

Becas de introducción a la investigación para estudiantes universitario JAE INTRO CSIC 2024

Descripción: Becas de introducción a la investigación para personas estudiantes universitarias con alto nivel de rendimiento académico. Las becas se conceden en régimen de concurrencia competitiva y de acuerdo con los principios de transparencia, objetividad y publicidad.

El plan de formación derivado de la concesión de estas becas se desarrollará en los grupos de investigación de las EI del CSIC, enmarcados en las 3 áreas globales del CSIC (Vida, Sociedad y Materia). Se posibilitará que dicho plan de formación esté orientado al posterior desarrollo de la tesis doctoral en el CSIC.

ACCESO CONVOCATORIA: <https://sede.csic.gob.es/intro2024>

PLAZO PRESENTACIÓN SOLICITUDES: del 20 de abril al 20 de mayo

Oferta de becas Jae intro 2024 Instituto de biología evolutiva: <https://www.ibe.upf-csic.es/>

| REFERENCIA | INVESTIGADOR | CORREO ELECTRONICO | INSTITUTO | TITULO PROGRAMA FORMATIVO | MEMORIA PROGRAMA FORMATIVO | WEB |
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| JAEINT24_EX_1601 | CAMPO GARCIA-RAMOS, JAVIER DEL | idelcampo@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | El proteoma oculto del holobionte coralino | En el del Campo Lab estudiamos la ecología y evolución de la microbiota simbiote de organismos marinos con un foco particular en corales, pero no exclusivamente. En el marco del programa JAE intro queremos ofrecer la oportunidad a los participantes de iniciarse en el estudio de la simbiosis y de la importancia que tiene esta para la conservación, en especial en el contexto actual de cambio climático. Introduciremos al alumno/a a los fundamentos teóricos del campo: diversidad de corales, principales simbiotes de corales, el impacto de la simbiosis en la susceptibilidad o resistencia de los corales al cambio climático, patógenos y probióticos microbianos de corales. Presentaremos al alumno/a las principales metodologías para el estudio de los simbiotes de corales: cultivo microbiano, métodos de extracción de ácidos nucleicos, procesamiento de ácidos nucleicos y análisis computacionales para llevar a cabo estudios de microbioma, metagenómica, transcriptómica, genómica, filogenómica, etc. En el marco de la JAE intro el alumno/a llevará a cabo un proyecto en que analizará datos de genómicos de corales y de sus simbiotes para poner en práctica los conocimientos adquiridos y para desarrollar sus habilidades como investigador/a. Durante su proyecto el alumno/a llevará a cabo de primera mano análisis de datos de proteomas de corales y simbiotes utilizando modelos de procesamiento de lenguaje natural con el objetivo de | delcampolab.com |

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| | | | | | <p>revelar el “dark proteome” del holobionte coralino, revelando así nuevas funciones que hasta ahora han pasado desapercibidas mediante análisis tradicionales.</p> <p>En paralelo, el alumno/a hará una rotación de una semana con cada uno de los miembros senior del laboratorio (2 en total) para ver como llevan a cabo otro tipo de proyectos que van desde la transcriptómica de células individuales de corales bajo estrés térmico a la hibridación fluorescente <i>in-situ</i> de bacterias patógenas en corales. La intención de esta rotación es que el alumno/a tenga una experiencia tan amplia como sea posible de la investigación que llevamos a cabo. El alumno participará activamente de la vida del laboratorio, participando de los lab meetings semanales y de los journal clubs quincenales, así como cualquier otra actividad que el laboratorio lleve a cabo.</p> | |
| JAEINT24_EX_0341 | CARRANZA GIL-DOLZ DEL CASTELLAR, SALVADOR | salvador.carranza@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | <p>Unleashing the secrets of Iberian snakes: exploring their venom evolution through multi-omics</p> | <p>Snake venom is a biological mixture of compounds with numerous purposes, including hunting and self-defense. The composition of this "biochemical weapon system" shows high complexity and diversity, resulting in a variable biochemical and toxicological profile that determines the pathological response. This response spans from local and systematic complications to neurotoxic reactions and poses such a threat that the World Health Organization (WHO) listed snakebites as a priority Neglected Tropical Disease in 2017. The effects produced after envenomation are very species specific, with great intra- and interspecific variability in the genes related to venom synthesis located in the venom gland. Therefore, it is crucial to understand their systematics and phylogeny to continue toxicological research and improve snakebite treatment. Antivenoms may lack effectiveness or even be dangerous for the patient when applied to the wrong species' envenomation. Additionally, due to their diverse evolutionary history and consequent variability, venomous animals are fascinating models for understanding fundamental processes, including gene duplication, convergent evolution, genotype-phenotype mapping, and cell and tissue development.</p> <p>Moreover, the bioactivities of many toxins make them promising leads for the discovery of new human therapeutics. Although snake venom gene evolution has been studied intensively over the past several decades, most previous studies have lacked the context of complete snake genomes and the full context of gene expression across diverse snake tissues. This has led to conclusions that are now under question, such as the legitimacy of the Toxicofera clade. Instead, the use of high-quality genomes of venomous snakes, combined with transcriptomic and proteomic data, will enable the generation of a comprehensive catalog of venom-gland-specific toxin genes—the so-called "venom-ome-specific toxins." These genes show venom-gland-specific expression and therefore most probably encode the minimal core venom effector proteins. The overall aim of this thesis is to produce and compare high-</p> | https://www.ibe.upf-csic.es/biodiversity |

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| | | | | | quality genomes, transcriptomic, and proteomic data for all snake genera present in the Iberian Peninsula and for all venomous snake species native to this territory. By doing this, it aspires to generate a comprehensive catalog of "venom-ome-specific toxins," an invaluable resource to shed light on the evolution of snake toxic arsenals. | |
| JAEINT24_EX_1296 | CASACUBERTA SUÑER, MARIA ELENA | elena.casacuberta@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | Unraveling the origin of animals | <p>Ever wonder how animals went from single-celled organisms to amazing multicellular creatures? We, at the MultiCellGenome lab, are diving deep into the secret lives of the closest unicellular relatives to animals. We work with four groups of unicellular organisms that could be the next big stars in cell biology and evolutionary research! We use a multidisciplinary approach to understand how both genes and cellular processes changed during evolution.</p> <p>We've developed transformation and genome-editing techniques, which basically means you can test your own ideas about how these organisms work! Imagine unlocking the secrets of how these single-celled ancestors morphed into the first animals! Check out these links for some pictures and videos of these unicellular relatives of animals: Link to MultiCellGenome Flickr: https://www.flickr.com/people/146564503@N06/ Link to MultiCellGenome YouTube: https://www.youtube.com/user/multicellgenomeLab Link to a recent research paper: https://www.sciencedirect.com/science/article/pii/S0960982221008903 If you are a JAE-Intro student, you could join our project and become an expert on these emerging models. You will answer questions about their life cycles, how they change throughout their lives, and even edit their genomes to see what happens! Plus, you will learn awesome techniques like molecular biology, cell culture, microscopy, and computational tools.</p> | https://multicellgenome.com |
| JAEINT24_EX_0714 | Comas Martínez, David | david.comas@upf.edu | INSTITUTO DE BIOLOGIA EVOLUTIVA | Genética de poblaciones y diversidad en la población romaní | <p>La demografía de la población romaní (también conocidos con el sobrenombre de gitanos) está caracterizada por sucesivos cuellos de botella y procesos de mezcla con poblaciones vecinas. El impacto de su particular historia demográfica tiene implicaciones en el riesgo genético para enfermedades. Se ha demostrado que los grupos romaní presentan determinadas enfermedades mendelianas como resultado de prácticas endogámicas pero también se ha observado la presencia de variantes genéticas ligeramente deletéreas (incluyendo variantes metabólicas y cardiovasculares) como resultado de una relajación de la selección purificadora debido a cuellos de botella durante su historia demográfica. En este proyecto pretendemos explorar la influencia de la demografía en la presencia y distribución de variantes genéticas asociadas a enfermedades en diferentes grupos romaní. Se pretende demostrar si la demografía particular de estos grupos (caracterizada por múltiples efectos fundadores, cuellos de botella y</p> | https://www.ibe.upf-csic.es/comas |

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| | | | | | mezclas con poblaciones vecinas) ha supuesto un incremento de variantes deletéreas asociadas con enfermedades mendelianas y complejas. En el proyecto se analizarán datos genómicos de genomas completos de distintos grupos romaní para poder testar hipótesis demográficas y su asociación con la enfermedad. El proyecto representa una aproximación genómica de los efectos evolutivos que la demografía de la población romaní ha tenido en la salud y la enfermedad de la población actual. | |
| JAEINT24_EX_1423 | FERNANDEZ GARCIA, ROSA MARIA | rosa.fernandez@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | How did land animals arise? Understanding the marine-terrestrial transition in the animal kingdom through a genomic approach | Terrestrialization – the colonization of the land habitat by plants and animals – is amongst the most important events in the history of life. Understanding terrestrialization is, therefore, key to understanding the origin of terrestrial biodiversity. From marine ancestors, animals colonized the land multiple times and in different moments of Earth’s history. In order for animals living in aquatic environments to colonize land, a number of physiological barriers need to be overcome, including massive changes to methods of respiration, water management and osmoregulation, reproduction or digestion, among other extreme physiological and metabolic changes. The main goal of this project is to shed light on the genomic basis of terrestrialization across animals. By comparing the genomes of terrestrial species to their marine phylogenetic siblings, we can understand which genes changed across evolutionary time and how they did it. In this context, the objectives of the TFM project are (i) to interrogate multiple genomes and transcriptomes representing different animal lineages through a phylogenomic spyglass, (ii) to annotate genes potentially related to osmoregulation, reproduction, digestion or excretion, and (iii) to explore how, when and how often these genes have been gained, duplicated or lost across the Animal Tree of Life. Tasks to perform: - De novo assembly of genomic datasets - Orthology inference. - Phylogenomic reconstruction of gene families. - Comparative genomics analyses. | www.metazomics.com |
| JAEINT24_EX_0446 | FERRANDEZ ROLDAN, ALFONSO | alfonso.ferrandez@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | Insect choriogenesis | Research fields: The Project in our laboratory includes Genetics, Genetic Engineering, Transgenesis, Evolution, Bioinformatics. Project: The success of many insects in invading new areas and becoming pests is related to their high ability to produce a large number of eggs in a short period. To combat these pests, it is crucial to understand the biology and evolution of insect reproduction, particularly the mechanisms of oogenesis. In insects there are two types of ovaries, the panoistic and the meroistic, which differ in structure and type of cells forming the ovarian follicle that will become the egg. During insect oogenesis, the ovarian follicle receives a series of signals to initiate its capacitation that will subsequently lead to maturity and oviposition. Along this process, a series of genes must be transcribed and translated in the correct place and time in the ovarian follicle. While some of these genes have a conserved structure and function in both panoistic and meroistic ovaries, others | https://www.biologiaevolutiva.org/mdpiulachs/ |

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| | | | | | <p>are specific to one of these types. In our laboratory we work with the cockroach <i>Blattella germanica</i>, an insect model with panoistic ovaries, the most primitive ovary type of insects, to decipher how the transition from the panoistic to the meroistic ovary type occurred in evolution. Specifically, we are interested in the regulation of the choriogenesis, a crucial step for oogenesis that involves the synthesis of the multiple layers of the chorion that are secreted and deposited in the surface of the oocyte. This extracellular matrix confers a highly specialized protective shield for the embryo, allowing gas exchange while preventing water loss during embryo development. In the project that we propose, we will analyze genes related to chorion synthesis and their regulation by hormones and non-coding RNAs.</p> <p>The student will learn from the most basic technics of molecular genetics (PCR, cloning, sequencing, in vitro transcription, in situ hybridization) to the most advanced applications (interference RNA and DIPA-CRISPR).</p> | |
| JAEINT24_EX_0917 | GONZALEZ PEREZ, JOSEFA | josefa.gonzalez@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | Genomica de la adaptacion a medios urbanos y naturales | <p>El proyecto de formación se enmarca en el proyecto científico del grupo que tiene como objetivo identificar las bases genómicas de la adaptación al ambiente. Utilizando como organismos de estudio <i>Drosophila melanogaster</i> y mosquitos del complejo <i>Anopheles</i> utilizamos una combinación de técnicas -ómicas (genómica, transcriptómica, ChIP-seq, ATAC-seq) y experimentales (enhancer assays, CRISPR/Cas9) para identificar los genes relevantes para la adaptación y sus mecanismos moleculares. Se podrá realizar tanto formación en el área bioinformática como experimental.</p> <p>El estudiante se incorporará a todas las actividades del laboratorio, que actualmente lidera una red europea en genómica de la adaptación, es parte de los consejos directivos de las dos mayores sociedades científicas evolutivas (SMBE y ESEB) y participa habitualmente en congresos nacionales e internacionales, así como en la docencia de cursos de postgrado. El estudiante tendrá además acceso a programas de formación de las dos instituciones a las que pertenece el instituto.</p> | www.gonzalezlab.eu |
| JAEINT24_EX_1400 | NAVARRO CUARTIELLAS, ARCADÍ | arcadi.navarro@upf.edu | INSTITUTO DE BIOLOGIA EVOLUTIVA | Exploring Pleiotropy Between Anthropometric and Lifestyle Markers and Disease in Human Populations — a Genomic Analysis | <p>Many phenotypical traits show correlation with the occurrence of certain diseases, and the underlying causes of these associations remain subjects of ongoing investigation. It has been established that complex traits and diseases have a highly polygenic architecture, and different phenotypes can be interconnected by the deep complexity of their genetic architecture. Pleiotropy is the phenomenon by which a genetic variant simultaneously affects two or more phenotypes. This may arise either by the direct involvement of the same locus to several phenotypes (horizontal pleiotropy), or through a causal chain from one intermediate phenotype to another (vertical pleiotropy).</p> | https://www.ibe.upf-csic.es/ |

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| | | | | | <p>Moreover, the role of pleiotropy extends beyond the immediate phenotypic associations, influencing natural selection and evolutionary trajectories, thereby contributing to outcomes that deviate from expected patterns in the absence of pleiotropic effects. Certain traits have been extensively documented to show correlation, and even causality, with complex diseases. However, the recent increase of interest on pleiotropy has raised discussions surrounding the potential influence of pleiotropy on previously established causal relationships between phenotypes. This research project aims to obtain GWAS data from the UK Biobank (UKBB) and other sources within the GWAS Catalogue and perform an extensive study on pleiotropy interconnecting related traits and diseases. Furthermore, the study intends to deepen our insights on the biological architecture underlying the pleiotropic relationships.</p> | |
| JAEINT24_EX_0414 | PIULACHS BAGA, M.DOLORES | md.piulachs@csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | piRNAs functions in insect oogenesis | <p>The piRNAs are a class of small non-coding RNAs (sncRNAs) described as genome lifeguards since they were associated with repression of transposon expression. Nowadays, the piRNA functions beyond protecting the genome are spread, even going so far as to evidence their involvement in some human illnesses, like cancer. The project we propose is to study the expression and function of some piRNAs expressed in the ovary of the cockroach <i>Blattella germanica</i> at the end of the gonadotropic cycle during the chorion synthesis. We have identified the piRNAs expressed in <i>B. germanica</i> ovaries using libraries built at different stages of ovary development. These stage libraries allowed us to establish the expression patterns of all piRNAs and to know which piRNAs are being expressed at key moments, which ones are the most important (at least quantitatively) at each stage, and which targets they are repressing. These data are key in understanding the function and regulation of piRNA during insect oogenesis. We will modify the piRNA expression using antisense oligonucleotides or DIPA-CRISPR to deplete it. We will increase piRNA levels by injecting synthetic piRNAs. In addition, since the piRNAs can regulate the expression of mRNAs, we will predict mRNA target candidates for each piRNA, using the transcriptomes available in the laboratory. We will study the action of the piRNA on their target mRNAs. The student will receive training in basic molecular methodologies, including cloning and expression studies by real-time-quantitative PCR. RNAi methodologies (including synthesis of dsRNA and treatment of the animals), DIPA-CRISPR, and immunohistochemistry (fluorescence microscopy).</p> | https://www.biologiaevolutiva.org/mdpiulachs/ |
| JAEINT24_EX_1298 | RUIZ TRILLO, IÑAKI | inaki.ruiz@ibe.upf-csic.es | INSTITUTO DE BIOLOGIA EVOLUTIVA | Unraveling the origin of animals | <p>Ever wonder how animals went from single-celled organisms to amazing multicellular creatures? We, at the MultiCellGenome lab, are diving deep into the secret lives of the closest unicellular relatives to animals. We work with four</p> | |

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| | | | | | <p>groups of unicellular organisms that could be the next big stars in cell biology and evolutionary research! We use a multidisciplinary approach to understand how both genes and cellular processes changed during evolution.</p> <p>We've developed transformation and genome editing techniques, which basically means you can test your own ideas about how these organisms work! Imagine unlocking the secrets of how these single-celled ancestors morphed into the first animals! Check out these links for some pictures and videos of these unicellular relatives of animals: Link to MultiCellGenome Flickr: https://www.flickr.com/people/146564503@N06/ Link to MultiCellGenome YouTube: https://www.youtube.com/user/multicellgenomeLab Link to a recent research paper: https://www.sciencedirect.com/science/article/pii/S0960982221008903 If you're a JAE-Intro student, you could join our project and become an expert on these emerging models. You'll answer questions about their life cycles, how they change throughout their lives, and even edit their genomes to see what happens! Plus, you'll learn awesome techniques like molecular biology, cell culture, microscopy, and computational tools.</p> | <p>https://multicellgenome.com</p> |
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