Biennial Report 2022_2023

INSTITUT de BIOLOGIA EVOLUTIVA
CSIC
upf.

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 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.

Founded 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 120 people and 25 research groups distributed in 5 scientific programs on Evolutionary Biology research.

Highlights

Sustainable science for an evolving planet

The IBE community is deeply engaged in the construction of the new IBE headquarters, scheduled for completion in 2026. This sustainable building, located nearby Barcelona's Ciutadella, will feature state-of-the-art facilities designed to support research across all dimensions of evolution.

3.500 m²	350	35
Usable projected area	People	Research groups

The new IBE building will be part of the **Antic Mercat del Peix complex**, focused on research and innovation in **precision medicine, biodiversity, and planetary well-being** and promoted by Pompeu Fabra University (UPF), the Barcelona Institute of Science and Technology (BIST), and the Institute of Evolutionary Biology (IBE, CSIC-UPF).

This scientific hub, which is part of the **Ciutadella del Coneixement**, will host **1,400 researchers**. It is expected to be operational by 2026 and will become a key component of the existing biomedical cluster along Barcelona's waterfront. All members involved in this transformative project are working to achieve the Leadership in Energy and Environmental Design (LEED) platinum **certification to sustainability**.

Render of the future IBE building.
Credit: ZFG Arquitects, MIRAG and Double Twist.

IBE crew, including director Salvador Carranza and deputy director Elena Bosch engaged with architects in the building design. Credit: Roser Marquez

Highlights

A growing and diverse community

The IBE aims to unite top international talent in the field of evolution through a collaborative and interdisciplinary approach. As part of its commitment, the IBE strives to foster a diverse community, where respect and integrity are the cornerstones of scientific progress.

In 2022-2023, the IBE welcomed two new principal researchers: **Tábita Hünemeier**, who leads the Human Population Genomics Lab, and **Òscar Lao**, the principal investigator of the Algorithms for Population Genomics Lab.

Oscar Lao
Credit: Pilar Rodríguez

Tábita Hünemeier
Credit: Pilar Rodríguez

Highlights

Working for biodiversity with social commitment

At the IBE, we address global biodiversity challenges by leading research with **evolutionary perspective**. Our work spans across genomics and big data to archaeology and field research, all aimed at unraveling the evolutionary mechanisms that generate biodiversity and promoting its conservation.

We put evolutionary science at the service of biodiversity for the future of our planet.

During 2022-2023, members of the IBE participated global genomics networks in conservation and adaptation, such as **ERGA**, **BIOSCAN**, the **Vertebrate Genome Project**, **DrosEU**, and the **Catalan Biogenome Project**. Our scientific personnel ha-ve been involved in world wide field work campaigns, from Papua New Guinea in the Pacific, to the Saudi Arabia desert, involving over **188 days of field work and 43 campaigns** during this period.

***Rosa Fernandez**, appointed as the Scientific Officer of the executive board at the ERGA consortium, hosted the first All Hands Biodiversity Genomics Europe (BGE) international meeting at the IBE headquarters. Credit: Pilar Rodríguez*

*IBE researchers of the Biology and Ecology of Abundant Protists Lab led by **Daniel Richter**, collecting water samples during a fieldwork campaign in the Caribbean Sea. Credit: Daniel J. Richter*

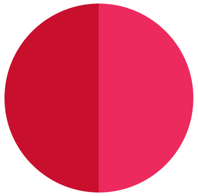
*IBE researcher of the Systematics, Biogeography and Evolution of Reptiles and Amphibians Lab led by **Salvador Carranza** exploring the Arabian desert in the United Arab Emirates. Credit: Bernat Burriel*

Meet our community

120

Total members

60 Women 50%



60 Men 50%

17% Foreign researchers

13 Nationalities

Data from 2023

	Total	Women	Men
Principal investigators	25	5	20
Postdoctoral researchers	15	7	8
Predoctoral researchers	37	16	21
Technical personnel	33	24	9
Admin & general services	10	8	2

Meet our community

A new generation of evolutionary biologists

In 2022-2023, IBE has continued to attract exceptionally talented scientists dedicated to exploring evolution from diverse perspectives. The remarkable achievements of IBE researchers have been recognized through numerous prestigious awards and honors from esteemed international organizations.

Notably, during this period, IBE reached a milestone of 4 ICREA researchers among its team and maintained 4 active ERC grants, highlighting the institute's commitment to high quality and innovation in evolutionary studies.

***Rosa Fernandez**, IBE Principal Investigator of the Metazoa Phylogenomics Lab, was awarded a prestigious Human Frontier Science Program (HFSP) Research Grant. Credit: Pilar Rodriguez*

***Carles Lalueza-Fox**, IBE Principal Investigator of the Paleogenomics Lab, wins the international prize "Fabio Frassetto". Credit: Carles Lalueza*

Scientific Highlights

In 2022-2023, the Institute of Evolutionary Biology (IBE) has reaffirmed its position as a leader in evolutionary research, making significant contributions to understanding the mechanisms that generate and sustain biodiversity.

Through groundbreaking publications, IBE has advanced knowledge in areas such as genomics, ancient DNA analysis, and population dynamics, offering new insights into species evolution and conservation. By harnessing the strength of global research networks, we have delved deeper into the complex interactions that drive evolutionary processes, laying the foundation for innovative approaches to addressing biodiversity loss and fostering planetary well-being.

211
Publications

→

54%
Led by IBE researchers

74%
Q1 Publications

Scientific Highlights

Biodiversity

Beetles’ genomic adaptations preceded cave entry

An international study led by IBE’s **Rosa Fernández** uncovers how subterranean beetles underwent significant genomic changes 6 to 30 million years before their cave adaptation. The findings reveal that gene gain, rather than loss, was crucial for adapting to subterranean life. The study also identifies both parallel and convergent evolution as key evolutionary processes, offering insights into the adaptation mechanisms of subterranean species.

Balart-García P., Aristide L., Bradford TM., Beasley-Hall P.G., Polak S., Cooper S.J.B., Fernández R. (2023). Parallel and convergent genomic changes underlie independent subterranean colonization across beetles. Nat Commun 14:3842. https://doi.org/10.1038/s41467-023-39603-1

Figure caption: Astagobius angustatus.
Credit to Tin Rožman.

The red fire ant is now established in Europe and could reach the UK

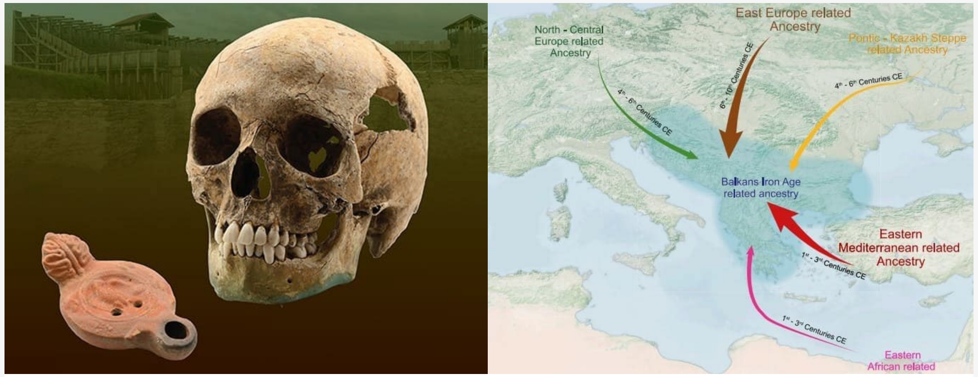
An international study led by **Roger Vila** at the IBE and published in Current Biology found 88 red fire ant colonies in Sicily, Italy. The research indicates that half of Europe's urban areas, including Barcelona, London, and Madrid, are suitable for this invasive species. Climate change may further expand its potential range for invasion.

Menchetti M., Schifani E., Alicata A., Cardador L., Sbrega E., Toro-Delgado E., Vila R. (2023). The fire ant *Solenopsis invicta* is established in Europe. Current Biology 33: R896-R897. https://doi.org/10.1016/j.cub.2023.07.036

Figure caption: Red fire ant.
Credit to Jesse Rorabaugh, public domain.

Scientific Highlights

Comparative and computational genomics



Ancient Balkan genomes trace the rise and fall of Roman Empire's frontier, reveal Slavic migrations to southeastern Europe

A multidisciplinary study co-led by IBE researcher **Carles Lalueza-Fox** reconstructs the genomic history of the Balkans during the first millennium CE. Analysis of 146 ancient genomes reveals significant Anatolian ancestry during Roman control and extensive Slavic migrations after Rome's fall. Published in Cell, the research shows these movements shaped the modern genetic landscape of the Balkans, transcending modern national boundaries.

Olalde I., Carrión P., Mikić I., (...), Lalueza-Fox C., Reich D. A genetic history of the Balkans from Roman frontier to Slavic migrations. (2023) Cell; 186(25):5472-5485.e9. 10.1016/j.cell.2023.10.018

Figure caption: On the left: Skull of an individual of East African ancestral origin discovered in Viminacium, with the oil lamp featuring an eagle found in his tomb. Credit: Miodrag Grbic. On the right: Geographic location where the individuals analyzed in this study were excavated and the different ancestry influences detected in different periods. Credit: Iñigo Olalde & Pablo Carrión.

Primates' DNA highlights applications for human health

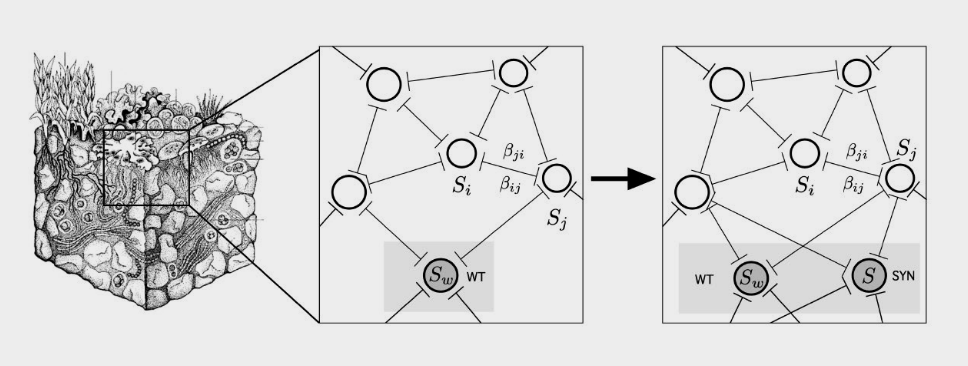
The genomes of 233 primate species provide key insights into primate evolution, human disease, and biodiversity conservation. Co-led by **Tomàs Marquès-Bonet** and participated by **Arcadi Navarro** at the IBE, this research is part of a *Science* Special Issue, featuring 3 led articles and 2 co-authored pieces. It presents the most comprehensive catalogue of primate genomic information to date and identifies a widespread recurrence of missense mutations once thought to be unique to humans, opening new avenues for future primate and human genomic research.

Kuderna L. F. K., (...), Marques-Bonet T. (2023) A global catalog of whole-genome diversity from 233 primate species. Science 380, 906-913. 10.1126/science.abn7829

Figure caption: White-fronted capuchin (Cebus unicolor) near Manaus, Brazil. Credit: Rebecca Still.

Scientific Highlights

Complex systems

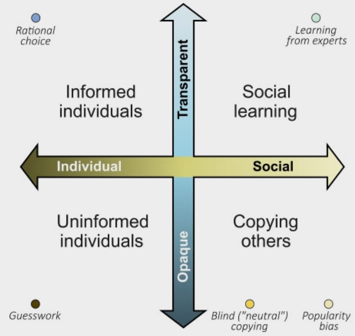


A model of ecological outcomes for introducing bioengineered species

A study led by IBE researcher **Ricard Solé** explores the effects of introducing engineered synthetic species into the environment, a promising approach to aid biodiversity and prevent mass extinction. By modelling a community's response to an engineered strain, the study reveals that species diversity acts as an ecological barrier limiting the spread of the introduced organism.

Maull V., Solé R. (2022). Network-level containment of single-species bioengineering. Philosophical Transactions of the Royal Society B: Biological Sciences, 377 (1853), 20210396. https://doi.org/10.1098/rstb.2021.0396

Figure caption: Representation of single-species engineering from a wild type present within a resident community in dryland's soil. Credit to Ricard Solé.



Imitation and access to information determine the evolution of society

IBE researcher **Sergi Valverde**, in collaboration with **Blai Vidiella** and **Salva Duran-Nebreda**, has proposed a new cultural evolution model that, for the first time, explains cultural leaps using the conceptual framework of punctuated evolution. In a series of empirical and theoretical studies, they demonstrate how the pace and nature of cultural innovation has been influenced by an interplay of imitation, access to information and population growth. In addition to explaining the historical adoption of new technologies, this model may also be used to predict future innovations.

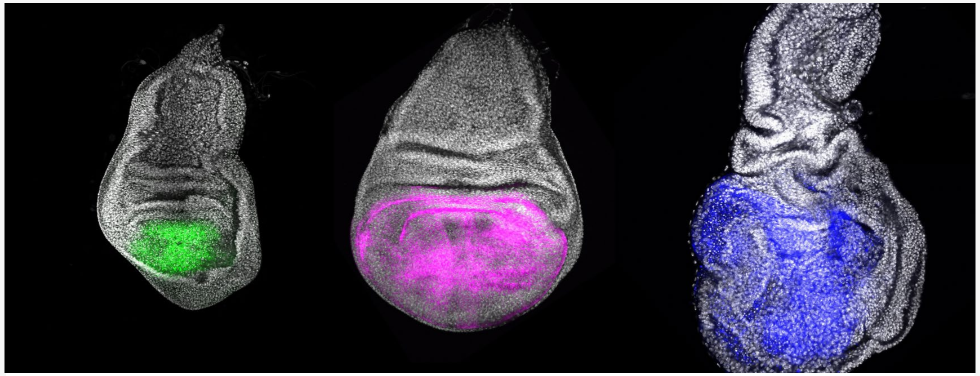
Vidiella B., Carrignon S., Bentley R. A., O'Brien M. J., Valverde S. (2022). A cultural evolutionary theory that explains both gradual and punctuated change. Journal of the Royal Society Interface, 19 (196), 20220570. https://doi.org/10.1098/rsif.2022.0570

Duran-Nebreda S., Bentley R.A., O'Brien M., Valverde S. (2022). Dilution of expertise in the rise and fall of collective innovation. Humanities and Social Sciences Communications, 9 (365). https://www.nature.com/articles/s41599-022-01380-5

Figure caption: The morphospace of cultural and technological evolution can be parametrized by different degrees of imitation and rationality, predicting a wide range of observed behaviours, from gradual ("rational choice") to neutral ("blind copying") to punctuated change ("learning from experts"). Credit to Blai Vidiella.

Scientific Highlights

Functional genomics and evolution

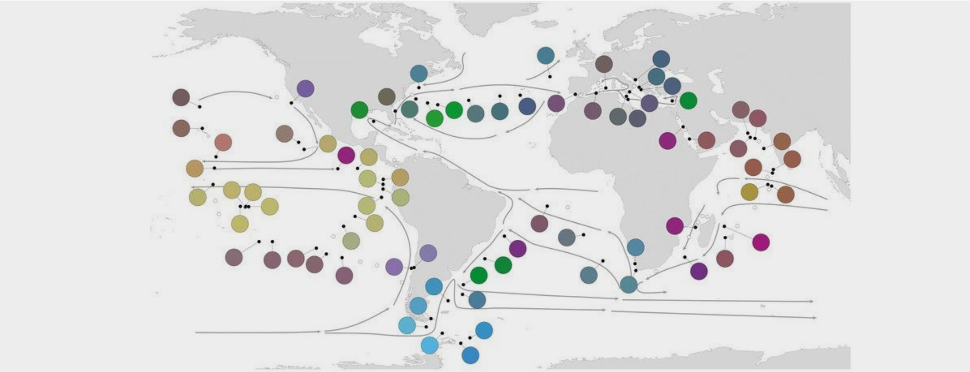


Chinmo, "the youth gene"

The study published in eLife and co-led by IBE researchers **Xavier Franch** and **David Martin**, has revealed that the Chinmo gene, responsible for the juvenile stage in insects, is present in mammals and could play a key role in cancerous processes. The research confirms that the Br-C and E93 genes regulate insect maturity, with roles analogous to promoters and suppressors of cancer in humans. These findings highlight the conserved nature of these genes across evolution and their potential role in the evolution of metamorphosis.

Chafino S., Giannios P., Casanova J., Martin D., Franch-Marro X. (2023). Antagonistic role of the BTB-zinc finger transcription factors chinmo and broad-complex in the juvenile/pupal transition and in growth control. eLife, 12, Article e84648. https://doi.org/10.7554/eLife.84648

Figure caption: Adult wing precursor imaginal cells of Drosophila melanogaster. The absence of Chinmo in the imaginal cells suppresses the growth of the wing (left) compared to the control wing (center), and overexpression of Chinmo leads to overgrowth (right). Credit to Panagiotis Giannios.



Plankton biogeography shaped by ocean currents

A study co-first authored by IBE researcher **Daniel J. Richter** reveals that ocean currents heavily influence global plankton distribution. Analysing metagenomic data from the Tara Oceans expedition, researchers found that plankton communities form distinct biogeographical provinces aligned with ocean current systems. This study shows that plankton diversity patterns are strongly linked to the movement of water over timescales of up to 1.5 years, offering new insights into marine ecosystem dynamics.

Richter D. J., Watteaux R., Vannier T., Leconte J., Frémont P., Reygondeau G., Maillet N., Henry N., Benoit G., Da Silva O., Delmont T. O., Fernàndez-Guerra A., Suweis S., Narci R., Berney C., Eveillard D., Gavory F., Guidi L., Labadie K., ... Jaillon O. (2022). Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems. eLife, 11, Article e78129. https://doi.org/10.7554/eLife.78129

Figure caption: Plankton biogeography, environmental variation, and ocean transport among Tara Oceans stations. Credit to Daniel Richter. CC BY 4.0.

Scientific Highlights

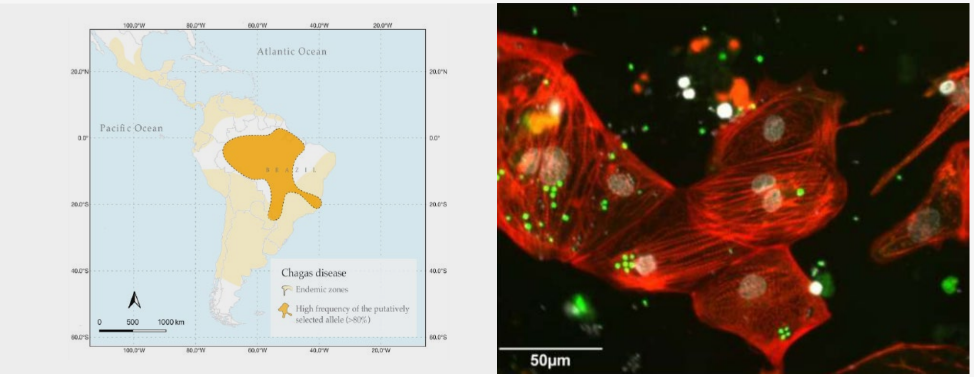
Populations genetics

Revealing the genetic adaptations of the populations of Peru

IBE researcher **Elena Bosch** co-led international research on the genetic adaptations of populations on the Pacific desert coast, the Andes Mountains range, and the Amazon rainforest of Peru. The study found evidence of genetic adaptation to the extreme altitude, climate, and the pathogens that coexist in the three ecological regions.

Caro-Consuegra R., Nieves-Colón M. A., Rawls E., Rubin-de-Celis V., Lizárraga B., Vidaurre T., Sandoval K., Fejerman L., Stone A. C., Moreno-Estrada A., Bosch E. (2022). Uncovering signals of positive selection in Peruvian populations from three ecological regions. Molecular Biology and Evolution, 39 (8), Article msac 158. https://doi.org/10.1093/molbev/msac158

Figure caption: Image composite of various ecological regions found across Peru. Left: image by LBM1948 with licence CC BY-SA 4.0 via Wikimedia Commons; Center: image by Bere von Awstburg with licence CC0 via Wikimedia Commons; Right: image by Jason Hollinger with licence CC BY 2.0 via Wikimedia Commons.



Genetic adaptations help Amazonian populations resist Chagas infection

An international study led by IBE principal investigator **Tábita Hünemeier** and participated by **David Comas** identified a *PPP3CA* gene variant that reduces Chagas infection risk in Amazonian populations. Functional studies showed the gene variant lowers parasite internalization in heart cells, suggesting natural selection for this resistance began 7,500 years ago. The research also uncovered genetic adaptations linked to cardiovascular, metabolic, and behavioral traits.

Couto-Silva, C. M., Nunes, K., Venturini, G., Araújo Castro E Silva, M., Pereira, L. V., Comas, D., Pereira, A., & Hünemeier, T. (2023). Indigenous people from Amazon show genetic signatures of pathogen-driven selection. Science Advances, 9 (10), Article eabo0234. https://doi.org/10.1126/sciadv.abo0234

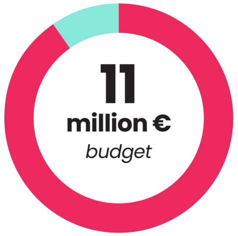
Figure caption: On the left: Frequency map of the PPP3CA gene variant. On the right: Heart cells during functional assays. Images provided by the authors and originally published in Science Advances. Distributed under the Creative Commons Attribution-NonCommercial 4.0 License (CC BY-NC).

Funding and projects

New external funds raised in 2022-2023

During 2022-2023, the IBE successfully acquired funding for a broad range of innovative projects, secured via competitive and non-competitive grants from a variety of public and private organizations.

External funding raised in 2022-2023



IBE researcher of the Microbial Ecology and Evolution Lab led by ***Javier del Campo***, feeding anemones.
Credit: Roser Marquez.

IBE researcher Valéria Marques of the Butterfly Diversity and Evolution Lab led by ***Roger Vila***, on a field campaign to Madeira exploring its butterfly biodiversity.
Credit: Roger Vila

Scientific life

Building a Strong Community at IBE

Fostering an engaged community lies at the heart of IBE's vision. In 2022-2023, numerous activities were organized to enrich scientific life and encourage meaningful connections within our community.

One highlight was the **biannual Retreat**, where IBE personnel spent two days off-site, engaging in stimulating presentations, thought-provoking discussions, and lively social gatherings with colleagues.

14

PhD
Theses defended

16

Undergraduated and
master students trained

4

International

12

National

Over the past two years, we also hosted **8 seminars**, **2 PhD Symposia**, and an **Evolution Course for PhD students**, all of which contributed to the academic growth and development of our members. Additionally, every fortnight, the community was invited to an informal break, creating opportunities for casual interactions and strengthening the social life of the center.

Our committees have also continued to make a significant impact on community life, each offering unique perspectives and valuable initiatives. A comprehensive record of their work can be accessed here.

These efforts collectively reflect IBE's unwavering dedication to cultivating collaboration and innovation within the community.

8
IBE Seminars

2
PhD Symposia

1
Evolution Course
for PhD students

1
Retreat

Communications & outreach

Data represents the summary of data corresponding to 2022 and 2023.

In 2022-2023, our research significantly boosted its media presence, earning recognition from specialist journals, mainstream media, and digital platforms, thereby underscoring our global impact. Additionally, our social media audience grew by 35% across platforms during this period.

Through our Public Engagement Program, we reached a **target audience of 48,466**, engaging 2990 participants in outreach activities, and broadcasting content across our channels, garnering over **39,900 views**.

We are proud to highlight that more than **45 IBE community members** actively contributed to this program, participating in **85 activities**, either with IBE leading or being a contributor.

56
News published
on IBE website

33
Press releases

222,874
Web page views

Press highlights

EL PERIÓDICO

Cómo una mutación genética protege de una infección a las poblaciones del Amazonas.
A study led by IBE researcher Tábita Hünemeier uncovers a key that could explain why some people are less susceptible to contracting Chagas disease.

RTVE

El mayor catálogo de ADN de primates de la historia abre las puertas de la genética y la salud humana.
IBE researcher Tomàs Marquès-Bonet takes part in the genome sequencing of over 800 individuals from 233 ape species around the world. This massive database will serve to predict to which extent a mutation is involved in an illness.

CNN WORLD

We knew this day would come': One of world's most invasive species reaches Europe.
A study led by IBE has confirmed the establishment of the invasive red fire ant in Europe, with numerous colonies found in Sicily. Likely originating from China or the U.S., the species could spread to urban areas across Europe, posing significant ecological and economic challenges.

LA VANGUARDIA

Una mariposa extinguida por la humanidad podría renacer tras secuenciarse su genoma.
Researchers from IBE and MCNB have successfully sequenced the complete genome of the Xerces blue butterfly, the first insect known to go extinct in historical times. This marks the first retrieval of an extinct insect's genome, potentially enabling its future de-extinction. The findings may also help assess the conservation status of current insect species.

ABC

El ADN de un hombre de hace 23.000 años sugiere que la península ibérica fue un refugio aislado en la Edad de Hielo.
Two international research teams, including researchers from IBE, analyzed ancient DNA from over 100 Eurasian hunter-gatherers. Their findings reveal that the Iberian Peninsula served as a climatic refuge during the Last Glacial Maximum of the Ice Age, contributing to the genetic continuity of European populations sustained by these Paleolithic survivors.

EL PERIÓDICO

¿Cómo ayudan unos genetistas de BCN a identificar víctimas en El Salvador?
Researchers from IBE, the Genomics Service at UPF and partner organizations have developed the first high-resolution genetic database in Central America. By analyzing genetic variation in 248 men and 143 women from El Salvador, the database provides a crucial tool for identifying victims of the civil war and emigrants who perish annually while attempting to cross the Mexico-US border.

Social Media

data 2023

7,196 → **+34%**

Followers on Social Media

Increase since 2021

Public engagement & science education

2022-2023

48,466
Target audience reached

2,990
Participants in outreach activities

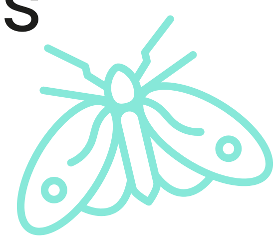
39,900
Views of content across all IBE channels

Ancient DNA
A window into our past.
An illustrated documentary

We were there too
Campaign for the International Day of Women an Girls in Science

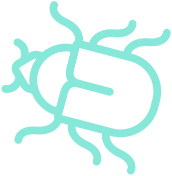
Setmana de la Ciència
IBE Open Doors

Research labs



Biodiversity

Butterfly Diversity and Evolution lab
Metazoa Phylogenomics lab
Microbial Ecology and Evolution
Phylogeny and Phylogeography of Mammals lab
Systematics, Biogeography and Evolution of Reptiles and Amphibians lab

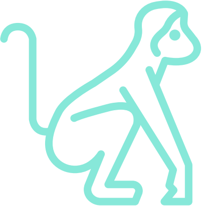


Comparative and Computational Genomics

Comparative Genomics lab
Evolutionary and Functional Genomics lab
Evolutionary Genomics lab
Paleogenomics lab

Complex Systems

Complex Systems lab
Evolution of Networks lab
Language Evolution lab

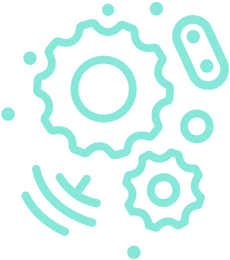


Functional Genomics and Evolution

Biology and Ecology of Abundant Protists lab
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

Population Genetics

Algorithms for Population Genomics
Evolutionary Population Genetics lab
Evolutionary Systems Biology lab
Genomics of Individuality lab
Human Genome Diversity lab



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