

## Comparative Genomics

Code: 42945  
ECTS Credits: 6

**2025/2026**

Degree	Type	Year
Cytogenetics and Reproductive Biology	OT	0

### Contact

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### Teachers

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### Teaching groups languages

You can view this information at the [end](#) of this document.

### Prerequisites

- BSc in Biology, Biomedical Sciences, Genetics or Biotechnology or in their equivalents in the curricula. Graduates or graduates of degrees in the field of Biosciences may also access.
- Basic knowledge of Catalan (level B1) or Spanish (level B1) (only for students who do not have Catalan or Spanish as their mother tongue).

### Objectives and Contextualisation

Comparative Genomics provides a broad perspective both in the evolution of species and in the origin of human diseases through the study of genomic sequences. The content of the module will address broad aspects of the area such as evolutionary cytogenetics, methodologies for studying genomes, as well as the latest advances in animal and plant comparative genomics. Comparative Genomics is a very dynamic and constantly evolving field, so the teaching methodology will include master classes of specialists that will present the latest advances in the subject as well as seminars by students where scientific articles are presented and discussed.

## Competences

- Apply the scientific method and critical reasoning to problem solving.
- Communicate and justify conclusions clearly and unambiguously to both specialist and non-specialist audiences.
- Continue the learning process, to a large extent autonomously.
- Design experiments, analyse data and interpret findings.
- Integrate knowledge and use it to make judgements in complex situations, with incomplete information, while keeping in mind social and ethical responsibilities.
- Interpret chromosome changes linked to evolutionary processes that formed the human karyotype (Specialisation in Cytogenetics).
- Interpret, resolve and report on clinical cases or scientific findings in the area of the master's degree.
- Show an ability to work in teams and interact with professionals from other specialist areas.
- Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
- Use acquired knowledge as a basis for originality in the application of ideas, often in a research context.
- Use and manage bibliography or ICT resources in the master's programme, in one's first language and in English.

## Learning Outcomes

1. Apply the scientific method and critical reasoning to problem solving.
2. Communicate and justify conclusions clearly and unambiguously to both specialist and non-specialist audiences.
3. Continue the learning process, to a large extent autonomously.
4. Design experiments, analyse data and interpret findings.
5. Integrate knowledge and use it to make judgements in complex situations, with incomplete information, while keeping in mind social and ethical responsibilities.
6. Recognise the karyotypic variability of animal and plant species and how human genomic architecture is linked to its evolutionary history.
7. Show an ability to work in teams and interact with professionals from other specialist areas.
8. Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
9. Use acquired knowledge as a basis for originality in the application of ideas, often in a research context.
10. Use and manage bibliography or ICT resources in the master's programme, in one's first language and in English.
11. Use the sources of data on the genomes of any species and interpret the fundamentals of bioinformatic analysis.
12. Write articles and report scientific findings in the area of evolutionary biology.

## Content

The contents of this subject include basic and specific concepts on evolutionary cytogenetics, advances in the area of comparative genomics, genome reconstruction models as well as the application of bioinformatics tools in the knowledge of animal and plant species.

Evolutionary cytogenetics. Chromosomal variability. Criteria of karyotype ordering. Chromosomal sex. Karyotype / species. Models of chromosomal speciation.

Methodologies for the study of genomes. Mass sequencing techniques. Study of the structural variations of the genome. Databases. Study of chromatin conformation (3C, 5C and Hi-C).

Animal Comparative Genomics. "In silico" study of complete genomes. Evolutionary breakpoints. Synthenic genomic blocks. Phylogenomics. Ratios of chromosomal evolution. Repetitive elements and recombination. Genomics of primates and other mammals.

Plant Comparative Genomics. Karyotypic diversity, genome structure, synthetic groups, genomic evolution of plant species.

Unless the requirements enforced by the health authorities demand a prioritization or reduction of these contents.

## Activities and Methodology

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Classes	30	1.2	4, 5, 3, 6, 9, 10, 11
Type: Supervised			
Material preparation	15	0.6	7, 10, 11
Type: Autonomous			
Bibliography	11	0.44	10, 11
Presentations	10	0.4	7, 12, 10
Reading of relevant papers	11	0.44	5, 3, 10, 11
Study	68	2.72	7, 8, 5, 3, 9, 10

The subject will be taught following the guidelines of the European Higher Education Area (EHEA). This implies an active participation of the students in their own learning process and will result in a participation of the students in class and an interaction between them and the teaching staff.

Comparative genomics is a very dynamic and constantly evolving field, so the teaching methodology will include master classes of specialists that will present the latest advances in the subject as well as seminars by students where scientific articles are presented and discussed. The following describes the organization and teaching methodology that will be followed.

1. Master classes: The content of the theory program will be taught in master classes. They will be made with audiovisual material prepared by the teacher.
2. Reading and commenting on articles and / or texts of interest: The master classes will be complemented with readings of scientific articles on the topics discussed.
3. Practical session on browsers of the human genome and HiC.
4. Elaboration of a paper.
5. Autonomous study.

Annotation: Within the schedule set by the centre or degree programme, 15 minutes of one class will be reserved for students to evaluate their lecturers and their courses or modules through questionnaires.

## Assessment

### Continous Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Attendance	5%	0.5	0.02	8, 2, 5
Oral dissertation	20%	1	0.04	1, 7, 12, 8, 9, 10, 11
Paper delivery	30%	1.75	0.07	1, 7, 4, 12, 8, 2, 5, 3, 6, 9, 10, 11
Written exams	45%	1.75	0.07	1, 4, 5, 3, 6, 11

Paper delivery: 30%

Oral dissertation: 20%

Written exams: 45%

Attendance and active participation: 5%

## Bibliography

<http://www.ncbi.nlm.nih.gov/>

<http://www.discoverlife.org/mp/20m?tree=Life&flags=all>

<http://www.ensembl.org/index.html>

<http://genome.ucsc.edu/>

<http://www.broadinstitute.org/scientific-community/science/projects/mammals-models/mammalian-genome-project>

<http://timetree.org/index.php>

<http://genome10k.soe.ucsc.edu/>

<http://www.mouseencode.org/>

<https://www.earthbiogenome.org/>

## Software

Ensembl ([https://www.ensembl.org/Homo\\_sapiens/Info/Index](https://www.ensembl.org/Homo_sapiens/Info/Index))

PopHuman (<https://pophuman.uab.cat/>)

UCSC (<http://genome.ucsc.edu/>)

## Groups and Languages

Please note that this information is provisional until 30 November 2025. You can check it through this [link](#). To consult the language you will need to enter the CODE of the subject.

Name	Group	Language	Semester	Turn
(TEm) Theory (master)	1	Catalan/Spanish	first semester	morning-mixed