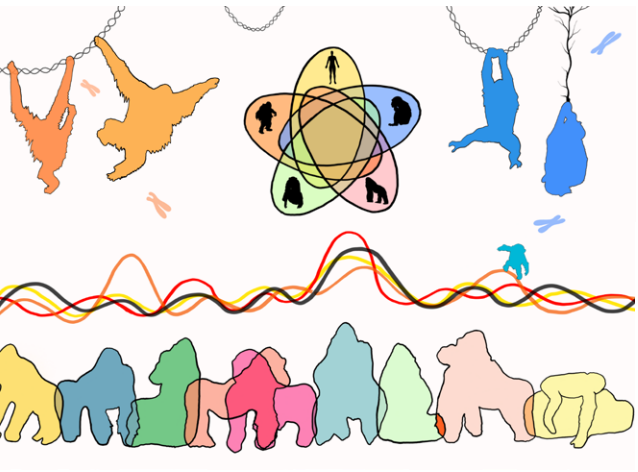


Fig. 1: *Drawing of co-author Alex Cagan to illustrate the action of adaptive selection in the apes*

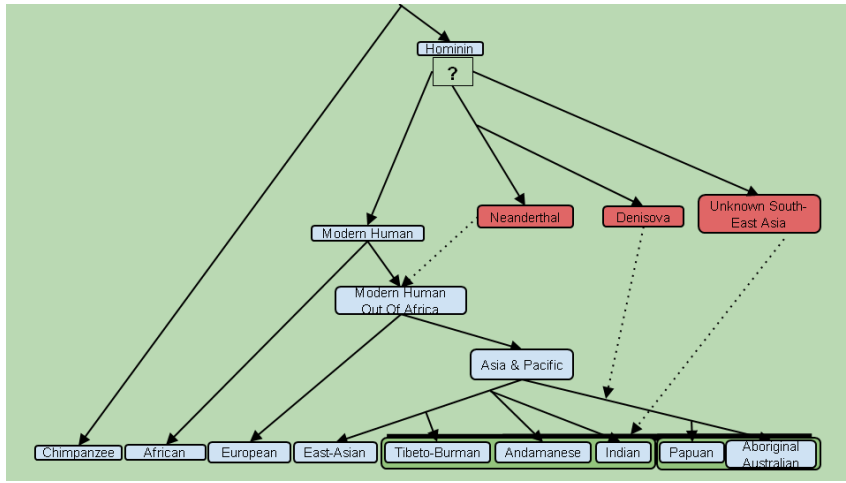


Fig. 2: *A new tree of humans, with the introgression of an unknown hominin is populations of South East Asia and Pacific, that could be* Homo erectus *or another extinct population, more related to Neanderthals than to modern humans.*

Calafell, F.; Anglada, R.; Bonet, N.; González-Ruiz, M.; Prats-Muñoz, G.; Lalueza-Fox, C.; Bertranpetit, J .; Malgosa, A. and Casals, F. 2016. An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936-1939). *Electrophoresis* 37(21): 2841-2847.

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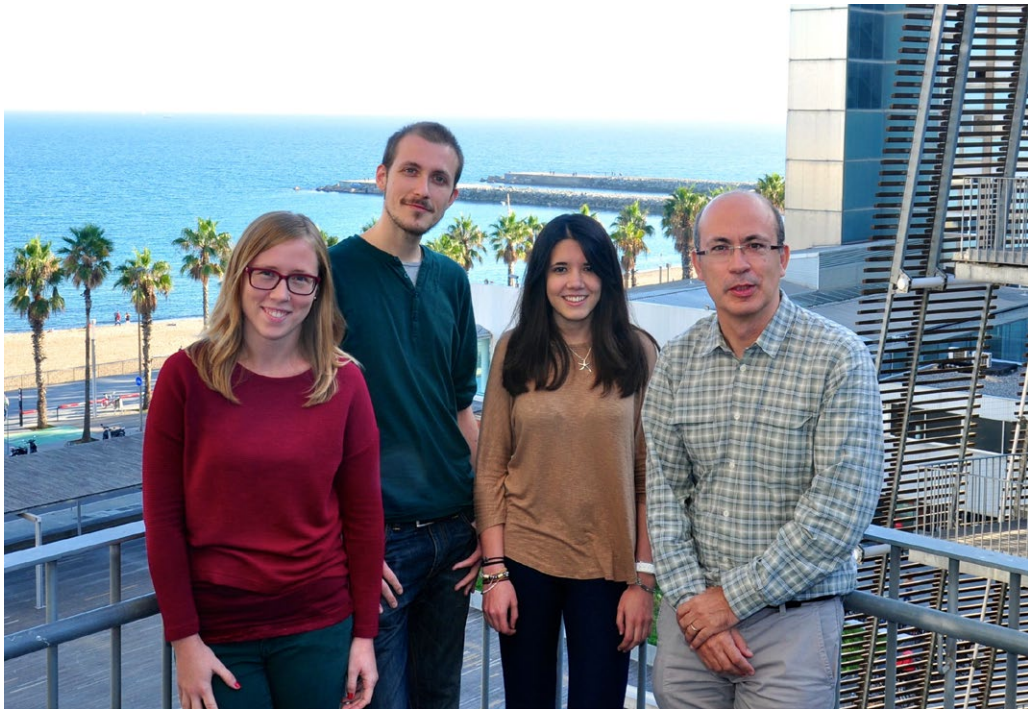
Funded Projects

- **Project Title:** Seleccion adaptativa en las poblaciones humanas
  Financed by: MICINN (BFU2016-77961-P)
  Years: 2016-2019
  PI: Jaume Bertranpetit and Elena Bosch
- **Project Title:** Genètica de les Poblacions Humanes
  Financed by: Generalitat de Catalunya (2014 SGR 866)
  Years: 2014-2016
  PI: Jaume Bertranpetit

group GENOMICS OF INDIVIDUALITY



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

group members

Francesc Calafell, *Group Leader*
Associate Professor, UPF

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

Research Outline

The general topics that interest us revolve around the genomics of individuality: what is there in our genomes that 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)? In particular, we focus on both sides of the Western Mediterranean, their genetic structure, and their contacts.

Research Lines

1. The Western Mediterranean genetic landscape

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

2. Phylogeography of the Y chromosome in the Western Mediterranean

The phylogeography of -chromosome haplogroups can be used to make inferences on the origin and dispersal of these tree branches, and, more importantly, on the history of the populations carrying them. We are analyzing two such branches, E-M81 and DF-27, which abound respectively in NW Africa and Iberia. Both have recent origins and have expanded explosively; we intend to ascertain the demographic history that produced them and deeply affected the populations that host them

Publications 2016

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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
  PIs: David Comas and Francesc Calafell

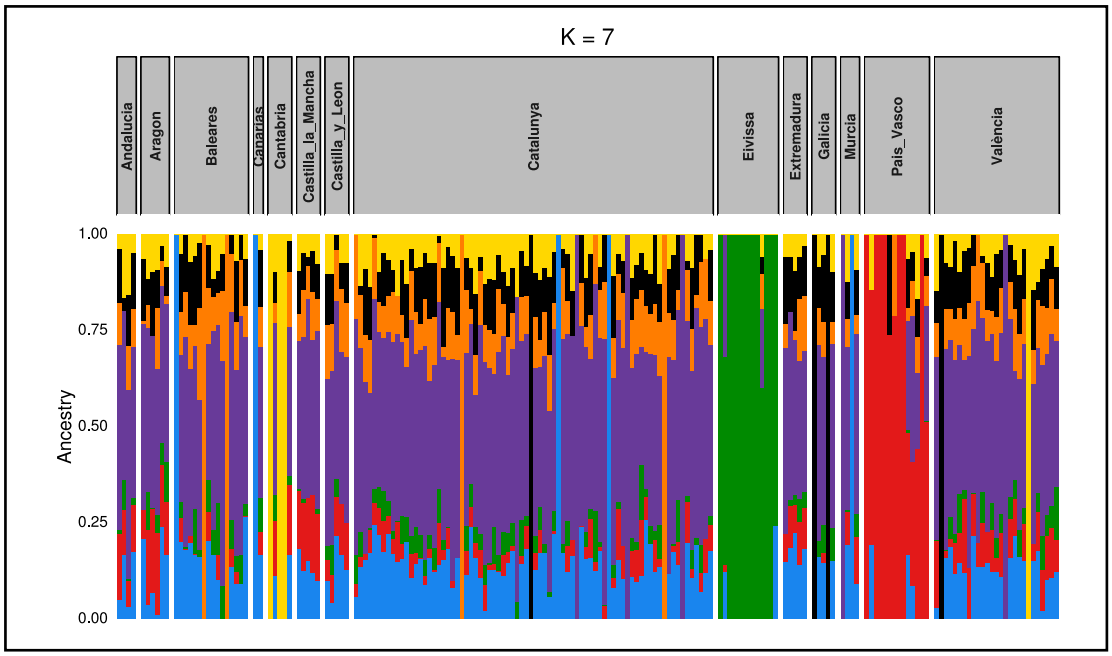
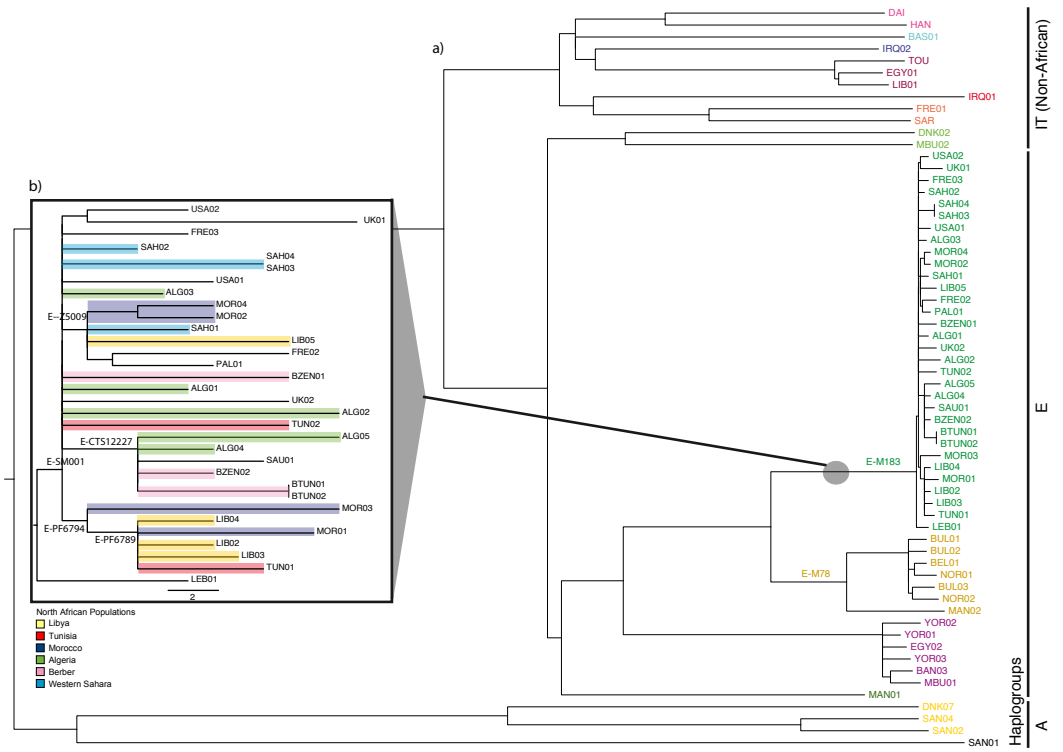


Fig.1: *Admixture plot showing the estimated proportions of three different ancestries (represented in color) for individuals (vertical lines) in several Spanish populations.*

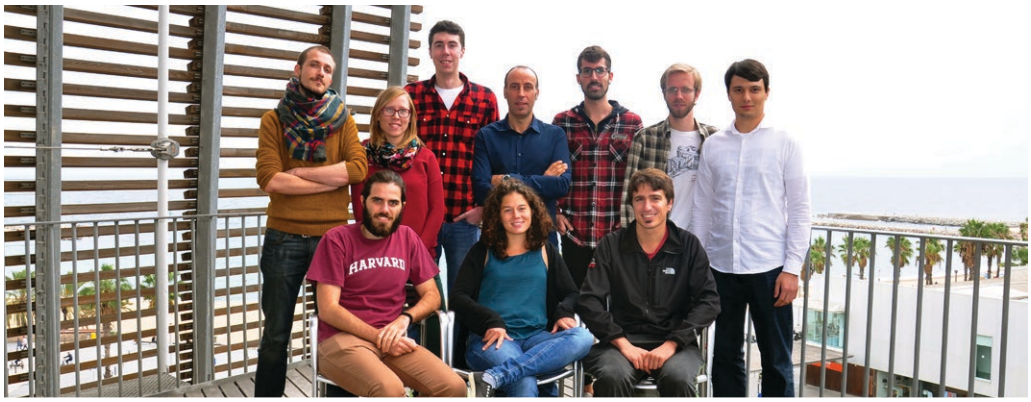
Author: *Simone Biagini*

Fig. 2: *Tree showing the phylogenetic relationships of Y chromosomes* obtained from full sequences. Inset: *E-M183 Y chromosomes.*

Author: *Neus Solé*



group HUMAN GENOME: DIVERSITY AND ADAPTATION



Top, from left to right and top to bottom: Simone Biagini, Neus Solé-Morata, Carles Llorca, David Comas, André Flores, Gerard Serra, Joao Pimenta, David Mas, Lara Rubio Araúna and Àlex Mas

Bottom, from left to right: Yolanda Espinosa, Alicia Gallego and Ignasi Torruella

group members

David Comas, *Group Leader*
Associate Professor, UPF

Subgroups

Human Genome Diversity

David Comas, Associate Professor, UPF
Simone Biagini, PhD Student, FPI Scholarship
André Flores, PhD Student, FI Scholarship
Àlex Mas, PhD Student, UFRGS Scholarship
Lara Rubio Arauna, PhD Student, UPF Scholarship
Gerard Serra, PhD Student, FI Scholarship
Neus Solé-Morata, PhD Student, FI Scholarship
Neus Font, Master Student, UPF
Carla García, Master Student, UPF
Carles Llorca, Master Student, UPF
David Mas, Master Student, UPF

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

Research Outline

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

Research Lines

Subgroup: Human Genome Diversity
1. Demographic history of European populations: differential migrations and genetic composition of some European minorities
2. Migrations and adaptations in North African populations
3. Genomic composition of African populations: demography and adaptation using complete genomes

Subgroup: microRNAs in Human Adaptation and Disease
1. Involvement of microRNA related mechanisms in human disease susceptibility
2. Molecular evolution of microRNAs in primates

Publications 2016

Colobran, R.; Franco-Jarava, C.; Martín-Nalda, A.; Baena, N.; Gabau, E.; Padilla, N.; de la Cruz, X.; Pujol-Borrell, R.; Comas, D.; Soler-Palacín, P. and Hernández-González, M. 2016. Novel mutations causing C5 deficiency in three north-African families. *Journal of Clinical Immunology* 36: 388-396.

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Funded Projects

- **Project Title:** Análisis genómico de la biodiversidad humana en el Mediterráneo: en la encrucijada entre tres continentes (CGL2013-44351-P)
  Financed by: Ministerio de Economía
  Years: 2014-2016
  PI: Francesc Calafell and David Comas
- **Project Title:** Práticas culturais e seu papel na saúde e na doença de populaçoes nativas americanas e de seus descendentes (405996/2013-6)
  Financed by: National Council for Scientific and Technological Development of the Ministry of Science, Technology and Innovation (CNPq/MCTI) of Brazil
  Years: 2014-2016
  PI: Maria Cátira Bortolini and David Comas
- **Project Title:** Genètica de les Poblacions Humanes
  Financed by: Generalitat de Catalunya (2014 SGR-866)
  Years: 2014-2018
  PI: Jaume Bertranpetit

Fig. 1: *The human population history of North African is revealed by genomic data.*

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Marc and Daniel catching Chamaeleon arabicus

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IBE HIGHLIGHTED PAPERS

Signatures of evolutionary adaptation in quantitative trait loci influencing trace element homeostasis in liver

Engelken, J.; Espadas, G.; Mancuso, FM.; Bonet, N.; Scherr, A.L.; Jímenez-Álvarez, V.; Codina-Solà, M.; Medina-Stacey, D.; Spataro, N.; Stoneking, M.; Calafell, F.; Sabidó, E. and Bosch, E. 2016. . *Molecular Biology and Evolution* 33(3): 738-754.

Micronutrients play an important role in our health and consequently their concentrations are tightly regulated in our body. This multidisciplinary work has studied the interaction between the content of different trace elements in liver, the expression of a number of proteins involved in their homeostasis at both RNA and protein level and their corresponding genetic variation in worldwide human populations. These results have been subsequently used to investigate adaptive responses to differential nutrient availability and potential dietary changes occurred in our past. Notably, the authors have found that the micronutrients with stronger adaptive responses are zinc and selenium.

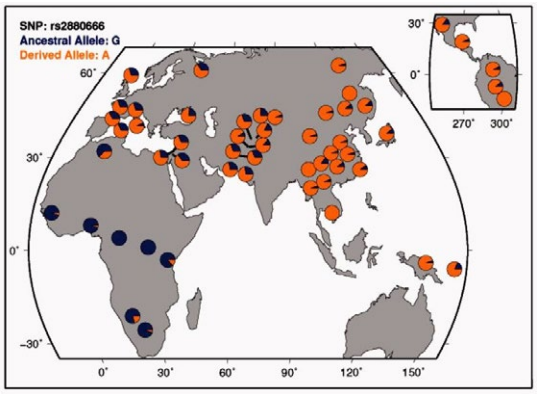


Fig. 1: *Worldwide distribution of allele frequencies as provided by the HGPD Selection Browser (http://hgdp.uchicago.edu) for a Zn nutriQTL detected around the zinc transporter gene SLC30A9, which shows one of the most significant signatures of adaptation found in Asians.*

Genomic analysis of Andamanese provides insight into ancient human migrations into Asia and adaptation

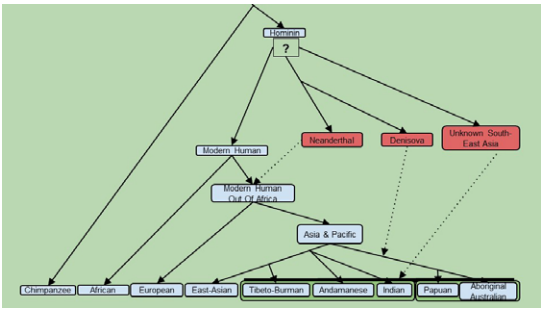
Mondal, M.; Casals, F.; Xu T.; Dall'Olio, G.M.; Pybus, M.; Netea, M.G.; Comas, D.; Laayouni, H.; Li, Q.; Majamder, P.P. and Bertranpetit, J. 2016. *Nature Genetics* 48: 1066-1070.

The genetic analysis of a group of individuals from the Andaman Islands in the Indian Ocean has revealed that their DNA contains fragments that do not correspond to modern humans who left Africa about 80,000 years ago. When comparing these sequences with those of Neanderthals and Denisovans, it has been seen that they also are clearly different. The research has concluded that this DNA belongs to an extinct hominid that shares a common ancestor with the other two but has a different history. This is new evidence that the human genome contains small amounts of information from extinct ancestors.

About 80,000 years ago, archaic *Homo sapiens* evolved into modern man in Africa. A small part of the population left the continent, resulting in all of the human settlements outside Africa. However, there were doubts as to whether Pygmies like the ones in the Andaman Islands came from an initial migration that would have been followed by other migrations. Thanks to the DNA sequences obtained in this study, this has been found not to be the case and so-called *Out of Africa*, from which all modern humans are descended, came about in a single migration.

The small stature of the Andamanese, therefore, is not explained by a founder effect, that is to say, that the first inhabitants were short and that is why their offspring are too. The scientific team has found genetic evidence that this event is the result of an evolutionary process of adaptation and natural selection. On a small island there is no place for the

whole trophic chain, so the large predators should disappear and the animals of lower levels become small, as it gives them selective advantages. This study provides conclusive genetic proof of this phenomenon, which gave rise to animals such as *Myotragus balearicus*, a 40 cm goat that who lived on the Balearic Islands, or metre-high elephants that had lived in Sicily. The current findings could also serve to explain the small stature of the fossil hominids of Flores island in Indonesia.



Mitochondrial DNA from the eradicated European Plasmodium vivax and P. falciparum from 70-year-old slides from the Ebro Delta in Spain

Gelabert, P.; Sandoval-Velasco, M.; Olalde, I.; Fregel, R.; Rieux, A.; Escosa, R.; Aranda, C.; Paaijmans, K.; Mueller, I.; Gilbert, M.T.P.; Lalueza-Fox, C. 2016. *Proc Natl Acad Sci USA* 113(41):11495-11500.

Malaria is one of the most severe public health problems worldwide and the major cause of death in many sub-Saharan countries. It was endemic in Europe until the second half of the 20th century, when it was eradicated across the continent. The evolutionary history of *Plasmodium vivax* and *Plasmodium falciparum*, the main causative agents of the disease is controversial, due to the lack of genetic information on these parasites in Europe. In 1925, the Catalan Autonomous Government established, at the Ebro Delta -a highly endemic malaria region- an anti-malaric center, directed by Dr. Ildefonso Canicio, who worked there for decades -eventually contracting the disease himself-. At his death in 1961, some of the microscopy slides with patient's blood drops he used to make for diagnostic purposes, were collected by his descendants and some of them were handed to researchers at the Institute of Evolutionary Biology. Next generation sequencing technologies were used to retrieve the complete mitochondrial genomes of both *Plasmodium* parasites and were analysed in the context of modern strain diversity. It was found that the most common contemporary *P. vivax* strains from South and Central America cluster with the extinct European strain, suggesting that malaria spread to this continent from Europe in post-Columbian times. Moreover, the *P. falciparum* European strain clusters with an Indian-specific strain, which supports historical accounts indicating that severe malaria entered Europe from the East during Classical Greek times. The analysis of additional slides, as well as the nuclear genome of *P. falciparum*, will help to unravel present-day resistant mutation to different drugs as well as estimate a mutation rate for this parasite that could help model adaptive rates to new treatments.

Fig. 1: *Two of the Giemsa-stained slides analyzed in this study, labeled CM and CA (inferior stain).*
Author: *Carles Lalueza-Fox*

Chimpanzee genomic diversity reveals ancient admixture with bonobos

de Manuel, M.; Kuhlwilm, M.; Frandsen, P.; [23 authors]; Navarro, A.; [7 authors]; Xue, Y.; Hvilsom, C. and Marques-Bonet, T. 2016. *Science* 354 (6311) 477-481.

Between 1.5 and 2 million years ago chimpanzees (*Pan troglodytes*) and bonobos (*Pan paniscus*) split from a common ancestor and evolved important strong physical and behavioural differences. To this day, the existence of gene flow between the species has not been considered due to the Congo River that physically separates the geographical distribution ranges of the species. This is the first study, then, to reveal admixture among the species similar to what has been reported between humans and Neanderthals. This has been possible thanks to the application of recent analytical tools to detect current and ancient admixture among groups.

The studied samples, comprising 75 complete genomes of chimpanzees and bonobos, cover 10 countries in Africa, from the westernmost to the easternmost region of the chimpanzee range. Here, we found that chimpanzees do have very strong geographical stratification of their genome diversity, and thus, the results have a direct application to the conservation of these species because they permit the detection of the origin of chimpanzees confiscated from illegal trafficking.

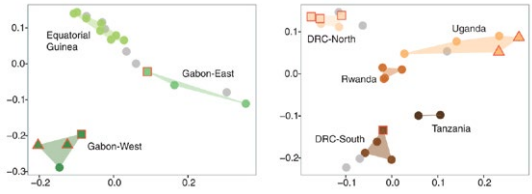


Fig. 1: *Geographic stratification of chimpanzee diversity. PCA plot of chromosome 21 SNP data for a set of central (left) and eastern (right) chimpanzees. Samples with unknown origin are colored in gray. The test samples (squares) were found to cluster perfectly with genome data for known samples (dots) (deManuel et al. Science 2016). Triangles correspond to SNP data from fecal samples.*

Integrative analyses unveil speciation linked to host plant shift in *Spialia* butterflies

Hernández-Roldán J.L.; Dapporto, L.; Dincă, V.; Vicente J.C.; Hornett, E.A.; Šichová, J.; Lukhtanov, V.A.; Talavera, G.; Vila, R. 2016. *Molecular Ecology* 25(17):4267-84.

Describing a new species of butterfly for Europe is quite an exceptional feat. In fact, the last butterfly species in the Iberian Peninsula was described over 20 years ago. However, discovering cryptic species in well-studied areas and taxonomic groups can have profound implications in understanding eco-evolutionary processes and in nature conservation because such groups often involve research models and act as flagship taxa for nature management.

The Butterfly Diversity and Evolution Lab, together with colleagues from several countries, used an array of techniques to study the butterflies in the *Spialia sertorius* species group (Lepidoptera, Hesperiidae). The integration of genetic, chemical, cytogenetic, morphological, ecological and microbiological data indicates that the *sertorius* species complex includes at least five species that differentiated during the last three million years. As a result, two taxa are reinstated as species and a new cryptic species, *Spialia rosae*, is described.

The new species is endemic of the Iberian Peninsula and is morphologically indistinguishable from the sympatric *S. sertorius*, but feeds on a different host plant (*Rosa* sp.). The sister species

show constant differences in DNA, chemical profiles and ecology, suggesting that *S. rosae* represents a case of ecological speciation involving larval host plant and altitudinal shift. Differences in infection by *Wolbachia*, a bacterial endosymbiont of insects that may generate cytoplasmic incompatibility, suggest that the speciation process could have been triggered by these bacteria. This study exemplifies how a multidisciplinary approach can reveal elusive cases of hidden diversity and reminds us that our knowledge of biodiversity is still incomplete even in well studied areas and taxonomic groups.

Testing the island effect on phenotypic diversification: insights from the *Hemidactylus* geckos of the Socotra Archipelago

Garcia-Porta, J., Šmíd, J., Sol, D., Fasola, M. and Carranza, S. 2016. *Scientific Reports* 6: 23729.

The existence of phenotypically bizarre species in islands – as the Dodo or the Galapagos tortoises– has always amazed naturalists and evolutionary biologists. This distinctiveness of so many island species has classically been linked to the impoverished species richness exhibited by islands, consequence of their geographic isolation. This would release new colonizers from competitors and enemies, enabling them the capacity to expand their niches and invade adaptive zones that are normally occupied in the continent, triggering extreme levels of morphological diversification.

In this study, we test the hypothesis of the existence of an "island effect" on phenotypic traits using a completely sampled mainland-island system, the arid clade of *Hemidactylus*, a group of geckos mainly distributed across Africa, Arabia and the Socotra Archipelago. To this effect, we generated a new molecular phylogeny of the group on which we mapped body size and head proportions. We then explored whether island and continental taxa shared the same morphospace and differed in their disparities and tempos of evolution. The results showed that the insular species produced the most extreme sizes of the radiation, involving accelerated rates of evolution and higher disparities compared with most continental groups. In contrast, head proportions exhibited constant evolutionary rates across the radiation and similar disparities in islands compared with the continent. These results, although generally consistent with the notion that islands promote high morphological disparity, reveal at the same time a complex scenario in which different traits may experience different evolutionary patterns in the same mainland-island system and that continental groups do not always present low levels of morphological diversification compared to insular groups.

Fig. 1: Hemidactylus pumilio. *Endemic to Socotra Island, it is the smallest species of the arid clade of* Hemidactylus.

Photo: *Fabio Pupin*

The Dynamic Regulatory Genome of *Capsaspora owczarzaki* and the Origin of Animal Multicellularity

Sebé-Pedrós, A.; Ballare, C.; Parra-Acero, H.; Chiva, C.; Tena, J.; Sabidó, E.; Gómez-Skarmeta, J.-L.; Di Croce, L.; and Ruiz-Trillo, I. 2016. *Cell 19;165(5):1224-37*

Evolution has given rise to astonishing diversity in the animal kingdom, from barely visible insects to towering elephants. All of this diversity arose from a single cell ancestor. This amazing fact begs the question: how did the first multicellular animal evolve from a single-cell ancestor to give rise to such diversity?

The Multicellgenome lab has developed a clever approach to unravel this intriguing mystery by comparing the genomes of animals to their closest unicellular relatives, such as the amoeba *Capsaspora owczarzaki*. Upon comparing the

genomes, the investigators found that many genes were shared between the two organisms (and therefore were already present in their common ancestor).

Given that the common ancestor already had a complex genetic repertoire, gene innovation alone cannot explain the origin of animal multicellularity. So what could explain the evolution of animal multicellularity? The researchers of the MCG Lab hypothesized that perhaps genomic regulation rather than gene repertoire was the key. To tackle this hypothesis, they carried out the first integrative analysis of the genome regulatory mechanisms of *Capsaspora*.

Interestingly, the authors found that this unicellular relative of animals shares many mechanisms of genome regulation with animals. The differences, however, were the most revealing part.

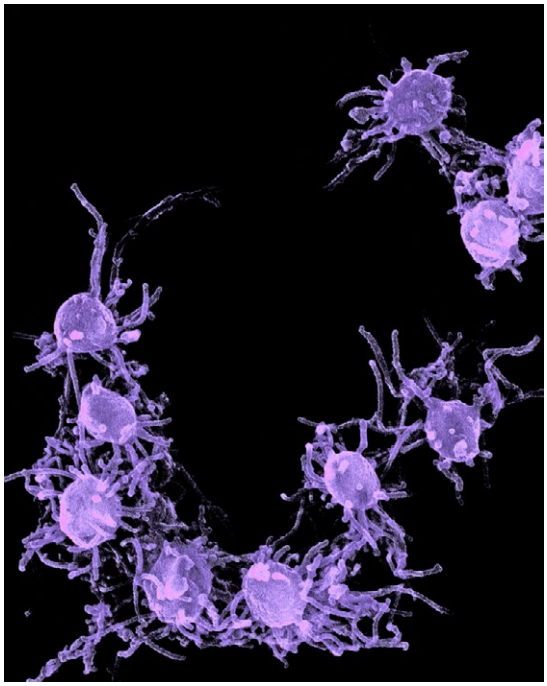


Fig. 1: *Capsaspora owczarzaki, which was isolated from the hemolymph of a Puerto Rico snail.*
Photo: *Arnau Sebé-Padrós*

A primary difference between *Capsaspora* and animals was the absence of distal cis-regulatory sites in the amoeba. It turns out that these sites, known as enhancers, are critical for the development of different cell types and tissues in animals. These enhancers may constitute the basis for the sophisticated gene regulation observed in animals, and may be the missing key to understanding evolution of multicellularity.

Further analyses in other unicellular relatives of animals will be critical to further describe the evolution of the animal-specific regulatory genome, which will allow the researchers to further unravel the mystery of how we as animals evolved from our unicellular ancestor.

The occurrence of the holometabolous pupal stage requires the interaction between E93, Krüppel-homolog 1 and Broad-Complex

Ureña, E., Chafino, S, Manjón, C., Franch-Marro, X. and Martín, D. 2016. *PLOS Genetics* 12(5): e1006020.

Insects are the most successful and diversified animal group, with more than two million species described (approximately half of all animal species reported). One of the reasons of this taxonomic richness lies in the appearance of specific novel phenotypic characters known as *key innovations* that has allowed the adaptive radiation of insect species. Several lines of evidence suggest that *complete metamorphosis*, which includes the occurrence of a specific stage, the pupa, is a key innovation that has had the most relevant effect on insect diversity through evolution. Considering the phylogenetic relationships among insects, it is generally accepted that insects that display complete metamorphosis (holometabolous insects) form a monophyletic group that evolved from an ancestor exhibiting incomplete metamorphosis (hemimetabolous insects) approximately 300 million years ago. Unfortunately, despite its evolutionary relevance, the nature of the changes underlying the appearance of holometaboly, including the formation of the pupa, remains a puzzling problem in evolutionary and developmental biology.
A few years ago, the David Martín and Xavier Franch-Marro's lab, successfully identified and

characterized the transcription factor E93 as the critical factor that instructs cells to differentiate into the adult fate during the metamorphic stage in hemimetabolous and holometabolous insects. Now, using the holometabolous insects *Tribolium castaneum* and *Drosophila melanogaster* as models, the same group has shown that the genetic interaction between E93 and two other critical metamorphic transcription factors, *Krüppel-homolog 1* and *Broad-Complex*, underlie the formation of the pupa in holometabolous insects. Experiments showed that a transient peak of *Kr-h1* at the end of the final larval stage, a particular event specific of holometabolous insects, prevents the precocious up-regulation of *E93*, thus pausing the implementation of the adult differentiation program, and allowing the strong up-regulation of *Broad-Complex*, which is critical for the correct formation of the pupa. In addition, by using the hemimetabolous insect *Blattella germanica*, they also demonstrate that the functional relation between *E93*, *Krüppel-homolog 1*, and *Broad-Complex* is evolutionarily conserved, suggesting that the occurrence of the pupal stage has been facilitated by the co-option of regulatory mechanisms already present in hemimetabolous insects. Overall, the results presented in the paper provide a molecular framework to explain how complete metamorphosis is regulated, thus shedding light into the evolution of complete metamorphosis.

Fig. 1: *Electron microscopy image of a pupa (left) and adult (right) of the flour beetle* Tribolium castaneum.

The major synthetic evolutionary transitions

Solé, R. 2016. *Philos Trans R Soc Lond B Biol Sci* 371(1701).

The evolution of life has been marked by a number of major innovation events, also known as Major Evolutionary Transitions. These include for example the origin of cells, multicellular life forms, sight, cooperation, cognition, language and even consciousness.

Understanding the nature of these transitions and their unique or universal character is a big challenge. It could be argued that there's only a single evolution experiment, since we have only this planet as a case study. Using tools from molecular genetics, phylogenetic analysis and systems biology, it is possible to reconstruct a great deal of past events, but innovations require a proper theoretical framework to gather a full understanding of their origins. An alternative approach is provided by a "synthetic" path grounded in our potential for engineering, simulating or building artificial alternatives or Major Synthetic Transitions.

Using synthetic biology, artificial life models or evolutionary robotics, it is possible to recreate the conditions predating major innovations. Artificial multicellularity, robotic grammars or protocells are examples of the potential innovations that can be created in the lab. By using this alternative approach, we can answer crucial questions concerning the universal (or even inevitable) character of some transitions and how they can actually occur through evolutionary dynamics.

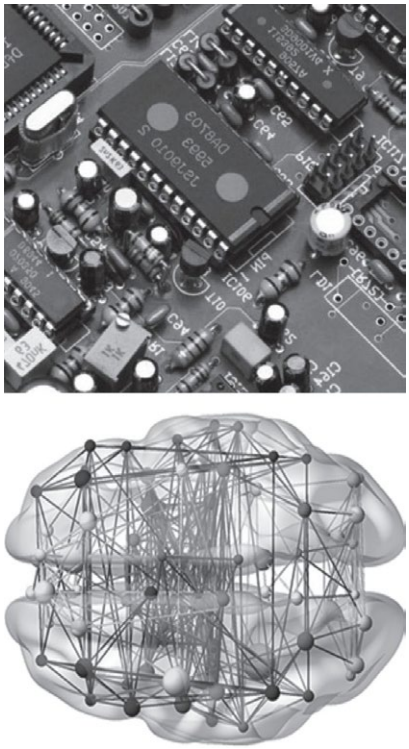


Fig. 1: *Electronic circuits (top) are the iconic representations of standard computing machines. Brains (bottom) and computer circuits have been often compared as implementations of hardware systems capable of performing computations.*

Author: *Ricard Solé*

Major Transitions in Information Technology

Valverde, S. 2016. *Philos Trans R Soc Lond B Biol Sci* 371(1701)

Although the evolution of technology has been only marginally represented in most evolutionary views, we should not forget that technology offers a rather good fossil record at different scales, and this is particularly true for information technology (IT) both within hardware and software designs. We can study the time-dependent traits developed through the history of IT since the 1950s using novel techniques from complex networks theory. These methods reveal punctuated patterns of evolution marked by bursts in diversification. Technological transitions are associated with innovations (both in hardware and software) and the method used to uncover the underlying phylogenetic trees is grounded on a simple topological approximation that largely ignores most of the fine-grained information contained by each invention. This result encourages us to think that a 'tree of technology' might eventually be characterized and fully compared with the tree of life. Although many key issues have yet to be resolved, it is argued that the structure of technological evolution shares fundamental features with the structure of biological evolution.

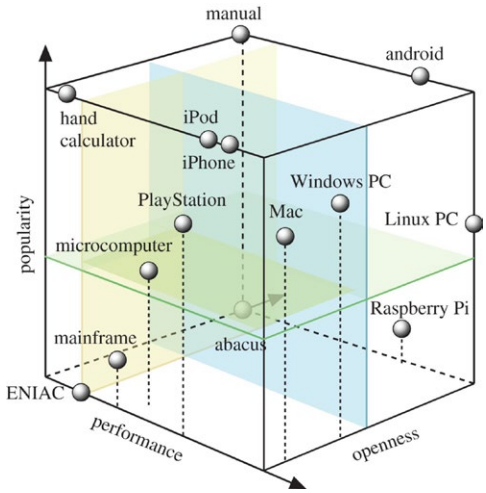


Fig. 1: *The evolution of information technology (IT) allows for a quantitative and theoretical approach to technological transitions.*

Author: *Sergi Valverde*

IBE COLLECTIONS

Another year, the scientists in the Animal Biodiversity and Evolution Program have worked hard to continue increasing the size and quality of the IBE collections. This continuous effort can be now seen reflected in the astounding, please number of specimens that their collections have reached. Currently, the insects are still the champions of the collection with more than 120,000 specimens of Coleoptera (Fig. 1) and more than 70,000 of Lepidoptera, plus a smaller representation of Hymenoptera and other insect Orders. The second animal group with more specimens in the collection are the reptiles and amphibians, with more than 11,300 and 2,440 tissue samples respectively. Finally, the collection is enriched with ca. 1,500 DNA samples of mammals. In terms of species numbers, we have ca. 5,000 species of Coleoptera, 950 of reptiles and 180 amphibians. The number of Lepidoptera species this year has been increased to ca. 1,300 species.

Fig. 1: *Some dry specimens in one of our researchers collection.*

One of the main activities carried out with the collection during 2016 has been continuing with the organization and arrangement of samples for different groups. This task has been in the hands of a new technician, Elena Plana, since late 2016, after Jaume Badia left the position last summer to pursue an MSc. The new person in charge of the collection has acquired new responsibilities with an emphasis in ordering the collections, and she is currently helping with the inventory, arrangement, and databasing of specimens. Besides, the materials used to preserve the specimens are being studied (and changed if necessary) in order to improve the durability of the collection by taking measures to keep the specimens under the best preservation conditions.

The collection technician is also helping with the Program's activities that the protocol of Nagoya. The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (ABS) is a supplementary agreement to the Convention on Biological Diversity. It provides a transparent legal framework for the effective implementation of one of the three objectives of the CBD: the fair and equitable sharing of benefits arising from the utilization of genetic resources. The protocol entered into force on 12 October 2014 and although it contributes to the conservation and sustainable use of biodiversity it makes it difficult for the scientific community to obtain the necessary permits to collect specimens, even when their activities do not pursue any economic benefit, as it happens with the Program's research.

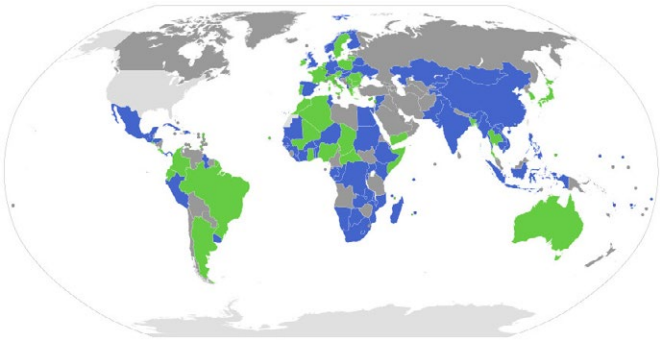


Fig. 2: *Nagoya Protocol on ABS.* *Parties,* *Only signed but not ratified,* *non signatory but Biological Diversity Convention party, non signatory,* *non-Biological Diversity Convention party.*

The fact that lots of countries have joined the Protocol in different periods (Fig. 2) and the lack of standardization (each country is building their own legal framework of necessary measures to allow collecting samples in their jurisdiction), made necessary an extensive research to know each countries' processes and requirements. We are building this knowledge progressively by establishing a network of relevant contacts with whom to negotiate the specimen transfer agreements in these countries where the scientists of the ABE program develop their activity. Moreover, and also related with the provisions of the Nagoya protocol, we have established a Collection Policy and material transfer agreements, both almost ready to be accessed and used on the IBE website.

Developments and discoveries of 2016

In 2016, the researchers in the Animal Biodiversity and Evolution program have travelled around the Globe and received material from many colleagues to increase the representation of species in their respective collections. Some of the international expeditions carried out in 2016 include:

Fig. 3: *Sampling locations for the new collection specimens obtained by IBE members during 2016.*

Cyprus

As part of the project on the evolutionary transitions on aquatic Coleoptera, the water beetle group conducted field work in Cyprus, mainly to collect their (few) endemic species and those on the extensive saline coastal lagoons and marshes of the south of the island.

Aeolian Islands

Roger and colleagues assisted the 2016 Butterfly Week. This initiative that involves international researchers and citizens allowed the crew to share their knowledge and projects with them, and, at the same time, explore the fauna of these islands.

Kamchatka

Our ant expert, Sämi Schar, travelled to Kamchatka looking for some ant populations. Since the focus of his research are ants with a Holarctic distribution, Beringia (the land and maritime area that bounds Russia, Canada, Chukchi Sea and Kamchatka Peninsula) is a potential area of dispersal across continents where he expected to find some key species for his project.

Slovakia and Hungary

Our beetle researchers sampled the western Carpathians, between Slovakia and Hungary, mainly to collect species in freshwater streams, some of them endemic to these mountains.

Scandinavia

Some members of the butterfly group drove all over Scandinavia in order to find the last species they needed to complete their EUGENMAP project (European Genetic Map of Butterflies).

Poland, Slovakia, Czech Republic and Germany
Joan Carles Hinojosa and his collaborator crossed all these countries in a long expedition to collect butterflies in central Europe.

Oman and UAE
Some members of the reptile group performed a new expedition to the arid and inhospitable south-eastern Arabia. Long hot days and sleepless nights were rewarded with the discovery of three new species of reptiles.

The ABE scientists devote a significant amount of time to taxonomic research. During 2016, this was reflected in the description of seven new animal species, including:

Beetles (Coleoptera)
Aphaobius haraldi Faille et al. 2016

Calligrapha pavimentata Gómez-Zurita 2016

Calligrapha zapoteca Gómez-Zurita 2016

Butterflies (Lepidoptera)
Spialia rosae Hernández-Roldán et al. 2016

Reptiles (Reptilia)
Asaccus gardneri Carranza et al. 2016
Asaccus margaritae Carranza et al. 2016
Rhynchocalamus dayanae Tamar et al. 2016

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Fig. 7: *Margarita Metallinou*

Fig. 8: *Asaccus gardneri*

Fig. 9: *Asaccus margaritae*

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Tamar, K.; Šmíd, J.; Göçmen, B.; Meiri, S. and Carranza, S. (2016). An integrative systematic revision and biogeography of *Rhynchocalamus* snakes (Reptilia, Colubridae) with a description of a new species from Israel. *PeerJ* 4: e2769.

Advancing the taxonomic knowledge about animals is one of the objectives of the Animal Biodiversity and Evolution Programme and, as a result of that, new species of animals are described every year. Among all seven new species described during 2016 we would like to highlight the discovery of two new geckos from Arabia, one of them named after the late Margarita Metallinou, a former PhD student of the programme that passed away in an accident in 2015.

Discovery of two new endemic species of Musandam: *Asaccus gardneri* and *Asaccus Margaritae* (Carranza et al 2016)

On 2016, Salvador Carranza together with some members of his research team of the Systematics, Biogeography and Evolution of Reptiles and Amphibians and collaborators from the Centre for Endangered Arabian Wildlife, Environment and Protected Areas Authority, Sharjah, United Arab Emirates described two new species of geckos from the Hajar Mountains in southeast Arabia. As a result of their nocturnal habits and morphological similarity they eluded scientists for decades until last year, when a comprehensive study using an integrative approach including morphological and molecular data showed that what was previously considered a single species, *Asaccus caudivolvulus*, was in fact an assemblage of three species that started diversifying in the northern Hajar Mountains more than 12.7 Million years ago. As a result of this discovery and the corresponding taxonomic revision, the species *A. caudivolvulus* was restricted to a small coastal area of the UAE and at risk from heavy development, while the two new species described were found widely distributed across the northern tip of the Hajar Mountains and seem to segregate in altitude when found in close proximity in the Musandam Peninsula (Oman). Similarly to other integrative analyses of the reptiles of the Hajar mountains, this study highlights the high level of diversity and endemicity of this arid mountain range, underscoring its status as one of the top hotspots of reptile diversity in Arabia and one of the mountain ranges with the highest diversity in the world. Of the two new species, one was named *Asaccus gardneri,* after Dr. Drew Gardner for his contribution to Arabian herpetology and the other one was named *Asaccus margaritae,* to honor Dr. Margarita Metallinou, who was involved in the earlier stages of the research, having collected this new species during a 2013 expedition to Arabia.

We would like to dedicate a few lines to the memory of Dr. Margarita Metallinou (1985-2015). She was a promising young systematic herpetologist whose career was tragically cut short by a wildlife accident while doing fieldwork in Africa in July 2015. Her legacy in the IBE started on 2008, when she joined the laboratory of Salvador Carranza to do her master's thesis on the phylogeny, biogeography and evolution of the geckos of the genus *Stenodactylus*. As part of her work she had the chance to participate in a field expedition to Morocco and she immediately fell in love with the arid reptile faunas and the endless flat vistas of the Sahara desert. Later, while doing her PhD in the same laboratory she discovered taxonomy was also one of her passions.

In her short career, Margarita contributed significantly to the phylogenetics and taxonomy of the lizards of Africa and Arabia and she helped inspire other young systematic herpetologists, especially women. Moreover, her laboratory, analytical and field skills as well as her outgoing, engaging and nurturing personality made her leave all the fortunate who knew her full of gratefulness for the enrichment she brought to their lives.

THESES, COURSES AND SEMINARS

Doctoral Thesis presented during 2016

- **PhD Student:** Tiago Loureiro de Carvalho
  Title: « Tandem Repeat variation in human and great ape populations and its impact on gene expression divergence »
  Thesis Director: Tomàs Marquès-Bonet
  Institution & Date: Universitat Pompeu Fabra, 21st January 2016
- **PhD Student:** Salva Duran
  Title: Artificiall multicellularity and pattern formation
  Thesis Director: Ricard Solé
  Institution & Date: Universitat Pompeu Fabra, 15th January 2016
- **PhD Student:** Laín Guío
  Title: The transposon Búrrí-fheh in Drosophílø melanogøsteri adaptive phenotypes, molecular mechanisms, and genetic inheritance
  Thesis Director: Josefa Gonzalez
  Institution & Date: Universitat de Barcelona 17st March 2016
- **PhD Student:** Max Carbonell
  Title: Engineering Principles for Synthetic Biology
  Thesis Director: Carlos Rodriguez-Caso and Javier Macia
  Institution & Date: Universitat Pompeu Fabra 13 June 2016
- **PhD Student:** Luis F. Seoane
  Title: Multiobjective Optimization in Models of Synthetic and Natural Living Systems
  Thesis Director: Ricard Sole Vicente
  Institution & Date: Universitat Pompeu Fabra 13 May 2016
- **PhD Student:** Iñigo Olalde
  Title: From the Mesolithic to the Bronze Age: unraveling 5,000 years of European population history with paleogenomics
  Thesis Director: Carles Lalueza-Fox
  Institution & Date: Universitat Pompeu Fabra 22 July 2016
- **PhD Student:** Ignasi Torruella
  Title: « Genetic variation in human miRNAs: functional consequences and involvement in Cancer »
  Thesis Director: Yolanda Espinosa Parrilla
  Institution & Date: Universitat Pompeu Fabra 28 October 2016
- **PhD Student:** Nino Spataro
  Title: « Human genetic disorders: linking Mendelian and complex diseases »
  Thesis Director: Elena Bosch
  Institution & Date: Universitat Pompeu Fabra 26 October 2016
- **PhD Student:** Alicia Gallego
  Title: « Addressing functional and evolutionary implications of microRNA variation at the DNA and RNA levels in primates
  Thesis Director: Yolanda Espinosa Parrilla
  Institution&Date: Universitat Pompeu Fabra 14 November 2016
- **PhD Student:** Juan A. Rodriguez
  Title: « Testing two evolutionary theories of ageing by using public genome-wide data »
  Thesis Directors: Elena Bosch y Arcadi Navarro
  Institution & Date: Universitat Pompeu Fabra 24 January 2017
- **PhD Student:** Andrey Rudoy
  Title: « Evolution of the male genitalia in the genus linnebius leach1815, Family hidraenidae (coleoptera) »
  Thesis Directors: Ignacio Ribera
  Institution & Date: Universitat Barcelona 17 October 2016
- **PhD Student:** Mayukh Mondal
  Title: New Insights into Human Migration, Demography and Adaptation of Indian and South Asian populations from genome analyses
  Thesis Director: Jaume Bertranpetit , Ferran Casals
  Institution & Date: Universitat Pompeu Fabra 21 November 2016

- **PhD Student:** Guillem de Valles Ibáñez
  Title: Evolutionary analysis of the genome load of loss-of-function variants and their contribution to immunodeficiencies
  Thesis Director: Tomas Marques , Ferran Casals
  Institution & Date: Universitat Pompeu Fabra 16 December 2016
- **PhD Student:** Diego Hartasánchez
  Title: Modeling and simulation of interlocus gene conversion
  Thesis Director: Arcadi Navarro
  Institution & Date: Universitat Pompeu Fabra 22 November 2016
- **PhD Student:** David Garcia Vazquez
  Title: Range expansions in the evolutionary history of western palaearctic aquatic coleoptera
  Thesis Director: Ignacio Ribera Galan
  Institution & Date: Universitat Barcelona 16 December 2016
- **PhD Student:** Gissela de la Cadena
  Title: Eliminación de impedimentos taxonómicos y ecológicos en hot-sopts de biodiversidad mediante herramientas moleculares ; los Chrysomelidae y sus asociaciones tróficas en el bosque tropical de Nicaragua
  Thesis Director: Jesús Gomez-Zurita and Anna Papadopoulou
  Institution & Date: Universitat Barcelona 22 December 2016

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: Salvador Carranza
- 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
- Interdisciplinary Seminars (5 ECTS).
  Coordinator: Yolanda Espinosa Parrilla.
- Introduction to the University and to the Biomedical Engineering (6 ECTS
  Coordinator: Javier Macía
- Principles of Biological Design (2 ECTS).
  Coordinator: Ricard Solé
- Evolutionary Algorithms (4 ECTS).
  Coordinator: Sergi Valverde
- Cell and Tissue Engineering (5 ECTs).
  Coordinator: Ricard Solé

Bachelor's Degree in Bioinformatics (Universitat Pompeu Fabra-UB-UPC)

- Biostatistics and Data Analysis (4 ECTS). Coordinator: Hafid Laayouni
- Introduction to Bioinformatics (6 ECTS). Coordinator: Hafid Laayouni

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 the Universitat de Barcelona.

- Biomedical Data Analysis (5 ECTS). Coordinator: Hafid Laayouni
- Applied Genomics: Genome-Phenome Analysis for Human Health (5 ECTS). Coordinator: Ferran Casals
- 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:** I. Ruiz-Trillo , S. Carranza
- **Master:** "Cell biology"; Universitat Autónoma de Barcelona (UAB) **Teacher:** J. González
- **Master:** Human Biology; Universitat de Barscelona (UB) / Universitat Autònoma de Barcelona (UAB). **Teacher:** Francesc Calafell, Carles Lalueza
- **Master:** Genetic Counselling; IDEC/UPF. **Teacher:** Francesc Calafell
- **Master:** Genetics and Genomics, Universitat de Barcelona (UB). **Teacher:** Iñaki Ruiz-Trillo
- **Postgraduate course:** "Lessons from the variation in the genome". University of Ferrara **Teacher:** Jaume Bertranpetit
- **Postgraduate Course:** Filogenias y Genealogías de DNA: Reconstrucción y Aplicaciones; Universitat de Barcelona (UB). **Teachers:** J. Castresana, S. Carranza

Last but not least, every year IBE hosts several undergraduate and master students. Along 2016 IBE has hosted a total of 36 students. In particular:

- 8 High school juniors" - financed by "Fundació La Caixa-la Pedrera" through "Programa Joves i Ciència (3) -, Institut la Guineueta (1), escola Freta(2), escola st gervasi (1), escola St Josep (1).
- 15 undergraduate students (practicums) from: Universitat de Barcelona (9), Universitat Autònoma de Barcelona (3), Universitat de València (1), Universitat de Vic (2)
- 13 master students from: Universitat Pompeu Fabra (6), Universitat de Barcelona (4), Universidad autònoma de Barcelona (1), Universidad de Sevilla (1), Universitat de Vic (1)
- 8 ERASMUS students from: Università di Bologna (1), Universidad de Szent Istvan University (1), University of Creta (2), Universida de Firenze (2), Democritus University of Thrace (1), University of Athens (1)

Seminars

Speaker	Title	Institution	Date
Takaaki Daimon	Evolution of hormonal regulation of insect molting & metamorphosis: insights from knockout silkworms	University of Tokyo	13/1
Martin Sikora	Reconstructing 40,000 years of Eurasian population history from ancient DNA	Centre for GeoGenetics, University of Copenhagen	22/1
Enrico Cappellini	Paleoproteomics, state of the art and perspectives	Centre for GeoGenetics, University of Copenhagen	29/1
John McClutcheon	Degenerative genome evolution in endosymbionts: either stop it, slow it down, or go extinct	University of Montana	15/2
José Luis García-Pérez	LINE-1 Retrotransposition in Fanconi Anemia patients	GENYO, Granada, Spain	18/3
Ángeles de Cara	Detecting selection with haplotype-based methods: benchmarking polygenic selection and application to Heliconius butterflies	Museum National d'Histoire Naturelle, Paris	9/5
Erich Jarvis	Using Whole Genomes to Resolve a Vertebrate Family Tree and Genetics of Complex Traits	Duke University Medical Center	25/5
Dietmar Fernández Orth	Genomics and Bioinformatics. Next Generation Sequencing applications	Hospital Clínic, Barcelona	7/9
Magda Gayà-Vidal	Nucleotide variation analysis of human polymorphic inversions reveals a high degree of inversion recurrence	Research Center in Biodiversity and Genetic Resources (CIBIO), Vairão, Porto	9/9
Tábita Hünemeier	Genetic Signature of Natural Selection in the First Americans	Universidade de Sao Paulo	12/9
Irene Hernando	Transcriptional mechanisms during mouse early development revealed by single-cell RNA sequencing	Babraham Institute, Cambridge	19/9
Erica Bianco	Exploring pig demography using NGS data	Center of Research in Agrigenomic (CRAG)	20/10
Arnau Sebé-Pedrós	Early metazoan cell type evolution by single cell RNA-seq analysis	Weizmann Institute of Science	21/10

Speaker	Title	Institution	Date
Christelle Vangenot	Comparison of molecular diversity patterns of two multigenic families in chimpanzees and humans	University of Geneva	28/10
Maarten Larmuseau	Genetic genealogy - Interdisciplinary research on the relationship between DNA and family history	KU Leuven	15/12
Marcos Gallego-Llorente	Tracing the origin and spread of the Neolithic using ancient genomes	Department of Zoology University of Cambridge	19/12
Eric Libby	The evolution of biological complexity	Santa Fe Institute	22/12

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 and Josefa González, as joint coordinators of the Training and Outreach Unit.

TRAINING ACTIVITES

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

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

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

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

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

OUTREACH ACTIVITIES

The Institute of Evolutionary Biology is committed to informing and educating the general public about the research being carried out at the Institute. During 2016, IBE organized and participated in several outreach activities.

Top Ciencia exhibition in the CosmoCaixa museum

During one year, IBE research was highlighted at Cosmocaixa, the science museum of Barcelona managed by "la Caixa" Foundation, in a space of the museum that is aimed at promoting scientific careers and showing Spanish cutting-edge research. The Top Ciència area was composed of different audio-visual and interactive materials to know better what evolutionary biology is and what kind of research IBE scientists perform.

Melanogaster Catch The Fly

MCTF is the first European citizen science network in adaptation genomics. It offers the possibility to participate in scientific experiments with leading researchers in this field of biology, such as Dr González and her team at the Laboratory of Evolutionary and Functional Genomics. MCTF started in 2016 with the participation of young students from two Spanish high schools collecting fruit fly samples from fruit fields from their area, classifying them and sending them to analyse to the González Lab.

Barcelona International Youth Science Challenge

11th to 22nd July 2016

BIYSC is an international gathering in Barcelona of bright young researchers from all over the world. They meet together for two weeks to be inspired by internationally eminent science and technology leaders and to take part in specific Science and Technology challenges lead by top international Research Centres in Barcelona. IBE participated with a course named "Uncovering the hidden diversity of the oceans" and led by scientists from the Multicellgenome lab.

El llarg viatge de la papallona Vanessa cardui

This outreach video illustrates the longest migratory journey of any species of insects: the round-trip migration of the Vanessa cardui (Painted lady) butterfly between northern Europe and the African savannah. More info: https://goo.gl/flcRka.

Explora el Bosc

12th July 2016

IBE prepared a course about diversity and evolution called "Explora el Bosc", in collaboration with the "Exploratori dels Recursos de la Naturalesa" in Berga. The day began with presentations about biodiversity, insect collecting and animal identification. Then we move to the Obaga de Queralt to implement the knowledge acquired, although especiments collected were released in order not to disturb the ecosystem.

Saló de l'Ensenyament (teaching fair)
9th to 13th March 2016.
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.

PRBB Open Day
October 1st, 2016.
Organized by: Parc de Recerca Biomèdica de Barcelona (PRBB)

The IBE participated with several activities, including the scientific conferences "Com veiem la selecció natural a l'era del genoma (o allò que Darwin no sabia)" by Jaume Bertranpetit and "La manipulació genètica, una eina necessària per entendre la vida", by Elena Casacuberta.

Science Week
11th to 20th November 2016
Our participation started with several outrach seminars at Catalan shools as far as Prats del Lluçanès. The Open House sessions at CMIMA took place on 22 and 23 November, including the labs lead by Iñaki Ruiz-Trillo and Elena Casacuberta. We also took the opportunity to exhibit the photography collection "Butterflies in a click" at the CMIMA hall. Finally, on 16 November, IBE hosted the premiere screening of the film "The Fly Room" with an introduction by the director Alexis Gambis.

Organitzen: INSTITUT de BIOLOGIA EVOLUTIVA · IBE · CSIC · PRBB Barcelona Biomedical Research Park

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 2016, five students spend the summer at the IBE labs.

La Ciència Al Teu Món

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

Activities for students in collaboration with the PRBB

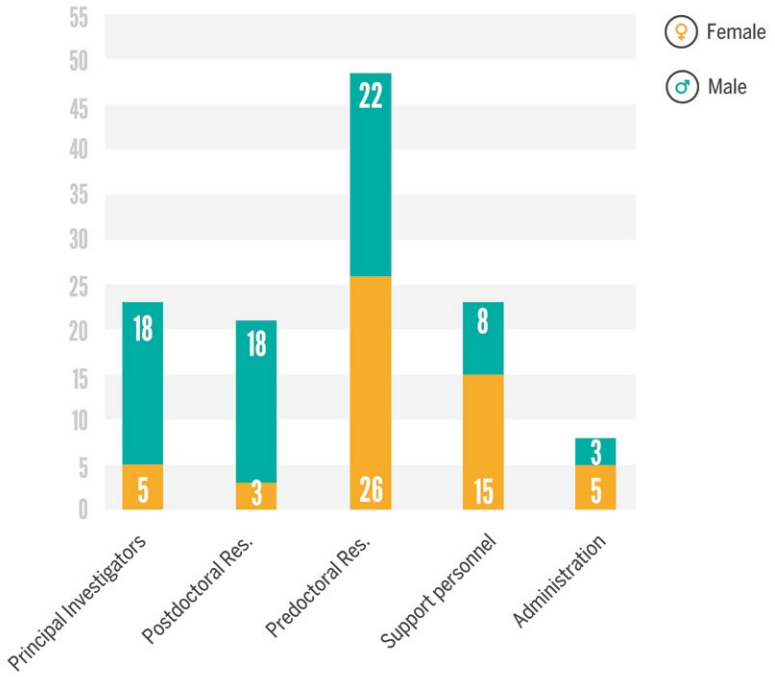
The PRBB provides a programme of activities for high school students. As part of the initiative **Escolab**, IBE offered high school students the chance to get to know the PRBB and some of its facilities and lines of research. The programme consists of a brief presentation of the park, a visit to one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

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

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

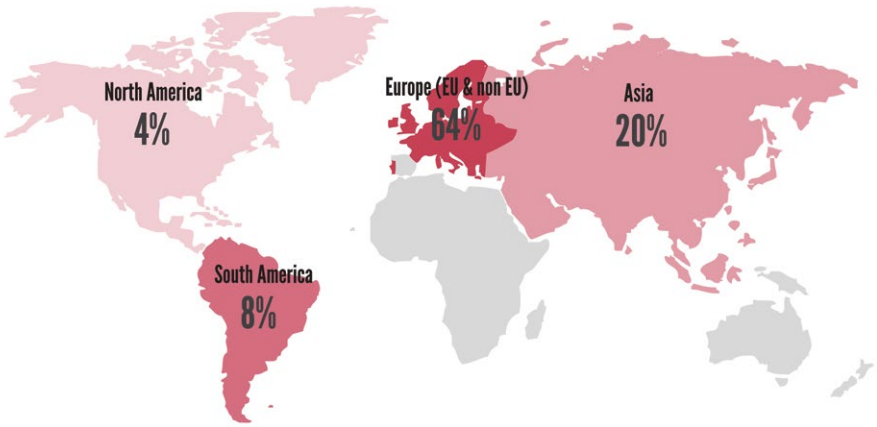
IBE IN NUMBERS

DISTRIBUTION OF 2016 PERSONNEL BY CATEGORIES AND GENDER



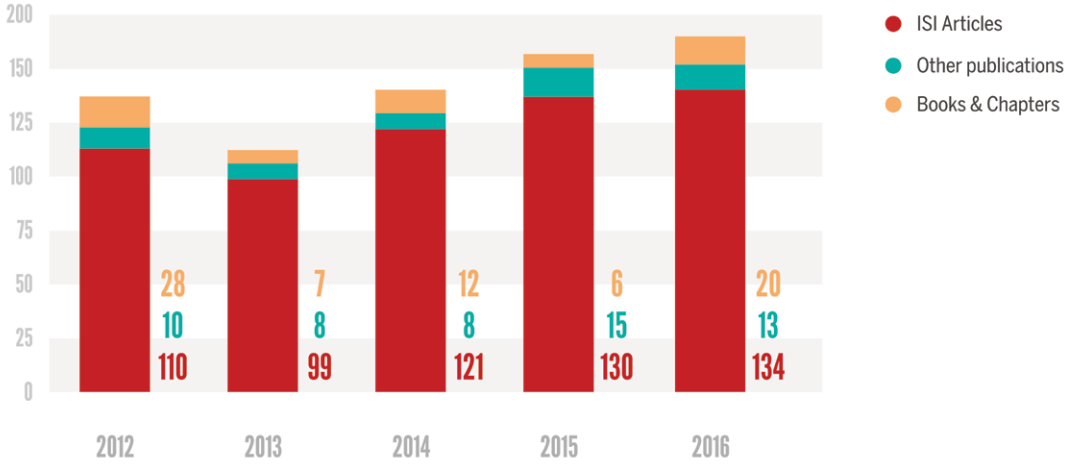
2016 INTERNATIONALISATION

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

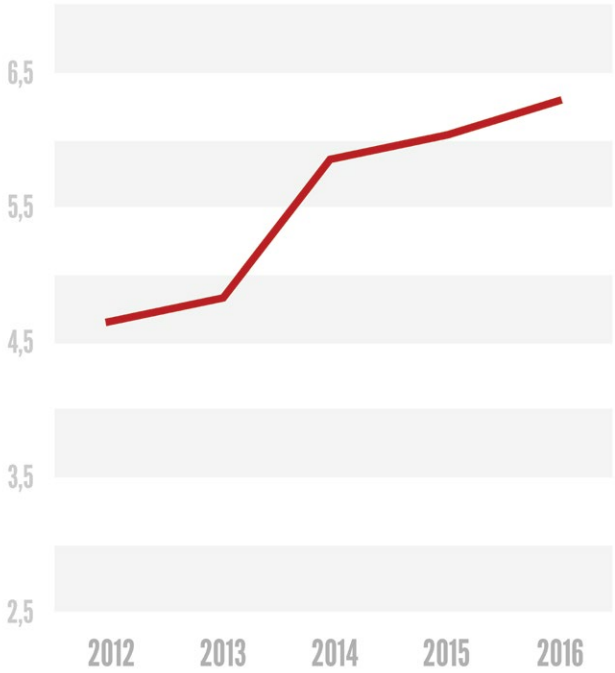


EVOLUTION IN NUMBER OF THESES DEFENDED EACH YEAR

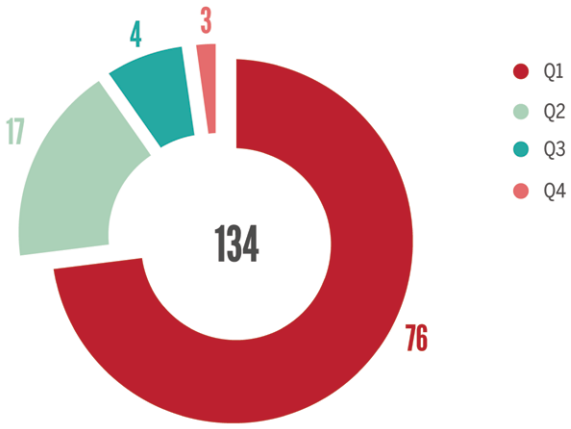
EVOLUTION OF PUBLICATIONS DISTRIBUTION PER KIND OF PUBLICATION



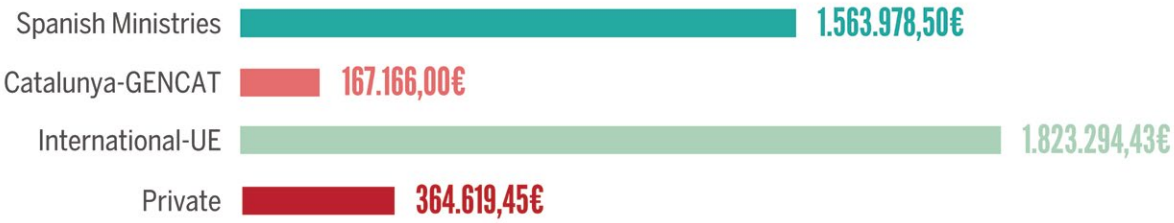
EVOLUTION OF MEAN IMPACT FACTOR FOR ISI PUBLICATIONS



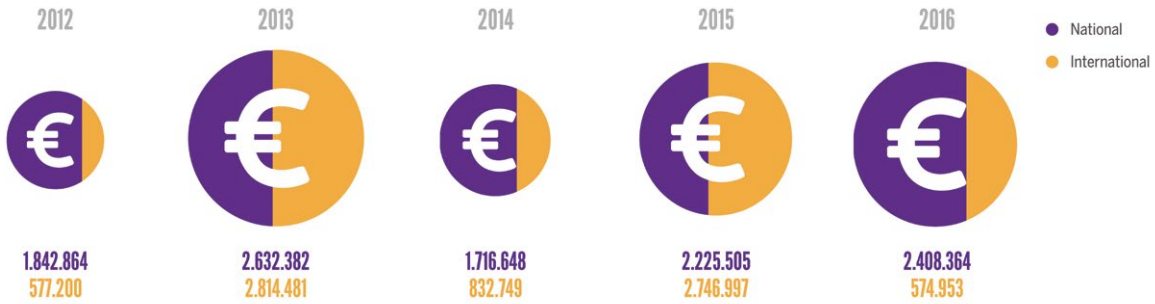
DISTRIBUTION OF 2016 ISI ARTICLES ACORDING TO THEIR QUARTILE



DISTRIBUTION OF ANNUAL COMPETITIVE FUNDS OF ONGOING PROJECTS IN 2016 ACCORDING TO THE ORIGIN OF FUNDS (FELLOWSHIPS NOT INCLUDED)



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



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