



UNIVERSITÀ DEGLI STUDI DI PALERMO

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| DEPARTMENT | Scienze e Tecnologie Biologiche, Chimiche e Farmaceutiche | | |
| ACADEMIC YEAR | 2021/2022 | | |
| MASTER'S DEGREE (MSC) | BIODIVERSITY AND ENVIRONMENTAL BIOLOGY | | |
| INTEGRATED COURSE | GENETICS AND GENOMICS - INTEGRATED COURSE | | |
| CODE | 18619 | | |
| MODULES | Yes | | |
| NUMBER OF MODULES | 2 | | |
| SCIENTIFIC SECTOR(S) | BIO/18, BIO/03 | | |
| HEAD PROFESSOR(S) | FEO SALVATORE | Professore Ordinario | Univ. di PALERMO |
| OTHER PROFESSOR(S) | FEO SALVATORE | Professore Ordinario | Univ. di PALERMO |
| | PALLA FRANCO | Professore Associato | Univ. di PALERMO |
| CREDITS | 9 | | |
| PROPAEDEUTICAL SUBJECTS | | | |
| MUTUALIZATION | | | |
| YEAR | 1 | | |
| TERM (SEMESTER) | 2° semester | | |
| ATTENDANCE | Not mandatory | | |
| EVALUATION | Out of 30 | | |
| TEACHER OFFICE HOURS | <p>FEO SALVATORE</p> <p>Monday 12:00 14:00 Via Real Mastranza, Caltanissetta</p> <p>Tuesday 10:00 12:00 Viale delle Scienze Dip. STEBICEF, Palermo</p> <p>Wednesday 12:00 14:00 Via Real Mastranza, Caltanissetta</p> <p>Thursday 10:00 12:00 Viale delle Scienze Dip. STEBICEF, Palermo</p> <p>PALLA FRANCO</p> <p>Monday 15:00 17:00 Studio del docente, Dipartimento STEBICEF - Sez Botanica ed Ecologia vegetale, via Archirafi 38 - I piano, 90123 Palermo</p> <p>Wednesday 15:00 17:00 Studio del docente, Dipartimento STEBICEF - Sez Botanica ed Ecologia vegetale, via Archirafi 38 - I piano, 90123 Palermo</p> <p>Friday 14:00 16:00 Studio del docente, Dipartimento STEBICEF - Sez Botanica ed Ecologia vegetale, via Archirafi 38 - I piano, 90123 Palermo</p> | | |

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| PREREQUISITES | The student to attend this course must have a good knowledge of basic genetics and molecular biology together with a good understanding of the principal cellular process occurring in prokaryotic and eukaryotic cells |
| LEARNING OUTCOMES | <p>Knowledge and understanding: Understanding the molecular events underlying the evolution of nucleic acids and proteins; access to their study methods through databases. Ability to understand how to use families of genes, RNA and proteins as models for the study of evolution and biodiversity.</p> <p>Applying knowledge and understanding: The course aims to make the student able to assimilate and elaborate critically the acquired knowledge, aimed at understanding the molecular logic.</p> <p>Making judgments: Students are guided to learn critically and responsibly everything is explained to them in the classroom and enrich their judgment through the reading and discussion of publications in highly qualified journals on scientific problems of wide media coverage in order to better develop and mature development of the discipline and tackle scientific problems.</p> <p>Communication skills: The course aims to develop the student's ability to present in a clear and rigorous, the knowledge gained. At the end of the course students should be able to enunciate properly and with appropriate vocabulary definitions, issues and mechanisms relating to the content of the course itself.</p> <p>Learning skills: Learning skills will be monitored throughout the course through participatory class discussion and in-course tests. The course aims to develop learning skills to undertake higher level studies and acquire tools and strategies for the expansion of their knowledge in the field of biological disciplines useful to promote and develop research activities.</p> |
| ASSESSMENT METHODS | <p>The tests that contribute to student assessment are: one written tests (to be held in the middle "test in progress" of the course) and an oral presentation, using power point, in the classroom at the end of course on a topic agreed with the teacher. The final exam grade, out of thirty, will be averaged by the grades obtained in the written test and in the oral presentation.</p> <p>The student who gives up or fails at least one of two written tests must undergo an oral examination on the entire program and produces the power point presentation.</p> <p>The tests described above are proposed to assess whether the student has acquired knowledge and understanding of the topics, has attained ability to interpret and to judge independently and has gained adequate analytical and communication skills.</p> <p>The following evaluation criteria will be used for the final grade:</p> <ul style="list-style-type: none">- Excellent: 30 - 30 cum laude Outcome: excellent knowledge of the topics, excellent language properties, good analytical ability, the student is able to apply knowledge for solve the proposed problems- Very good: 26-29 Outcome: good knowledge of the topics, full ownership of language, good analytical ability, the student is able to apply knowledge for solve the proposed problems- Good: 24-25 Outcome: good knowledge of the topics, good language properties, limited ability to independently apply knowledge to solve the problems proposed- Satisfactory: 21-23 Outcome: the candidate does not have full mastery of the main topics but neither possesses the knowledge, satisfactory language properties, low ability to independently apply the acquired knowledge for the resolution of problems- Sufficient: 18-20 Outcome: basic knowledge of the main topics and of the technical language, little or no ability to autonomously apply the acquired knowledge- Insufficient Outcome: The candidate does not have an acceptable knowledge of the topics treated during the course. |
| TEACHING METHODS | Lectures, class work |

MODULE MOLECULAR APPLICATIONS AND GMO

Prof. FRANCO PALLA

SUGGESTED BIBLIOGRAPHY

Browwn T.A. 2016. Biotecnologie molecolari-II edizione. Zanichelli
 Dale J. W. et al 2013. Dai Geni ai Genomi, III edizione. EdiSES
 Lesk A.M. 2009. Introduzione alla genomica. Zanichelli
 Lenhinger .Biochimica Iv ed. Zanichelli
 Watson J.D. et al 2009. Biologia Molecolare del gene, VI edizione. Zanichelli
 Dispense (cartacee e multimediali), video tematici, pubblicazioni scientifiche fornite dal docente.

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| AMBIT | 20879-Attività formative affini o integrative |
| INDIVIDUAL STUDY (Hrs) | 47 |
| COURSE ACTIVITY (Hrs) | 28 |

EDUCATIONAL OBJECTIVES OF THE MODULE

The course aims to provide necessary knowledge to understand the structure of genomes DNA (cellular, mitochondrial, chloroplast), to identify. Define the sequences useful for molecular identification of individuals, for the construction of dendrograms and phylogenetic trees. Lectures are conducted in order to evaluate and choosing the technological protocols appropriate to the study of the genomic DNA and the study of homologies of DNA sequences. The possible applications are critically examined and the use of methodological protocols for the construction of genetically modified plant. Their impact on the environment, human and animal health, considering also non-target insects, is considered in the light of the implementations in security and the increased supply of GMO. During the exercises are used technological procedures related to the issues addressed during the classroom lessons.

SYLLABUS

| Hrs | Frontal teaching |
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| 2 | Genomic DNA structure in procariotyc and eukariotyc cells. Nuclear, mitochondrial and cloroplastic genomes |
| 3 | Genome analysis, loci, meolecular markers (ITS, ISSR, CYO, rcbL) |
| 2 | Genetically Modified Organisms and microorganisms (GMO-GMMO). Plant genetic engineering: methods and application. In vitro culture, selection and analysis of transgenic plants Arabdopsis thaliana as vegetal molecular system. |
| 3 | Methods for the detection of GM events in food for human (corn and soybean flavours) and animals (simple and compound feed). |
| 2 | Quantitative Fluorescent – PCR (Syber green, Taqman protocols) DNA sequencing Sanger, Next generation sequencing, Pyrosequencing |
| 2 | DNA sequencing methods: Sanger, NGS Pyrosequencing |
| 2 | Insect-resistant plants. Effect of GM crops on non-target insects, affect on biodiversity |
| Hrs | Practice |
| 4 | Vegetal tissues preparatio: leaf, seeds, flavours, animal feeds. Genomic DNA extraction from plant matrixs. Genomic DNA extraction from insect tissues. Genomic DNA extraction from microbial cells. |
| 4 | Target sequences in nuclear, mitochondrial, chloroplastic genomes. In vitro amplification of molecular markers specific to the genome of eukaryotic cells (animal, plant) and prokaryotic. Sequence analysis and electrophoretic profiles. Drafting of dendrograms and phylogenetic trees |
| 4 | "DNA amplificability test" PCR and multiplex-PCR, to reveal trangenic genes in animal-vegetal matrix |

MODULE GENETICS APPLICATIONS

Prof. SALVATORE FEO

SUGGESTED BIBLIOGRAPHY

- J. Pevsner: Bioinformatics and Functional Genomics, Wiley Balckwell 2015, ISBN: 978-1-118-58178-0
 - T. Strachan, A. Read: Genetica Molecolare Umana, Zanichelli 2021, ISBN: 9788808520302
 - Articoli ed altro materiale monografico in lingua inglese verra' fornito dal docente durante il corso.

- J. Pevsner: Bioinformatics and Functional Genomics, Wiley Balckwell 2015, ISBN: 978-1-118-58178-0
 - T. Strachan, A. Read: Human Molecular Genetics, CRC Press 2018, ISBN: 9780429827471
 - During the course, the teacher will provide articles and other monographic material in English.

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| AMBIT | 50507-Discipline del settore biomolecolare |
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| INDIVIDUAL STUDY (Hrs) | 98 |
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| COURSE ACTIVITY (Hrs) | 52 |
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EDUCATIONAL OBJECTIVES OF THE MODULE

Objective of the Genetic Applications course is to provide knowledge and informations on the structure and organization of the genomes in order to define the phylogenetic relationships between different organisms, their evolutionary history and the molecular mechanisms behind evolution .

SYLLABUS

| Hrs | Frontal teaching |
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| 8 | Introduction to the course . Principles of the genetic analysis . Model organisms and the organization of their genomes : Yeast , Drosophila , Caenorhabditis , Arabidopsis , Mouse . Using genomic databases : FlyBase , Wormbase , TAIR and MGI . |
| 10 | Techniques for the global analysis of genomes and their plasticity (array-CGH , ChIP-on-Chip, exome, new generation sequencing, etc.). The microarray technology: microarrays for the study of SNPs, the global expression (mRNA and miRNA), the CNVs and the DNA-protein interactions. The gene expression database and statistical analysis of data. |
| 10 | Comparative genomics and molecular phylogeny: phylogenetic trees based on DNA and proteins sequence comparison . Application of molecular phylogeny: the genetic origins of modern humans; techniques for ancient DNA sequencing, NGS (New generation sequencing) .The metagenomic, the Environmental gene tags - EGTs. |
| 12 | Eukaryotic genomes evolution. Mechanisms of genome evolution: Gene duplication, Whole genome duplication, Transposable elements, Mutation, Pseudogenes, Exon shuffling, Genome reduction and gene loss. Genome evolution and speciation. Classification systems for genes, structure and function, the gene families. |
| Hrs | Practice |
| 12 | Computational Systems Biology. An overview and discussion of current bioinformatics resources most relevant to functional genomics investigations will be provided. These will include information on using genome browsers (EMBL-EBI – Ensembl, NCBI –Genome, UCSC – Encode), gene/protein annotation (GenCards), microarray/sequencing data repositories (NCBI-GEO, EMBL-EBI – Array express) and pathway analysis (DAVID, WEBGESTALT). Instruction on the integration of data into interaction and regulatory networks and systems biology approaches to mining and modelling of these data. |