UNIVERSITÀ
DEGLI STUDI DI MILANO-BICOCCA

SYLLABUS DEL CORSO

Biologia Molecolare Applicata

2425-1-F0802Q039

Aims

The course is organized in two modules dealing with chromatin organization and some of the processes involved in the control of gene expression. Particular emphasis will be devoted to methods and biotechnological applications.

Knowledge and understanding.
Students will learn chromatin organization and the molecular mechanisms of gene expression and epigenetic regulation in eukaryotic organisms. They will learn about the organization of complex genomes, the methods of their analysis, as well as, of the corresponding trascrittome.

Applying knowledge and understanding.
Students will be able to apply the acquired knowledge in other courses and in laboratory experiences and to use the comprehension skill in subsequent studies and/or research activities.

Making judgments.
Students will be able to process what they have learned and be able to recognize situations and
problems in which the acquired knowledge can be used.

Communication skills.
At the end of the course, students will be able to express themselves appropriately in the description of issues related to the molecular biology and its applications by using language properties, as well as, self-confidence.

Learning skills
At the end of the course, students will be able to survey the scientific literature related to the topics covered and will be able to analyze, apply and integrate the acquired knowledge with what learned in related courses.

Contents

Gene expression analysis and differential gene expression identification.
Chromatin organization and gene expression.
Low and high resolution analysis techniques for studying chromatin organization.
Gene targeting in mammals, transgenic animals.
Mechanisms of silencing (iRNA, ribozymes etc).
High-throughput sequencing methods.
Analysis of high-throughput sequencing data.

Detailed program

First module- Prof. Marina Vai
1. Gene expression analysis and differential gene expression identification. Competitive RT-PCR. Real Time PCR (sybr green and fluorescent probes). Melting curves. DNA arrays (oligos and cDNA): analysis and applications to Red Biotechnology (microarray-based diagnostic/prognostic tests) and Green Biotechnology (genomics approach to discover rose scent-related genes).
2. Chromatin organization and gene expression. The nucleosome. Chromatin modifications. The histone code. Histone modifications and transcription. The SAGA complex. Silencing: a model for silent chromatin assembly in yeast. Altered gene silencing/chromatin remodelling and disease. Deacetylases and cancer. CpG islands and transcription. DNA methylation in disease (fragile X, Rett syndrome).
3. Low and high resolution analysis techniques for studying chromatin organization. Methylation-sensitive restriction enzymes. Bisulfite-based methods: Methylation Specific PCR, Methyl-Light. Chromatin Immunoprecipitation (ChIP).ChIP on chips. Methylated DNA immunoprecipitation. DNA methylation arrays.

Second Module- Prof. Mattia Pelizzola
1. Expression in pluricellular eukaryotes. Transgenic animals. Knock-out and knock-in in mouse. Genome targeting and modification: Zinc-finger nucleases, TALEN and CRISPR-Cas9.
2. Gene expression silencing. Antisense oligonucleotides, ribozymes and interferent RNA. Molecular basis for RNA interference.
3.Genome organization and high-throughput sequencing methods: sequencing by synthesis via Illumina, sequencing by nanopores. Applications of high-throughput sequencing: gene expression profiling (RNA-seq), single cell expression profiling (scRNA-seq), binding of factors to DNA and chromatin, and modifications of chromatin (ChIP-seq).
4. Concepts of high-throughput sequencing data analysis: sequencing depth, quality controls, reads alignment, samples normalization, absolute and differential expression, identification of binding sites factors recognizing DNA and chromatin, calling of chromatin modifications.
5. The RNA life cycle: co- and post-transcriptional regulation of gene expression programs, synthesis of nascent RNA, processing of premature RNA, degradation of mature RNA, the role of RNA polymerase 2.
6. Epitranscriptional modifications of RNA: modifications of coding and non-coding RNAs, writers/erasers/readers of RNA modifications. Biotechnological applications: production of RNA vaccines and anti-cancer drugs.

Prerequisites

Background: basic notions of Molecular Biology.
Prerequisites: none

Teaching form

28 x 2 hours-lectures composed by:
- a section of delivered didactics (Didattica erogativa, DE) focused on the presentation-illustration of contents by the lecturer
- a section of interactive teaching (Didattica Interattiva, DI) including teaching interventions supplementary to delivered didactic activities and short interventions by trainees.

Didactic activities are conveyed by means of face-to-face lectures.
Teaching language: Italian.

Textbook and teaching resource

Selected scientific papers and slides will be available at the e-learning platform of the course

Recommended textbooks:

- J.D. Watson et al. “Biologia molecolare del gene” Zanichelli
- G. Capranico et al. “Biologia Molecolare” EdiSES
- T.A. Brown “Biotecnologie molecolari” Zanichelli
- M. Romani “Epigenetica” Zanichelli
- M.H. Citterich et al. “Fondamenti di Bioinformatica” Zanichelli

Semester

Second semester

Assessment method

Oral examination. Students will be asked to discuss a scientific paper on one of the topics covered during the course, followed by a conventional query on the course content. The ability to appropriately describe the scientific results, as well as their critical analysis will be positively evaluated.

Office hours

Contact. On demand, by telephone or e-mail request to the lecturers.

Sustainable Development Goals

GOOD HEALTH AND WELL-BEING