Who we are
We are a research institute working to understand the evolutionary mechanisms that generate biodiversity and to promote its conservation.

The Institute of Evolutionary Biology (IBE) is dedicated to understanding the processes and mechanisms that generate biodiversity and the genetic basis of evolution. Our work is helping to unravel how evolution works and to translate discoveries into new ways to conserve biodiversity.

Funded in 2008, the IBE is a unique partnership between the Spanish National Research Council (CSIC) and the Pompeu Fabra University (UPF). It brings together more than 130 people and 23 research groups distributed in 5 scientific programs on Evolutionary Biology research.

July 2018 has marked the 10th anniversary of IBE, which brought along a special agenda to celebrate our ten years of excellence in Evolutionary Biology research.
A walk through our 10 years

INSTITUTIONAL
IBE Foundation

2008

AWARDS
Teaching Quality prize
Awarded to Francesc Calafell, from the Genomics of Individuality Lab by the Consell Social UPF.

2009

FUNDING
First ERC grant by an IBE researcher
Tomàs Marquès-Bonet from the Comparative Genomics lab was awarded a Starting Grant from the European Research Council (ERC) to understand the origins of genomic variants and phenotypical differences among primate species.

2010

RESEARCH
First Nature paper
A burst of segmental duplications in the genome of the African great ape ancestor.

2009

ICREA Academia prize
Francesc Calafell, from the Genomics of Individuality Lab, was awarded an ICREA Academia prize.
Since 2008, these prizes recognize the research achievements of 25 professors of all disciplines in Catalan universities, and consist in prize money, supplemental research funds, and an overhead contribution to the host university, all for five years.
A walk through our 10 years

INSTITUTIONAL

Four labs join IBE

Josefa González
Evolutionary and Functional Genomics Lab
Luc Steels
Language Evolution Lab
Roger Vila
Butterfly Diversity and Evolution Lab
Iñaki Ruiz-Trillo
Multicell Genome Lab

FUNDING

IBE granted two Marie Curie Actions

Luc Steels, from the Language Evolution Lab, and Josefa González, from the Evolutionary and Functional Genomics lab, were awarded a Marie Curie Action to host talented foreign researchers and to create strategic partnerships with leading institutions worldwide.

AWARDS

ICREA Academia prize

David Comas, from the Human Genome Diversity Lab, was awarded an ICREA Academia prize.

Since 2008, these prizes recognize the research achievements of 25 professors of all disciplines in Catalan universities, and consist in prize money, supplemental research funds, and an overhead contribution to the host university, all for five years.

INSTITUTIONAL

2013

First IBE PhD Training Course

FUNDING

ERC Grant

Ricard Solé from the Complex Systems lab was awarded an Advanced Grant from the European Research Council (ERC) to study the evolutionary origins of complex systems, using both mathematical models and experimental approaches based on synthetic biology.
A walk through our 10 years

**AWARDS**
- **Teaching Quality prize**
  Awarded to Elena Bosch, from Evolutionary Population Genetics Lab by the Consell Social UPF.
- **EMBO Young Investigator Award**
  Tomàs Marquès-Bonet, from the Comparative Genomics lab, was selected for the EMBO Young Investigator award.
- **First Marie Curie Postdoctoral Researcher**
  Granted to Gerard Talavera to work on the Phylogeography and population genomics of the butterfly Vanessa cardui.

**FUNDING**
- **ERC Grant**
  Iñaki Ruiz-Trillo from the Multicell Genome Lab was awarded a Consolidator Grant from the European Research Council (ERC) to unravel the unicellular prehistory of metazoans with functional analyses and single-cell genomics.

**INSTITUTIONAL**
- **An IBE Retreat for the better**
  The annual IBE retreat came along Diversity and Good practices-Scientific Integrity commissions’ creation.
- **IBE’s Communication Unit creation**

---

**2013**

**2014**

**2015**
A walk through our 10 years

**FUNDING**
- ERC Grant

Josefa González from the Evolutionary and Functional Genomics Lab was awarded a Consolidator Grant from the European Research Council (ERC) to study adaptation in Drosophila.

**RESEARCH**
- First Science paper

Chimpanzee genomic diversity reveals ancient admixture with bonobos.


**AWARDS**
- ICREA Academia Prize

Elena Bosch, from the Evolutionary Population Genetics Lab, was awarded an ICREA Academia prize.

**AWARDS**
- Narcís Monturiol Medal

Jaume Bertranpetit from the Evolutionary Systems Biology Lab receives the Narcís Monturiol Medal.

Given by the Catalan Government since 1982, these awards recognize the contribution of Catalan organisations and authorities to the fields of science and technology.

**OUTREACH**
- IBE research highlighted at CosmoCaixa museum

During one year, IBE got an exhibition at Top Ciència, a space of Cosmocaixa aimed at promoting scientific careers and showing Spanish cutting-edge research.
A walk through our 10 years

**AWARDS**
- **ICREA Academia Prize**
  David Comas, from the Human Genome Diversity Lab, was awarded an ICREA Academia prize.

**AWARDS**
- **Howard Hughes Medical Institute (HHMI) award**
  Tomàs Marquès-Bonet, Director of the IBE, awarded by the Howard Hughes Medical Institute (HHMI).
  The prize was awarded to 41 candidates chosen from between 1600 nominations from all over the world, rewarding the career of young scientists. The prestigious American institution considers them the leaders of the future.

**INSTITUTIONAL**
- **New Director**
  Researcher Tomàs Marquès-Bonet was appointed the new director of the Institute of Evolutionary Biology.

**RESEARCH**
- **First Cell paper**
  The Dynamic Regulatory Genome of *Capsaspora* and the Origin of Animal Multicellularity.
  Arnau Sebé-Pedrós, Cecilia Ballaré, Helena Parra-Acero, Cristina Chiva, Juan J. Tena, Eduard Sabido, José Luis Gómez-Skarmeta, Luciano Di Croce and Iñaki Ruiz-Trillo; Cell 165, 1224–1237, May 19, 2016

**AWARDS**
- **2017 EMBO Membership**
  Iñaki Ruiz-Trillo, from the Multicell Genome Lab, became a member of EMBO, which supports talented researchers in recognition of their research excellence.
A walk through our 10 years

**Research**
- **2017**: IBE participates in 13 high impact papers
  - IBE researchers participated in the research of 6 Science and 7 Nature papers.

**Outreach**
- **2017**: Women in Evolution
  - Gender Awareness day entitled “Women in Evolution”, with the presence of outstanding women working in different areas of Evolutionary Biology.

**Institutional**
- **2018**: First PhD Symposium of IBE
- **2018**: One more lab for the Complex Systems program
  - Sergi Valverde, Evolution of Technology lab.

**Awards**
- **2018**: Narcís Monturio Medal
  - Xavier Bellés from the Evolution of Insect Metamorphosis lab and Carles Lalueza-Fox from the Paleogenomics lab receive the Narcís Monturio Medal.

**Outreach**
- **2018**: Special collaboration with ARA Catalan newspaper
  - ARA devoted its Sunday edition to evolutionary biology and to IBE.
  - It included an interview to IBE director Tomàs Marquès-Bonet, as well as six other pages, two interactives and one video dealing with several aspects of human evolution.
10 years in numbers

**Funding**

> 200 FUNDED RESEARCH PROJECTS

**Publications**

> 1,500 INDEXED PUBLICATIONS

- 4 ERC GRANTS
- 5 ICREA RESEARCHERS
- 36 NATURE, SCIENCE AND CELL PUBLICATIONS
10 years in numbers

Conservation projects

> 150 NEW TAXA CLASSIFIED (Genera, Species and Subspecies)

Awards

3 NARCÍS MONTURIOL MEDALS, 2016, 2018

1 HOWARD HUGHES MEDICAL INSTITUTE IEC AWARD, 2017

1 EMBO MEMBERSHIP, 2017

1 EMBO YOUNG INVESTIGATOR AWARD, 2013
Foreword

The following is an excerpt of the speech by Tomàs Marquès-Bonet, director of the Institute of Evolutionary Biology (IBE: CSIC-UPF), during the 10th year anniversary celebration.

Dear colleagues, dear friends, fellow scientists. Here we are, 10 years later.

It is a pleasure to be celebrating our 10th anniversary. To be precise: it is a pleasure that the IBE exists and it is an honor to be part of it. We are first and foremost scientists, and the IBE is just a way that allows us to fulfill our dream and our mission: to do science. That is what the IBE is about: Science. It is only a small part of Science, if you want: Evolutionary Biology. But still a very exciting, wonderful and diverse Science.

What kind of science? Excellent Science, difficult Science, delightful science... and sometimes even brilliant and ground-breaking Science.


And I can go on... Science to satisfy human curiosity, to advance knowledge, to contribute to progress, to serve our society, to improve our life and the life of our fellow citizens. Looking back at our relatively short life, that is exactly what we have done and we keep doing: Science. Today, 10 years after our foundation (thanks Xavier Bellés and Jaume Bertranpetit) we all should be proud of having done this Science.

We are small. Only 23 research groups, slightly over 120 researchers and our mission: to do science... and still are, a continuous fight; a permanent struggle with 2 different locations and 2
In the foreword, the author acknowledges the achievements of the Institution for Biodiversity Evolution (IBE) over the last 10 years. The author expresses pride in the institution's work, despite the challenges faced in obtaining funding and managing expectations. The author highlights the importance of maintaining a clear focus on excellence and passion in science. The author also thanks the mother institutions, the UPF and the CSIC, for their support and encourages future generations of scientists to contribute to the vital project of science.
Oman calling for a new reptile conservation plan.

IBE researchers led by Salvador Carranza have used an exceptional database including 5,359 records of 101 species of Oman’s terrestrial reptiles to assess the effectiveness of the protected areas in preserving this unique arid fauna. Their results indicate that Oman’s 22 protected areas cover only 3.91% of the country and include within their limits 63.37% of terrestrial reptiles and 50% of all endemics, highlighting that large areas of Oman lie outside protected areas and leaving many species unprotected. Their work calls for an urgent evaluation of the coverage of the current protected areas and the identification of further priority-protected territories for reptiles.


Percentage of Oman terrestrial reptile species’ distribution area included within a protected area. Dashed lines indicate the conservation target of 17% and 12% of the total species’ distribution area within a protected area.
Materials stored in museum collections can provide unique opportunities to document vanished genetic diversity and help direct conservation, as shown in a recent work of an IBE research lab, led by Roger Vila. In this work, IBE researchers used mitochondrial DNA from over 100-year-old museum specimens of the extinct Melanargia russiae (Esper’s marbled white) to determine which extant population should be used as source for its reintroduction in Hungary, where it was extirpated over a century ago.


Download article
What could have extended human lifespan? Researchers identify 25 genetic candidates.

Potentially, human beings can live for up to 120 years, whereas some closer primates live for half that period. In order to help explaining these longevity differences, IBE researchers led by Arcadi Navarro have identified some of the genes that may have been crucial in extending the life of our species. A new method has allowed identifying 25 candidate mutations, located in genes associated with wound healing, blood coagulation and cardiovascular disorders. The work confirms that some genetic variants that help us in the initial stages of life become harmful once the reproductive stage has ended. Authors suggest that these 25 genes could be candidates to develop new therapeutic targets for treating aging-related diseases, highlighting the potential of an evolutionary approach to medicine.

Copper Age Iberians 'exported' their culture - but not their genes - all over Europe.

The largest genomic study to date shows that the first Beaker expansion was one of cultural diffusion. Prehistoric Iberians 'exported' their culture throughout central Europe without exporting their genes. These are the main conclusions of an international study in which an IBE research team led by Carles Lalueza-Fox was involved. The findings show that the culture that produced these bell-shaped beakers extended from Iberia to central Europe without a significant movement of populations, although the Beaker culture would spread to other places through migrations at a later date. The diffusion of the Beaker culture from Iberia is the first example of a cultural phenomenon transmitted as an idea, basically due to a matter of social prestige.

Article: Iñigo Olalde, [...[103 authors]...] Carles Lalueza-Fox, David Reich. The Beaker Phenomenon and the Genomic Transformation of Northwest Europe. Nature. doi: 10.1038/nature25738
Copy-and-paste dynamics, at the heart of evolutionary change.

One of the challenges that evolutionary processes pose is the understanding of its open-ended nature, which allows for an unlimited increase of its complexity. In a recent article, an IBE research team led by Ricard Solé points at tinkering and reusing of existing parts as a mechanism to explore novel designs and promote evolutionary change. This copy-and-paste dynamics would provide the delicate balance between memory and innovation that characterize open-ended evolution processes, in the same way that grammar both enhances and constrains the combinatorial potential of human language.

The architecture of mutualistic networks as an evolutionary spandrel.

In biology, it is often assumed that all traits are adapted for the purpose they are used for. However, some traits can also evolve for a purpose and end up carrying out another function, or just be by-products of other trait’s adaptation. Often these traits are called evolutionary spandrels, in an analogy to the spandrels found in cathedrals - beautifully decorated but originally meant to be just a support between the roofs and the bows. Now an article from an IBE team led by Ricard Solé and first-authored by Sergi Valverde suggests that networks of mutualistic species - like plants and animals - might actually represent evolutionary spandrels. In their work, IBE researchers could reproduce the structural patterns of mutualistic networks by a simple dynamical model with no selection-driven coevolution of traits, pointing at these patterns as evolutionary byproducts of the network generative process.

A new set of genetic tools to study the origins of multicellularity.

How animals emerged from their unicellular ancestor remains a major evolutionary question. We know that the unicellular ancestor of animals had an unexpectedly complex genetic repertoire, including many genes that are key to animal development and multicellularity, but these analyses are hampered by the lack of genetic tools. Now a team of IBE researchers, led by Iñaki Ruiz-Trillo, have developed the first set of genetic tools that will convert Capsaspora - one of the closest unicellular relatives of animals - into a unique model to investigate the origin and evolution of animal multicellularity.


Download article
Identified a regulatory mechanism conserved throughout insect evolution.

IBE Researchers led by Xavier Bellés, Maria Dolors Piulachs and José Luis Maestro have identified a highly conserved regulatory mechanism involved in many physiological functions as well as in the protection of cells against genetic threats. Proteins Argonaute 1 and 2 were known to be respectively responsible for microRNA and short interfering RNA mechanisms. However, this was demonstrated only in the fruit fly, Drosophila melanogaster, a most modified insect that emerged some 100 million years ago. Now the IBE teams have found that the same sorting specialization operates in the German cockroach, Blattella germanica, a much less modified insect that emerged some 200 million years before the fruit flies. The findings imply that the above specialization is evolutionary conserved, at least from cockroach to flies, and might stem from the last common ancestor of extant insects.

Chimpanzee genome reveals the footprints of natural selection.

One of the most surprising advances of biology is the possibility of finding in the genome the footprints of natural selection. Recently, IBE researchers led by Jaume Bertranpetit have analysed these traits in the four subspecies of chimpanzees. For that they applied many different positive selection tests to whole genome sequences and trained a machine learning algorithm with extensive computer simulations of different selective scenarios. Results showed shared signals of selection in all subspecies, particularly in genes associated with immunity and muscle function. However, the analysis also reflected the unique demographic and adaptive history of each subspecies, targeting genes associated with male reproduction and DNA repair. With these results, IBE researchers have created a complete genome browser that can be used as a community resource.

Population genetics

Rh- didn't give Basques an evolutionary advantage.

Within Europe, Basques are one of the few populations to stand out genetically. This was first pointed out already in the 1940s, when blood testing in Basque refugees from the Spanish Civil War showed that they had a world record for Rh-. Now IBE researchers led by David Comas set out to test whether this was due just to random effects amplified by the small population size of the Basques, or whether somehow Rh- gave Basques some selective advantage. The usual footprints that adaptation leaves in the genome were not found around the Rh gene in Basques, so the authors conclude that there isn't anything exceptional happening with Rh in the Basque Country.

Article: Flores-Bello A.; Mas-Ponte D.; Rosu M.E.; Bosch E.; Calafell F.; Comas D. 2018. Sequence diversity of the Rh blood group system in Basques. European Journal of Human Genetics. doi: 10.1038/s41431-018-0232-1
2018 in numbers

Staff

**128** TOTAL MEMBERS

- **6** ADMINISTRATION
- **122** SCIENTIFIC STAFF

**50,4% MEN**

**49,6% WOMEN**

**SCIENTIFIC STAFF**

by professional category

- **PRINCIPAL INVESTIGATORS**
- **POSTDOCTORAL RESEARCHERS**
- **PREDOCTORAL RESEARCHERS**
- **SUPPORT PERSONNEL**

- **INTERNATIONAL**

- **FOREIGN RESEARCHERS**

- 24% NATIONALITIES ARE REPRESENTED AT IBE

- 19
2018 in numbers

**Publications**
- **128 Publications**
- **59 Publications** led by IBE researchers
- **69 Collaborations**
- **88 Q1 Publications (SJR 2018)**

**Competitive and private funding**
- **51 National and International Research Projects**
- **18 International**
- **33 National**

**Competitive Funds of Ongoing Projects**
- **International**: 2.01 million €
- **National**: 1.24 million €

**New Competitive Funds Raised in 2018**
- **International**: 0.75 million €
- **National**: 1.93 million €

**Budget**
- **3.25 million €**
- **2.68 million €**
<table>
<thead>
<tr>
<th>Event Type</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>PhD Theses Defended</td>
<td>16</td>
</tr>
<tr>
<td>IBE Seminars</td>
<td>7</td>
</tr>
<tr>
<td>PhD Training Course</td>
<td>1</td>
</tr>
<tr>
<td>IBE PhD Symposium</td>
<td>1</td>
</tr>
<tr>
<td>10-Year Celebration Party</td>
<td>1</td>
</tr>
</tbody>
</table>
2018 Communication and Outreach

MEDIA RELATIONS

14 PRESS RELEASES

SOCIAL MEDIA

Twitter
1,940 Followers

Facebook
600 Followers

Linkedin
441 Followers

PUBLIC ENGAGEMENT & SCIENCE EDUCATION

30 PARTICIPATION IN ACTIVITIES

4,070 TARGET AUDIENCE REACHED

www.ibe.upf-csic.es/in-the-media

Highlights

Openday, Biojunior & Yomo

Byisc & Joves Ciència

Women in science 2018

Simposi d’herpetologia

Collaboration Ara newspaper

Science at Christmas
Research labs

1. Animal Biodiversity and Evolution
   - Butterfly Diversity and Evolution lab
   - Herbivore Beetle Evolution lab
   - Phylogeny and Phylogeography of Mammals lab
   - Systematics, Biogeography and Evolution of Reptiles lab
   - Water and Cave Beetle Evolution lab

2. Comparative and Computational Genomics
   - Evolutionary and Functional Genomics lab
   - Comparative Genomics lab
   - Paleogenomics lab

3. Complex Systems
   - Complex Systems lab
   - Evolution of Technology lab
   - Language Evolution lab

4. Functional Genomics and Evolution
   - Evolution and Developmental Biology lab
   - Evolution of Insect Metamorphosis lab
   - Evolution of the Eukaryote Genome lab
   - Insect Reproduction lab
   - Multicellgenome lab
   - Nutritional Signals in Insects lab

5. Population Genetics
   - Evolutionary Population Genetics lab
   - Evolutionary Systems Biology lab
   - Genomics of Individuality lab
   - Human Genome Diversity lab
Research labs

MEMBERS OF THE GROUP (Active in 2018)

Postdoctoral Researchers
Gerard Talavera, Markus Franzén

Predoctoral Researchers
Joan Carles Hinojosa

Research Technician
Mattia Menchetti

Laboratory Technicians
Cecília Corbella, Josep Lluís Roca

Undergraduate Student (Erasmus Mundus Programme)
Isaac Kay-Lavelle (Visitor)

HIGHLIGHTS OF 2018

During 2018 we contributed to several major collaborative breakthroughs, including: 1) the first phylogenomic analysis for butterflies, 2) demonstrating that ecological specialization drives diversification in Lycaenidae, 3) support for a time-dependent model of diapause regulation using transcriptomics, and 4) the discovery of inverted meiosis as a means to rescue fitness in chromosomal hybrids. In studies led by our lab we assessed the reintroduction of a species, showed that Vanessa cardui migrates in a round-trip across the Sahara, and that Holarctic ant species are fewer than thought.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

2018-2019: Código de barras de lepidópteros (Insecta: Lepidoptera) en el departamento de Arequipa y sur de Perú. Proyectos de investigación básica o aplicada en ingenierías y ciencias biomédicas. Principal investigator: A.L. Lazo. 250,000 Peruvian Soles

2018-2020: The longest butterfly migration: monitoring and conservation of the Painted Lady butterfly breeding sanctuaries in tropical Africa (WW1-300R-18). RFPs for
Long-Distance Animal Migration. National Geographic Society. Principal investigator: Gerard Talavera. $147,000

2018: Mediterranean butterflies meet the lions: An African monitoring network to study and preserve trans-Saharan migrations (WW1-300R-18). Barcelona Zoo Foundation Pric Grant Application. Principal investigator: Gerard Talavera. 8,000€


FIGURE CAPTION
Butterfly Diversity and Evolution Lab members have built an international monitoring network to study the seasonal movements of the migratory butterfly Vanessa cardui. The project is led by Gerard Talavera and funded by the National Geographic Society and the Barcelona Zoo Foundation.
Herbivore Beetle Evolution lab

MEMBERS OF THE GROUP (Active in 2018)
Postdoctoral Researcher
Federico A. Agrain
Laboratory Technician
Anabela Cardoso
Master Student
José M. Herranz Alzueta
Erasmus Undergraduate Student
Nefeli Zervou (Visitor)

HIGHLIGHTS OF 2018
This year has been one of transition between two projects of a very different nature. I moved from a species-level epidemiological study trying to link Wolbachia infections with the origins of unisexuality in North American Calligrapha, to a full-fledged phylogenetic study of an entire leaf beetle subfamily, the Eumolpinae, across the world, but with a special focus on the western Pacific. We have wrapped-up the results from the ending project in a number of studies that dissociate Wolbachia from unisexuality and started piling-up data for the Eumolpinae phylogeny, starting in New Zealand.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS
CGL2014-52937-P (Ministry of Economy): Do maternally inherited endosymbionts have a role in the origin and maintenance of unisexuality in Calligrapha (Coleoptera: Chrysomelidae)? 1 January 2015 to 30 June 2018. P.I.: Jesús Gómez-Zurita.

CGL2017-83324-P (Ministry of Economy): Molecular phylogeny of the Eumolpinae (Coleoptera: Chrysomelidae) and study of their evolution in the Western Pacific islands. 1 January 2018 to 31 December 2021.


FIGURE CAPTION
Sampling leaf beetles from the vegetation in New Zealand primary forest. Anabela and Jesús inspect the beating tray in Bushy Park (Kai Iwi, Whanganui). These samples hold the key to the relationships and the history of this isolated fauna with surrounding archipelagos.
ANIMAL BIODIVERSITY
AND EVOLUTION

Phylogeny and Phylogeography
of Mammals lab

PRINCIPAL INVESTIGATOR
José Castresana
CSIC Research Scientist

MEMBERS OF THE GROUP (Active in 2018)
Predoctoral Researcher
Alfonso Balmori
Research Technician
Lídia Escoda

HIGHLIGHTS OF 2018

Our main goal is the application of 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 studying the population structure, kinship relationships, and connectivity patterns in some species of great conservation importance, such as the Pyrenean desman. More recently, we have also studied the diet of this species (see figure) and compared its phylogeography with that of another Iberian endemism, the Cabrera water shrew.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: Secuenciación del genoma del desmán ibérico para su aplicación en estudios de evolución poblacional y conservación.
Funded by: Plan Nacional I+D+i del Ministerio de Economía, Industria y Competitividad
Reference: CGL2017-84799-P
PI: José Castresana
Date: January 2018 - December 2020

Title: Biodiversitat Animal i Evolució.
Funded by: Generalitat de Catalunya, Grups de Recerca (SGR)
Reference: 2017-SGR-991
PI: Salvador Carranza
Date: January 2018 - December 2019

FIGURE CAPTION

We are studying the diet of the Pyrenean desman using the excrements found in its natural habitat, small mountain rivers, and applying an NGS-based metabarcoding approach. Among the most abundant prey we found are species of Ephemeroptera, Diptera, Trichoptera, Coleoptera, Plecoptera, Neuropteraida, Annelida, and Crustacea. On average, 17 different prey species were identified per excrement (Hawlitschek et al. 2018).
ANIMAL BIODIVERSITY AND EVOLUTION

Systematics, Biogeography and Evolution of Reptiles lab

MEMBERS OF THE GROUP (Active in 2018)

Postdoctoral Researchers
Panagiotis Kornilios, Pedro Tarroso, Raquel Vasconcelos
Predoctoral Researchers
Héctor Tejero, Luis Machado
Research Technicians
Karin Tamar, Marc Simó
Laboratory Technician
Josep Lluís Roca Romeu
Master Students
Bernat Burriel, Carolina Molina, Pelagia Mitsi
Undergraduate Student
Laia Perez Sorribes

HIGHLIGHTS OF 2018

During this 2018, we have contributed to a better knowledge of the reptile diversity of the arid areas of Arabia, describing two new lacertid lizards endemic to southern Arabia and one gecko endemic to the Hajar Mountains from southeastern Arabia. Our work has shown that diversity in arid Arabia is much higher than what was previously thought, being the Hajar Mountains one of the top hotspots of reptile endemcity in the world. Besides describing diversity, we have also produced two comprehensive works on the diversity, distribution and conservation of the reptile species from Oman and Socotra Island.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: Animal Biology and Evolution.
Financed by: Generalitat de Catalunya (AGAUR) (2017SGR991)
Participants: Institute of Evolutionary Biology (CSIC-UPF).
Duration: 2017-2020
PI: Salvador Carranza

Title: An integrative approach to the conservation of the endangered Arabian populations of the gecko Teratoscincus keyserlingii.
Financed by: Mohammed bin Zayed Species Conservation Fund Project number: 172515524
Participants: Institute of Evolutionary Biology (CSIC-UPF), Department of Nature Conservation, Sharjah (United Arab Emirates)
Duration: May 2017 – October 2018
PI: Salvador Carranza

Title: Arabian reptiles as a model to investigate how biodiversity is generated and maintained in arid areas.
Financed by: Ministerio de Educación y Ciencia (CGL2015-70390-P)
Participants: Institute of Evolutionary Biology (CSIC-UPF), University of Barcelona; CIBIO, Centro de Investigación em Biodiversidade e Recursos Genéticos da Universidade do Porto; University of Granada; South African National Biodiversity Institute, South Africa.
Duration: 2016-2018
PI: Salvador Carranza

FIGURE CAPTION
Picture of Teratoscincus Keyserlingii (Keyserlingi’s wonder gecko) taken at Sharjah (United Arab Emirates), within the framework of Mohammed bin Zayed Species conservation project (www.speciesconservation.org/case-studies-projects/keyserlings-wonder-gecko/15524)
Research labs

ANIMAL BIODIVERSITY AND EVOLUTION

Water and Cave Beetle Evolution lab

MEMBERS OF THE GROUP (Active in 2018)

Predoctoral Researchers
Adrián Villastrigo, Pau Balart, Xiaozhu Luo (Visitor)
Laboratory Technician
Anabela Cardoso
Postgraduate Student
Alessandro Nardi (Visitor)

HIGHLIGHTS OF 2018

During 2018 we continued our research in the two main lines of the lab, (1) the evolution of habitat transitions in aquatic Coleoptera, with studies on the multiple origins of tolerance to salinity within a phylogenetic framework and (2) evolutionary convergence in cave beetles. In this line we studied from convergent biogeographic patterns in Western Mediterranean lineages of subterranean beetles to the evolution of the central nervous system in blind species, the latter in collaboration with the University of Jena (Germany).

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: Convergent evolution in subterranean Coleoptera. 
Financed by: MINECO 
Total Funding: 151,000€ 
PI: Ignacio Ribera

Title: Grup de recerca consolidate en Biodiversitat Animal y Evolució. 
Financed by: Generalitat de Catalunya 
Total Funding: 37,650,80€ 
PI: Ignacio Ribera

FIGURE CAPTION

Evolution of the central nervous system in subterranean beetles, as reconstructed with CT microscans. The reduction and final loss of eyes and optical lobes are clearly visible.
COMPARATIVE AND COMPUTATIONAL GENOMICS

Evolutionary and Functional Genomics lab

PRINCIPAL INVESTIGATOR
Josefa González
CSIC Tenured Scientist

MEMBERS OF THE GROUP (Active in 2018)
Postdoctoral Researchers
Gabriel Rech, Sara Guirao-Rico, Lain Guio, Judit Salces, Llewellyn Green
Predoctoral Researchers
Míriam Merenciano, Vivien Hórvath, María Bogaerts-Márquez
Research Technician
Carlos Vargas
Laboratory Technician
Laura Aguilera
Undergraduate Student
Marcela Celis
Visiting student
Marta Ruszkiewicz

HIGHLIGHTS OF 2018
We have contributed to the discovery of a new An. gambiae complex species. We have spearheaded the analysis of the most comprehensive European Drosophila melanogaster genomic dataset and described a new longitudinal pattern in genetic variation. Lab members have received multiple fellowships and awards, such as an EMBO fellowship. We have contributed to 12 conferences and seminars. We have communicated our research to the general public in several outreach events. We have expanded our citizen science project to new schools in Spain, and our science and society project to new interested parties.

2018 SELECTED PUBLICATIONS


Kapun, M; Barrón, MC; Staubach, F; Vieira, J; Obbard, D; et al. *Genomic analysis of European Drosophila populations reveals longitudinal structure and continent-wide selection*. bioRxiv

https://www.biorxiv.org/content/10.1101/313759v3

2018 FUNDED PROJECTS

Research Projects

2016-2020

2018-2020
2016-2018

Networking Projects

2018-2022
Building on scientific literacy in evolution towards scientifically responsible Europeans. Co-IP. Josefa González. COST Action (CA17127).

2018-2020
Red temática en genómica de la adaptación (CGL2017-90681-REDT), co-P.I. Josefa González. MINECO.

2016-2021
Drosophila population genomics network. ESEB Special Topic Network. ESEB.co-P.I.: Josefa González

2017-2019
Comparative Evolutionary Genomics (2017 SGR 880)
co-P.I: Josefa González. Generalitat de Catalunya.

Science Outreach Projects

2018
Ciència i convivència: compendre el nostre entorn per sobreviure en una societat canviant (185005SS-006). Ajuntament de Barcelona.

2018
Tracking the genetic footprints of malaria mosquitoes ESEB Outreach Initiative Funds.

2018
AdaptNation, the European Drosophila community (FCT-17-12810). FECYT

FIGURE CAPTION
Research at the Gonzalez Lab combines -omics approaches with mechanistic and functional analysis mainly in the model organism Drosophila melanogaster.
COMPARATIVE AND COMPUTATIONAL GENOMICS

Comparative Genomics lab

PRINCIPAL INVESTIGATOR
Tomàs Marquès-Bonet and Arcadi Navarro
ICREA Research Professors

MEMBERS OF THE GROUP (Active in 2018)

Postdoctoral Researchers
Borja Esteve, Raquel García, David Alejandro Juan, Martin Kuhlwilm, Esther Lizano, Carlos Morcillo, Joseph Orkin, Gerard Muntané (visiting)

Predoctoral Researchers
Laura Batlle, Antoni de Dios, Paula Esteller, Luis José Ferrandez, Clàudia Fontserè, Lukas Kuderna, Irene Lobón, Aitor Serres, Manuel Solís, Marina Brasó, Txema Heredia, Marco Telford, Xavier Farré, Jonas Niemann (visiting)

Research Technicians
Marina Álvarez, Marc de Manuel, Francesc Xavier Marcos, Sojung Han

Visiting Master Student
Irune Ruiz

Erasmus visiting Student
Ferriol Calvet

HIGHLIGHTS OF 2018

During 2018 our team got engaged into several exciting projects, including the generation of genome assemblies for 10,000 vertebrates or the performance of the largest phylogeny-based genome-phenome study ever carried out, in which we will focus on ageing and use approaches spearheaded by us (Muntané et al. 2018). Also, we became part of the Earth Biogenome Project. In order to achieve all these goals our group is investigating novel assembly methods and investigating novel methods to generate genome datasets from non-invasive samples (Hernandez et al. 2018).

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

HHMI International Award to Tomàs Marquès-Bonet

MICINN Plan Estatal 2017- BFU2017-86471-P.
Population genetics from non-invasive samples.

NIHMH U01. PAR-14-174. Somatic Mutations in Human Brain.

FIGURE CAPTION

Across evolution, organisms keep changing drastically in many important aspects. Here we illustrate variation in Maximum Lifespan and Medium Adult Weight of several mammal lineages. All this variation dwarfs what we can achieve in the lab through genetic manipulation.

The evolution of such huge phenotypic variation needs to be understood. High-quality genome assemblies will allow linking it to genome variation and will shed light upon some age-old mysteries such as the evolution of senescence.
Research labs

MEMBERS OF THE GROUP (Active in 2018)

Predoctoral Researchers
Manuel Ferrando-Bernal, Antonio de Dios
Research Technician
Pere Gelabert

HIGHLIGHTS OF 2018

We published at Nature the largest ancient human dataset to date that explores a distinctive archaeological European horizon, the so-called Bell Beaker complex. We have been able to demonstrate that the spread of this complex was not mediated by migration in first instance, but later on, in a reflux from Central Europe to the periphery of the continent, was driven by population replacements. We have also been involved in a paleogenomic study on the Icelandic first settlers, published at Science, where we have shown a differential contribution of people from Scandinavian and Celtic origin.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: The genomic prehistory of the Iberian Peninsula
Funded by: SPGC - Programa Nacional de Promoción General del Conocimiento, Ministerio de Economía y Competitividad
Reference: BFU2015-64699-P
PI: Carles Lalueza-Fox
Date: 2016-2018

FIGURE CAPTION

A typical Bell Beaker cup.
MEMBERS OF THE GROUP (Active in 2018)

Postdoctoral Researchers
Nuria Conde Puevo, Raúl Montañez Martínez

Predoctoral Researchers
Guim Aguadé Gorgorió, Àina Ollé Vila, Jordi Piñero Fernandez, Blai Vidiella Rocamora

Research Technician
Luis Francisco Seoane Iglesias

Master student (visiting)
Victor Maull Miquel, Jordi Pla

Postdoctoral Researchers (visiting)
Martí Sánchez, Josep Sardanyes Cayuela

HIGHLIGHTS OF 2018

The Complex Systems lab focuses on understanding the evolutionary origins of complex systems, using both mathematical models and experimental approaches based on synthetic biology. This lab has proposed and developed the concept of Major Synthetic Transitions as a framework for exploring the origins of innovation in evolution using a parallel approach, namely our potential for building or simulating synthetic systems that can recreate past evolutionary events. This includes the origin of protocells, multicellular systems, symbiosis, cognition and language. Another research area addresses Unstable Evolutionary Dynamics, namely the dynamics of biological systems (particularly RNA viruses and cancer) that exhibit a tendency towards high genetic instability as part of their adaptation potential. The Complex Systems lab also introduced the concept of «Terraforming» endangered or human-made ecosystems to avoid catastrophic shifts. The success of this proposal will require the development of a new synthesis involving multiple scales and conceptual frameworks, ranging from synthetic biology and cellular circuits to ecological communities. Finally, it also studies the evolution of artificial systems, in both silico ecosystems and technological networks, in its search for a true definition of evolutionary dynamics and technological phylogenies.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: Microbial deployment of new-to-nature chemistries for refactoring the barriers between living and non-living matter (MADONNA (H2020-FET))
Funded by: EU-H2020
Date: 2018-2021

Title: Hacia una física de las grandes transacciones evolutivas (FIS2015-67616)
Funded by: Instituto de salud Carlos III
Date: 2016-2018

Title: Cellular Computation
Funded by: Fundación Marcelino Botín
Date: 2015-2019

Title: Evolució de Sistemes Complexos (2017 SGR 00866).
Grup de recerca pre-consolidat reconegut i finançat Generalitat de Catalunya.
Funded by: AGAUR (2017 SGR 00866)
Date: 2017-2020
Network thinking has been present ever since the time of Charles Darwin. Nature is a complex web of interaction species, coevolving together in space and time. Many studies have pointed out the existence of universal network traits, but there is no general explanation for their origin. A common explanation is that modularity and nestedness must be evolutionary adaptations. Our study in Nature Ecology and Evolution suggests an alternative. Following the classic work of S. J. Gould and R. C. Lewontin, we refer to these structural patterns as spandrels. Although network features originate as side-effects of generative rules (tinkering), selection can still use them in important and interesting ways.

2018 SELECTED PUBLICATIONS

MEMBERS OF THE GROUP (Active in 2018)
Research Assistant
Meritxell Margen

HIGHLIGHTS OF 2018
Part of the work has focused on strategic planning of future AI research at the request of the European Community and the Spanish Government. Within the H2020 AI4EU project, we participated in launching a European Observatory for Ethical, legal, socio-economic and cultural issues in AI. Emilia Garcia Casademont successfully defended her thesis about the origins of phrase structure based on the hypothesis that phrase structure is not an accidental structural property of language, but rather an adaptation of language systems to cope with combinatorial explosions in semantic interpretation.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS
Title: Comprensión de Lenguaje Artificial en Robots
Funded by: Ministerio de Economía y competitividad (MINECO)
Date: 2015-2019

Title: Evolució de Sistemes Complexos (2017 SGR 00866), Grup de Recerca pre-consolidat reconegut i finançat per la Generalitat de Catalunya.
Funded by: AGAUR (Generalitat de Catalunya)
Date: 2017-2020
Our lab is interested in understanding when an immature organism decides to become adult, and how such transformation is controlled, using the metamorphic transition in insects as the experimental model. During 2018, our group: (1) has characterized the critical role of the “Metamorphic Gene Network”, formed by the E93, Kr-h1 and Br-C genes, in the evolution of neoteny in the strepsipteran Xenos vesparum; (2) has characterized how the timing of metamorphic transition is regulated in the red flour beetle Tribolium castaneum; and (3) how the metamorphic process is regulated in the tracheal system and the wings of the fruitfly Drosophila melanogaster.

2018 SELECTED PUBLICATIONS


Evolution of Insects
Metamorphosis lab

PRINCIPAL INVESTIGATOR
Xavier Bellés
CSIC Research Professor

HIGHLIGHTS OF 2018

Co-leadership of an international consortium to sequence the genome of a cockroach (Blattella germanica) and a termite (Cryptotermes secundus). The comparative analysis gave key information about the evolution of insect eusociality. In addition, we compared 11 transcriptomes from B. germanica and Drosophila melanogaster, which revealed regularities in the evolution of modern insects. The proteins Argonaute 1 and Argonaute 2 are associated to the microRNA and RNAi pathways in D. melanogaster. Our studies have shown that this is also the case in the more primitive species B. germanica.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: Key transitions in the embryogenesis of a hemimetabolic insect. Juvenile Hormone, transcription factors and microRNAs.
Funded by: MINECO (Ministry of Science, Spain).
Reference: BCCGL2015-64727-P.
PI: Xavier Bellés
Date: 2016-2019

Title: Functional Genomics and Evolution (Ajuts de suport a la recerca de Catalunya, SGR).
Funded by: Generalitat de Catalunya, General Direction of Research, AGAUR. Catalan Government
Reference: 2017-SGR 1030
PI: Xavier Bellés (Grant)
Date: 2017-2018

Title: Modifying plants to produce interfering RNA.
Funded by: EU, COST Action 2015. 2016-2019. PIs: 48 PIs from 24 countries
Reference: 2017-SGR 1030
COST countries (Bruno Mezzetti: General Coordinator; Xavier Belles: Delegate for the Management Committee).

Title: JSPS Bilateral Joint Research Pro.
Funded by: Japan Society for the Promotion of Science (JSPS).
PI: Takaaki Daimon (Japan), Xavier Belles (Spain).
Date: 2017-2019

FIGURE CAPTION

Gene expression during the ontogeny of two extreme neopterans, the cockroach Blattella germanica (polyneopteran, hemimetabolan and short germ-band species), and the fly Drosophila melanogaster (endopterygote, holometabolan and long germ-band species). Genes associated with metamorphosis are predominantly expressed in late nymphal stages in B. germanica and in early-mid embryo in D. melanogaster. In B. germanica the maternal to zygotic transition (MZT) concentrates early in embryogenesis, when juvenile hormone factors are significantly expressed. In D. melanogaster, the MZT extends throughout embryogenesis, during which juvenile hormone factors appear unimportant. These differences may reflect broad trends in the evolution of development within neopterans, related to the germ-band type and the metamorphosis mode.
Evolution of the Eukaryote Genome lab

PRINCIPAL INVESTIGATOR
Elena Casacuberta
CSIC Tenured Scientist

MEMBERS OF THE GROUP (Active in 2018)

Postdoctoral Researcher
Sebastian Najle

Predoctoral Researcher
Silvia Chafino Aixa

Research Technicians
Aleksandra Kozyczkowska, Adrià Chorro, Josefa Cruz

HIGHLIGHTS OF 2018

During 2018 there were two teams in my lab. 1) Developing genetic tools for unicellular organisms. We have advanced towards a better understanding of the genome of the unicellular eukaryotes C. limacisporum, A. whisleri and C. fragantissima while developing genetic tools such as transient and stable transfection. 2) We have published a manuscript on the role of the E93 gene, “the adult specifier” in the female neoteny of the insect X. vesparum. Silvia Chafino, a PhD student from this team, defended her PhD at the University Pompeu Fabra obtaining a qualification of Excellent Cum Laude.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS


FIGURE CAPTION

Abeoforma whisleri transfected with AwH2bVenus
FUNCTIONAL GENOMICS
AND EVOLUTION

Insect Reproduction lab

PRINCIPAL INVESTIGATOR
Maria-Dolors Piulachs
CSIC Research Scientist

MEMBERS OF THE GROUP (Active in 2018)
Research Technician
José Carlos Montañés
Laboratory Technician
Viviana Pagone
Master Students
Fleur Chelemen, Ariadna Pedraza, Natalia Llonga
Undergraduate Student
Oscar Paniello

HIGHLIGHTS OF 2018

I participate in the consortium that have sequenced the genome of a cockroach (*Blattella germanica*) and a termite (*Cryptotermes secundus*), doing a comparative analysis of genomes that provides key information about the evolution of insect eusociality. We also sequenced and identified, for the first time, the piRNA from a cockroach, studying its expression through the different developmental stages of *B. germanica*, and we did a comparative analysis against the piRNA from holometabolan insects showing the low level of conservation of these small non-coding RNAs between species. I was nominated as member of the ECE Praesidium.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

Title: RNAi "a la carta" para el control de cucarachas.
Funded by: MINECO (Ministry of Science, Spain).
Reference: CGL2016-76011-R.
P: M.D. Piulachs y J.L. Maestro
Date: 2016-2019
99,000€
Title: **Modifying plants to produce interfering RNA.**
Funded by: CA COSTaction CA15223
PI: Bruno Mezzetti. (MD Piulachs Delegate for the Spanish Management Committee)
Date: 2016-2020

Title: **Functional Genomics and Evolution (Ajuts de suport a la recerca de Catalunya, SGR).**
Funded by: Generalitat de Catalunya, General Direction of Research, AGAUR, Catalan Government.
Reference: 2017-SGR 1030
Coordinator: Xavier Bellés
Date: 2017-2018

**FIGURE CAPTION**

Follicular cells in a basal ovarian follicle from a 7-day-old adult female. Green: F-Actins stained with Phalloidin-TRITC. Red: DNA staining with DAPI.
FUNCTIONAL GENOMICS
AND EVOLUTION

Multicellgenome
lab

PRINCIPAL INVESTIGATOR
Iñaki Ruiz Trillo
ICREA Research Professor

MEMBERS OF THE GROUP (Active in 2018)
Postdoctoral Researchers
Sebastián R. Najle, Andrej Ondracka, Michelle Leger, Omaya Dudin, Dan Richter, David López, Xavier Grau
Predoctoral Researchers
Núria Ros, Alicia S. Arroyo, Eduard Ocaña, Alberto Pérez, Konstantina Mitsi, Helena Parra
Research Technicians
Aleksandra Kozyczkowska, Maria Ferrer
Laboratory Technician
Meritxell Antó
Master student
Alfonso Mendaña

HIGHLIGHTS OF 2018

We developed the first genetic tools in a close relative of animals, the filasterean Capsaspora owczarzaki. We also provided a better genome assembly of this organism. This will open future research avenues to address the origin of animals.

We found that animal-type microRNAs and the genes to produce them are not metazoan-specific as previously thought, being present in some unicellular relatives of animals.

We found that the quantity of exon skipping increases significantly in bilaterian animals, compared to other eukaryotes, and is associated to the creation of functional proteins.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

PREMETAZOA EVOLUTION. Unravelling the unicellular prehistory of metazoans by functional analyses and single-cell genomics (ERC-2012-Co, European Research Council)

Origin of Animals: Unravelling the nature of the last unicellular ancestor through a genomic, proteomic and functional approach. (BFU2017-90114-P, MINECO)
New Genetic Tools for Marine Protists (GBMF4973.01, Betty and Gordon Moore Foundation)

SINGEK. Promoting SINGle cell GEnomics to explore the ecology and evolution of hidden microeukaryotes. (H2020-MSCA-ITN-2015, European Comission)

FIGURE CAPTION
Confocal microscopy images of Capsaspora transfected cells.
**FUNCTIONAL GENOMICS AND EVOLUTION**

**Nutritional Signals in Insects lab**

**PRINCIPAL INVESTIGATOR**

José Luis Maestro  
CSIC Tenured Scientist

---

**MEMBERS OF THE GROUP (Active in 2018)**

- Research Technician  
  José Carlos Montañés  
- Laboratory Technician  
  Viviana Pagone  
- Graduate Student  
  Carlos Rojano

---

**HIGHLIGHTS OF 2018**

**Endocrinology of insect vitellogenesis**

We identified juvenile hormone acid methyltransferase as a key enzyme in juvenile hormone synthesis in *Blattella germanica*. In addition, we uncovered differential expression and compensatory transcriptional regulation between different insulin-like peptides.

**RNAi pathway**

In collaboration with other IBE groups we discovered that the activities of Argonaute-1 (Ago1) and Ago2 in the miRNA and siRNA pathways have been conserved at least from cockroaches to flies, and we demonstrated that Ago2 is responsible for degrading but not for selecting siRNAs.

---

**2018 SELECTED PUBLICATIONS**


---

**2018 FUNDED PROJECTS**

**Title:** RNAi “a la carta” para el control de cucarachas.  
**Funded by:** MINECO (Ministry of Science, Spain).  
**Reference:** CGL2016-76011-R  
**Date:** 2016-2019  
**99.000€**

**Title:** Ajuts de suport a la recerca de Catalunya.  
**Funded by:** AGAUR. 2017-2019.  
**Reference:** 2017-SGR 1030  
**PI:** Xavier Bellés  
**Date:** 2017-2019

---

**FIGURE CAPTION**

Immunolocalization of BgILP5 in the brain of an adult *B. germanica* female showing labeled insulin-producing cells (IPCs) in the pars intercerebralis and the three spatial axes. Lower right bottom corner corresponds to the front. The figure is produced by superimposing 50 images using the Zeiss Axiolmager Z1 microscope (Apotome) software.
### POPULATION GENETICS

**Evolutionary Population Genetics lab**

**Principal Investigator**

**Elena Bosch Fusté**

UPF Associate Professor

---

**Research labs**

**Members of the Group (Active in 2018)**

- Predoctoral Researchers
  - Ana Roca-Umbert, Barbara Sinigaglia, Rocio Caro
  - Predoctoral Researcher (visiting)
    - Alina Urnikyte

**Highlights of 2018**

Exploring adaptation to high altitude: We used genomic data and computational tools to infer demographic events and signatures of positive selection in Native American populations, including two Andean groups.

Exploring adaptation to zinc deficiency: We analysed signatures of classical selective sweeps and polygenic selection in the 24 zinc transporter genes known in humans including populations living in zinc deficient areas.

Inferring adaptive phenotypes: We generated a knock-in mouse for a putative adaptive non-synonymous variant in the Andamanese, which is currently under further analysis.

**2018 Selected Publications**


**2018 Funded Projects**


**Figure Caption**

Signals of recent selection in the Yanomay (lowland) and Aymara (highland) Peruvian populations.
Research labs

MEMBERS OF THE GROUP (Active in 2018)
- Postdoctoral Researchers
  - Hafid Laayouni, Sandra Acosta, Begona Dobon
- Predoctoral Researchers
  - Jessica Nye, Sandra Walsh, Pablo Villegas
- Research Technician
  - Elisabeth Gabriela Agüileta

HIGHLIGHTS OF 2018

- Docteur Honoris Causa de l’Université Toulouse III Paul Sabatier. Received in 2018.
- Invited Keynote Speaker at the Barcelona VPH (Virtual Physiological Human) Summer School 2018. Digging into the information of the diversity of the human genome: from the reconstruction of human origins to the adaptation to the environment. 22nd June 2018.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS

- 2018 Maria de Maeztu. Project for the sequencing of the metagenome. Amount granted: 20,000€. PI J. Bertranpetit and R. Maldonado.
HIGHLIGHTS OF 2018

In 2018, we discovered that the human population of Eivissa (but not Majorca or Minorca) is as much genetic outlier as Basques are. By comparing genomewide SNP array data of living Eivissans with ancient DNA of Phoenician necropolises in the island, we could rule out that the Phoenician settlement of Eivissa caused this genetic differentiation. Instead, long runs of homozygosity in islanders pointed to genetic drift and population bottlenecks as the cause of this genetic distinctness.

2018 SELECTED PUBLICATIONS


Our group is focused on the analysis of the human genome 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. In this sense, during 2018 we have detected a founder mutation in Roma that causes a severe myopathy and we have addressed the migration patterns in North Africans using mtDNA. Finally, we have dissected at DNA level the RhD system in Basques, which has been a hallmark of their singularity.

2018 SELECTED PUBLICATIONS


2018 FUNDED PROJECTS


FIGURE CAPTION

A large crowd.