DEPARTMENT
of GENETICS
The Department of Genetics is one of the most active research departments at the University of Barcelona (UB). At present, it has 28 professors, which along with postdoctoral and recruited researchers, graduate and undergraduate students, technicians and administrative staff and services, form a group of more than 130 people.

The Department of Genetics at the UB was established in 1963, when Dr. Antoni Prevosti, then a CSIC scientist, became Full Professor of Genetics. Both the subject and the chair in Genetics were the first in a Spanish university. At the time of its formation, the Department pioneered the study of variability in natural populations using Drosophila as a model organism. Nowadays, research and teaching have expanded greatly. Using state of the art molecular tools and the latest generation of genomic approaches, as well as a wide variety of animal models, research in the Department addresses the scientific challenges expected to have a major impact on the XXI Century society: Biotechnology, Development and Regeneration, EVO-DEVO, Genetics and Evolutionary Genomics, and Human Molecular Genetics.

Teaching includes courses in the Degrees of Biology, Biomedical Sciences, Biochemistry, Biotechnology and Environmental Sciences, as well as various masters, such as Genetics and Genomics, Biodiversity, Biomedicine, and Molecular Biotechnology. The Department is also responsible for the PhD program in Genetics, which has the quality award of the Ministry of Education.
BIOTECHNOLOGY

What pathogens use virulence genes to cause disease in animals and plants? What is the role of resistance to heavy metals in virulence? What genes encode metal resistance proteins? Can we get disease-resistant crops?

The area of Biotechnology of the Department of Genetics includes two research groups aimed to study at the genetic and molecular levels (from genomics to proteomics) the mechanisms by which organisms respond and/or defend against various situations of stress, including infections, biological pathogens, such as inorganic - lack or excess metal ions. Knowledge of these processes is later applied in biotechnological strategies to modulate, enhance and optimize the response of organisms to metal homeostasis or plants diseases.
DEVELOPMENT and REGENERATION

How is pattern formation achieved during development and regeneration? How is cell plasticity controlled: genome versus epigenome?

The field of DEVELOPMENTAL BIOLOGY studies how a fully formed adult animal arises from a single cell. During this process, distinct tissues, organs and systems develop in a precise spatio-temporal manner to achieve particular morphologies. Some adult animals have the ability to REGENERATE some of these organs and systems after their traumatic loss.

Nowadays, research in development and regeneration focuses on signaling pathways, proliferation, cell death, organogenesis, epigenetics and stem cells. Many phylogenetically-conserved pathways play very similar roles in development, regeneration and the pathogenesis of cancer in various model organisms. To understand the function of these pathways we use Platyhelminthes and Drosophila. Our research spans from pattern formation during development and regeneration, including cell proliferation and differentiation, to studies of neural circuit assembly and synaptic specificity.

The approach to answer our questions is extremely multidisciplinary and takes advantage of state of the art genomic and genetic technologies, as well as the latest imaging methods and computer optimized image analysis.
EVO-DEVO and NEW ANIMAL MODELS

To what extent humans are similar or different to a mouse, a fish or a worm? How do genetic changes during development generate evolutionary innovations and create biodiversity?

The field of EVO-DEVO has been recognized in the MILLENIUM issue of Nature (2000) as one of the 10 disciplines that will have a greater future impact on the society of the XXI Century. EVO-DEVO studies how the evolution of the mechanisms of embryo development at the genetic, molecular, cellular and morphogenetic levels is responsible for the extraordinary diversity generated during the last 1.000 million years of animal and plant diversification.

EVO-DEVO, as we know it today, arises from the intersection of the fields of Genetic and Molecular Developmental Biology, Molecular Evolution and Comparative Genomics, and it is nourished by state-of-the-art novel “omic” technologies (genomics, transcriptomics, proteomics, epigenomics) and the recent advances of molecular techniques of Genetic Engineering, transgenesis and gene silencing.

EVO-DEVO research follows comparative developmental approaches using new animal models chosen ad hoc for their key phylogenetic position to illuminate the changes of the mechanisms of development responsible for morphological and functional innovations that might have facilitated the major evolutionary transitions of life forms in our planet.
EVOLUTIONARY GENETICS and GENOMICS

What are the genetic and genomic bases of adaptation and evolutionary novelties? How have genetic changes contributed to the diversity of life? What are the main evolutionary processes that have shaped genetic changes?

Evolutionary Genetics studies the genetic basis and mechanisms determining the adaptive process, the patterns of evolution and biodiversity. Within this general objective, at the Departament de Genètica we perform research in the fields of population genetics and genomics, phylogeography, phylogenetics and comparative genomics. Projects in these fields are conducted in a wide range of taxonomic groups that include both model and non-model species. In our research, we use experimental approaches based on classical methods of molecular biology and on the new “omics” technologies (genomics and transcriptomics), and also bioinformatics, including the development of computational tools and software.

Our research seeks to generate knowledge on fundamental questions in evolutionary genetics. More specifically, we aim to determine: a) the significance of genetic changes in coding and regulatory regions in adaptive evolution; b) the molecular origin of chromosomal inversions, and their role in speciation and adaptation; c) the role of multigenic families and gene networks in the origin of evolutionary novelties; d) the processes leading to population genetic structure and that determine the evolutionary history of species. Our research aims to achieve an inclusive vision of the evolution of populations and species, and the adaptation process, as well as of the acquisition of evolutionary novelties and the origin and maintenance of biodiversity.
HUMAN MOLECULAR GENETICS

What are the genetic basis of hereditary diseases? How can we approach the search of new genes causing lysosomal diseases, blindness, osteoporosis or migraine? How can we delve into the molecular causes of genetic diseases? Can we improve the diagnosis and design of effective therapies for these diseases?

These are scientific questions addressed by the group of Human Molecular Genetics at the Department of Genetics, formed by a large group of researchers who have spent years working to determine the genetic and molecular bases of monogenic diseases from lysosomal diseases (Gaucher, Sanfilippo type B or C Niemann-Pick type A / B and C) to hereditary disorders of vision due to retinal degeneration, and complex diseases, most prevalent, such as osteoporosis and neurological disorders (migraine, episodic ataxia, impaired neurotransmission) and behavioral (drug addictions, ADHD, autism and aggressive behavior).

We aim to answer what genes cause these diseases, which processes are altered when these genes have mutations, how can we diagnose genetic carriers in families, if we can address some cell or gene therapy to alleviate its effects or even if we might someday cure the patients. To achieve these goals, we employ a range of innovative techniques and accurate genetic diagnosis (sequencing exomes, building chips genetic diagnosis and search for new candidate genes), and define new therapeutic targets by biochemical, genetic and cellular studies that combine the construction of animal models (mouse, zebrafish) as well as cell-based assays (transfected cells, primary cultures, iPS cells).
RESEARCH PROJECTS
under the FELLOWSHIP PROGRAM
“RESEARCH SUMMER at GENETICS”

Biotechnology
Marc Valls
Silvia Atrian

Evolutionary Genetics and Genomics
Julio Rozas
Montserrat Aguadé and Carme Segarra
Marta Pascual
Marta Riutort

Development and Regeneration
Francesc Cebrià
Marta Morey
Florenç Serras
Emili Saló i Teresa Adell
Josep F Abril

EVO-DEVO and New Animal Models
Pere Martínez
Cristian Cañestro and Ricard Albalat
Jordi Garcia Fernàndez

Human Molecular Genetics
Susana Balcells
Daniel Grinberg
Gemma Marfany
Regulation of virulence genes of the phytopathogen *Ralstonia Solanacearum*

In recent years several studies have reported the genes from plant’s pathogens that are transcribed in response to host contact, but it is still unknown in which stage of the infection they act. In this project we want to identify the genes expressed by the bacterium *R. solanacearum* that allow them to colonize tomato plants and induce in them the disease of bacterial withering. We propose a transversal approach using techniques of molecular genetics, plant biology and microbiology to better understand how the bacteria cause the diseases and try to remedy it.

Metal-organism relationships: how and what for?

Half of the known proteins contain one or more metal ions, which are essential for their structure and/or function, or which have as main role metal ion binding in the organisms. The regulation of the genes/proteins that contribute in the metal metabolism is still highly unknown. In our laboratory, we investigate three subjects related to the biology of metals in organisms, as well as possible biomedical and biotechnological applications: (i) how does a protein recognize the correct metal to be coordinated? (metal specificity); (ii) how some copper proteins are infectivity and virulence determinants in pathogenic fungi; and (iii) the function in plants of some iron proteins.
Why can some animals regenerate and others not? Freshwater planarians are amazing worms, if they are cut in 10-20 pieces one week later we have 10-20 complete animals. This regenerative capacity is based upon a population of adult totipotent stem cells. In our lab we study, through RNAi, the function of the Epidermal Growth Factor Receptor (EGFR) signaling pathway and the nervous system on the regulation of stem cell proliferation and differentiation, as well as during the processes of morphogenesis and pattern formation that lead to the complete regeneration of an animal, including the brain.

How does the brain wire? In order to assemble functional circuits neurons need to establish specific connections with their synaptic partners. We use Drosophila to unravel the molecular mechanisms underlying this process. Our hypothesis is that the molecular differences between closely related neuronal subtypes contribute to their distinct connectivity. In a multidisciplinary approach, we take advantage of genomic technologies (i.e. RNAseq) to identify molecular differences between subtypes; genetics to identify cell-subtype specific gene batteries determining synaptic specificity; and the study of cis-regulatory regions to gain insight into the transcriptional strategies that bring about specific connectivity patterns.
DEVELOPMENT and REGENERATION

Genetic engineering of epithelial regeneration

Supervisor:
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Addressed to:
prospective TFG or TFM students

Understanding the molecular basis of epithelial regeneration is crucial for designing treatments for skin wounds, burns and epithelial pathologies. Using gene expression transactivators we can activate specific DNA constructs that can be used to discover the genes required for tissue repair. Specifically, we plan to investigate the requirement of JNK and Hippo signaling pathways in regeneration as well as the cross-talk between them. The main goal will be to use constructs that inhibit or enhance signaling activity and assess how essential are those pathways for tissue repair. Students interested will be using genetically engineered tools in living organisms, molecular biology techniques and bioimaging techniques including
DEVELOPMENT and REGENERATION

Patterning and growth control during regeneration

Planarians are flatworms well known for their extraordinary ability to regenerate any body part in a few days. From the XIX century, long before the ‘boom’ of regenerative medicine, we know that this capacity is due to the existence of adult totipotent stem cells. Recent studies indicate that to successfully accomplish regeneration, the proliferative response must be accompanied by the activation of signals that ensure growth control and proper patterning of missing organs. In our group we study the role of the Hippo and Wnt intercellular communication pathways, responsible for size control and axial establishment in embryos, during planarian regeneration.

Flushing planarian transcriptome dynamics into Systems Biology networks

Planarian Schmidtea mediterranea is well known by its amazing regeneration capabilities thanks to the presence of adult stem cells, the neoblasts. We have participated in different Omic approaches, mainly proteomics and transcriptomics, as well as the differential expression analysis of the planarian transcripts, focusing in the search of neoblast specific genes. We have started to draw a protocol to map planarian transcripts on KEGG pathways, but we want to explore other pathway databases, such as the protein-protein interactions, signaling or gene-regulatory networks, and make it more accessible through a dynamic web-based interface. Among those databases one can cite String, BioGrid and Reactome. Cross-referencing such pathway information on the genome or transcriptome browsers for this organism, can become a useful tool for molecular biologist in order to plan their experiments.
EVO-DEVO and New Animal Models

Evolution of the central nervous system in bilateral animals

This project aims to investigate the mechanisms that have allowed the appearance of centralized brains in bilateral animals. To address it, a systematic study on the neurogenesis of a group of animals with a “simple” nervous system, the Xenoacelomorpha, will be carried out. Recently, in collaboration with other international laboratories, we have sequenced the genome of 5 species of Xenoacelomorphs. These sequences have revealed a huge variety of genes involved in neurogenesis. Now, using techniques of protein and mRNA detection, we want to uncover how these genes contribute to the formation of a relatively simplified nervous system.

Animal models to perform functional analyses of gene loss during embryo development

Did you know that gene losses might be beneficial? Did you know that gene losses could confer resistance to AIDS or malaria, and cause evolutionary innovations as those that facilitated the origin of tetrapods or even humans? If you are attracted by the research in the fields of Genetic Engineering, Transgenesis, Molecular Genetics, Developmental Biology, Evo-Devo and Genomics, and you would like to work with new animal models, we invite you to investigate how gene losses have affected the mechanisms of embryonic development of the heart, or how gene losses might be important for adapting to global climate change. Are you interested?

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Addressed to:
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Supervisor:
Pere Martinez (pedro.martinez@ub.edu)

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EVO-DEVO and New Animal Models

Long non-coding RNAs and innovation in vertebrates

Supervisor: Jordi Garcia-Fernàndez (jordigarcia8@gmail.com)

Addressed to: prospective TFG or TFM students

This project will be based on transcriptomic analyses of animals placed at key points of the vertebrate lineage, to identify lncRNAs regulators. The comparative genomic analyses will be complemented with the study of the expression of the selected lncRNAs both in silico as well as during embryogenesis and adult organisms.
Origin and evolution of the multigenic families of the chemoreceptor system

Chemoreception is a biological process fundamental for survival and regulated by several multigenic families with a large number of gene gains and losses. In arthropods, the main families involved in taste and olfactory senses are the OBPs, CSPs and the chemoreceptor superfamily (ORs and GRs, mainly). In this project we will study different aspects about the evolutionary origin of the chemoreceptor system as well as the biological meaning of such significant gene turnover rates. We will use experimental (RNA-seq; genomics), bioinformatic and analytical tools (mainly of comparative genomics).

Population genomics, chromosomal evolution and adaptation

Adaptations are the result of natural selection that upon its action leaves a footprint in DNA variation. We are interested in unraveling these footprints both in gene networks and regions affected by chromosomal inversions, and thus in contributing to identify the genetic basis of adaptive traits. We are also interested in identifying the origin of chromosomal inversions and their impact on nucleotide variation in the genome. To answer these questions, we use experimental (molecular and genomics), analytical (of evolutionary genetics) and bioinformatics approaches.
Genetic population structure, adaptation and conservation

**Supervisor:**
Marta Pascual (martapascual@ub.edu)

**Addressed to:**
prospective TFG or TFM students

The analysis of the genetic population structure is fundamental to apply adequate conservation measures. In our group we study the connectivity among populations of different species using mitochondrial genes, microsatellite loci and SNPs and analyze the impact of environmental discontinuities on gene flow. This project aims to analyze, with the COI gene, several populations of the terrestrial snail *Xerocrassa montserratensis*, an endemic species of Catalonia listed as Vulnerable, with small and isolated populations mainly in the stony slopes of Montserrat and Sant Llorenç del Munt, to be able to use this knowledge for conservation purposes.

Phylogeographical analysis and study of a case of sympatric speciation in planarians

**Supervisor:**
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prospective TFG or TFM students

This project will consist in sequencing a mitochondrial and a nuclear gene from planarians from Corsica and Sardinia. In these islands we find two species of the genus *Dugesia* (*D. benazzii* and *D. hepta*), that can be distinguished only by their chromosome number (2n=16 and 2n=14, respectively). In a preliminary study we have seen that both species are very close genetically and live together in several rivers. Because of this, we want to carry out a more detailed molecular analysis to determine whether *D. hepta* has appeared only once from *D. benazzii*, indicating a real example of sympatric speciation due to a chromosomal re-arrangement. On the other hand, the populations of *D. benazzii* from Corsica are very different genetically from those from Sardinia, suggesting that, in fact, it could be a novel species. Thus, we will perform a study of species delimitation and, if needed, the description of the novel species. The molecular phylogenies obtained will allow us to establish a comparison of the evolutive history of these species with the geological history of the islands, which will let us to evaluate if this has been, at least in part, the responsible of the observed speciation.
Opitz C syndrome (or Opitz trigonocephaly) is a rare genetic disorder characterized by severe malformations, mental retardation and psychomotor retardation with a high rate of mortality. This syndrome is very rare (less than 60 cases described worldwide) and the responsible gene is unknown. The identification of this gene by exome analyses is the first step to understand this disease and look for possible therapies. In this project you will participate in the analyses of the exomes of 6 patients. Those variants found after exome massive sequencing will need to be verified by Sanger sequencing.

Lysosomal diseases comprise a group of heritable diseases caused by mutations in genes that code for lysosomal proteins. These mutations result in the accumulation of different substrates in the lysosomes, which in many diseases account for organomegaly, skeletal abnormalities and dysfunction of the central nervous system. Our group is currently focused in the generation of cellular and animal models for some of these diseases (Sanfilippo C, Gaucher, Niemann-Pick C) and the development of therapeutic strategies with these models and/or cells of patients.
HUMAN MOLECULAR GENETICS

Why mutations in retinal dystrophy genes cause blindness?

Supervisor

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Addressed to:

Prospective TFG or TFM students

Retinal dystrophies (RD) are the main cause of hereditary blindness in the adult. Mutations in more than 300 hundred genes cause RD, but the precise function in the retina is for many still unknown. We use transfections in cultured cells, cultured explants of mouse retinas, knockdown in zebrafish embryos, and genome editing in mouse to generate cell and animal models to address the functional characterization of RD genes.