

General Information	Studies in NUTRITION SCIENCE FOR HUMAN HEALTH		
Title of the subject	Nutrigenomics		
Degree Course (class)	Nutrition Science for Human Health		
ECTS credits	6		
Compulsory attendance	No		
Language	Italian		

Subject Teacher		
Name and Surname	Carmela Gissi	
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Place and time of reception	Campus di Via E. Orabona, 4 - Palazzo Dipartimenti Biologici; 1° floor From Monday to Friday by email appointment	
ECTS credits details	Discipline sector (SSD)	Area
	Molecular Biology (BIO/11)	Characterizing

Study plan schedule	Year of study plan		Semester	
	first		first	
Time management	Lessons	Laboratory	Exercises	Total
CFU	5	1		6
Total hours	40	12		62
In-class study hours				
Out-of-class study hours	85	13		98

Syllabus	
Prerequisites / Requirements	Basic knowledge of Physics, General and Organic Chemistry, Biochemistry, Anatomy and Human Physiology.

Expected learning outcomes (according to Dublin descriptors)	
Knowledge and understanding	- Knowledge of the correlations between nutrients and the human genome, with particular reference to both the regulation of gene expression by nutrients and the evolutionary changes of the genome due to diet.
Applying knowledge	- In-depth understanding of the functional significance of the interactions between foods and genome, with particular reference to the regulation of gene expression by foods and to the evolutionary changes of the genome due to diet.
Making informed judgments and choices	- Be able to evaluate the relevance and characteristics of the interactions between nutrition and genome. Being able to understand, analyze and evaluate the scientific and educational literature concerning nutrigenomics.
Communicating knowledge	- Ability to describe the interactions between diet and genome with simplicity and effectiveness, with particular reference to the modulation of gene expression, changes in the proteome, and the evolutionary adaptations of the human genome in relation to diet.
Capacities to continue learning	- Ability to learn from highly complex technical-scientific texts,

	monographs, scientific journals, IT tools and databases concerning genomics and nutrigenomics fields.
Study Program	
Content	<p>Nutrigenomics, nutrigenetics and "omics" sciences: definition and objectives.</p> <p>The genomics of eukaryotes</p> <p><u>Introduction</u> Genome projects and target organisms. Notes on the genomes of prokaryotes. Size of prokaryotic and eukaryotic genomes; size and complexity of eukaryotic genomes; the paradox of the value of C and its explanation; variability of gene density in eukaryotic genomes. The analysis of the transcriptome for the study of genomic characteristics</p> <p><u>The sequences that make up a genome</u> Concept of "coding" and "non-coding"; the structure of the protein gene in the light of genomic data; overlapping and cassette genes. Alternative splicing. Genes for "non-coding protein" RNA (ncRNA): microRNA, siRNA, piRNA, circRNA and long non-coding RNA (lncRNA). Transcription, transcript maturation and role in gene expression regulation of small and long ncRNA. The repetitive DNA and the transposable elements. DNA transposons, LTR retrotransposons, LINE and SINE elements: characteristics and mechanisms of transposition. Origin of the pseudogenes. Genomic distribution and characteristics of the transposable elements of the human genome. Alu of humans and other primates: origin, genomic distribution and role in the regulation of gene expression. RNA-editing and methylation of Alu sequences. Role of transposons and repeated elements for the plasticity and evolution of the genome and for the birth of new genes. Mini and microsatellites and their origin. The repeated DNA of centromeres and telomeres. Highly and moderately repetitive DNA. The satellite DNA of the centromeres. Segmental duplications. Single copy DNA and gene families.</p> <p>Regulation of gene expression in eukaryotes in relation to diet</p> <p><u>Epigenetic mechanisms</u> Chromatin and its characteristics, with the different levels of packaging. Euchromatin and heterochromatin. Chromatin remodeling by: histone modifications, action of "remodeling complexes", substitutions of histone variants. The histone code. The epigenetic inheritance. Action of lncRNA and small ncRNA in epigenetic silencing. DNA methylation and CpG islands. Epigenetic silencing by DNA methylation and imprinting. Compartmentalization and nuclear architecture: implications for the regulation of gene expression. High-throughput techniques for the study of chromatin status (ChIP-seq; identification of hypersensitive sites to DNaseI, etc). Techniques for the study of DNA methylation and of the entire methylome (bisulfite NGS and mapping).</p> <p><u>Regulation of the beginning of the transcription</u> Eukaryotic transcription by RNA Pol II: structure and functioning mechanism of Promoters, Enhancer, Silencer and Insulator. Basal</p>

transcription factors (basal TF), activators and co-activators of eukaryotic transcription. Domain structure of eukaryotic activators and co-activators. Combinatorial control of gene expression in eukaryotes: the modular structure of the cis-acting (promoters, enhancers, etc.) and trans-acting elements (basal transcription factors and activators). Techniques for the study of transcription factors and for the analysis of the transcriptome.

Signal transduction

The signal transduction pathways: characteristics and role in the regulation of cellular functions. The JAK-STAT signal transduction pathway. Signal transduction via cAMP and via phosphorylation. The MAPK cascade triggered by insulin. The nuclear receptors of steroid hormones.

The human genome

The human genome project and sequencing strategies: hierarchical sequencing and "whole-genome shotgun sequencing". Genetic and physical maps for hierarchical sequencing. Brief history of the human genome project: the competition between the public consortium and Celera Genomics.

The "1000 genomes" project for the study of human population variability. Annotation of human genetic variability: SNP (Single Nucleotide Polymorphisms), CNV (Copy Number Variations) and chromosomal rearrangements. Notes on the genomes of archaic hominids.

The ENCODE project for the annotation of the regulatory regions of the human genome.

DNA sequencing technologies for Nutrigenomics studies

Notes on DNA sequencing according to the Sanger method. New Generation Sequencing Platforms (NGS) and differences with the Sanger method. The second generation platforms: 454, Illumina, IonTorrent and SOLID. The Third Generation sequencing platforms: PacBio and Nanopore. Applications of NGS technologies in "omics" disciplines and for nutrigenomics.

Personalized nutrition and Nutriepigenomics

IPOP studies (Integrative Personal Omics Profiling). Diet-derived epigenetic modulators

Genomic adaptations to the diet

Genomic adaptations of human populations to the diet. The LCT gene and the persistence of lactase in adulthood. Mutations in the AMY1 gene for salivary amylase. Positive selection in the genes for smell and taste. Cultural aspects that have shaped the human genome

Microbiome

The human microbiome and its characteristics: variability of the human microbiome according to the anatomical site and age; acquisition of the

	<p>human microbiome in the early stages of life; inter-individual variability. The concept of taxonomic "core" and functional "core" of the microbiome. Metagenomics for the study of the human microbiome. The international projects "MetaHit" and "Human Microbiome Project".</p> <p>Metagenomics Metagenomics for the study of microbial biodiversity and microbiome. Main features of target-oriented metatagenomics (or metabarcoding) and shotgun metagenomics. Notes on functional metagenomics. The choice of the target sequence in target-oriented metagenomics: characteristics of the "DNA barcode". Reference databases for the "DNA barcode" and criteria underlying the taxonomic assignment ("binning") in metabarcoding experiments. Shotgun metagenomics: principles and objectives. Analysis criteria of the data produced for Shotgun Metagenomics: analysis of marker genes; "Binning"; gene prediction and functional annotation.</p> <p>Exercises - Consultation of the human genome through the UCSC genomic browser, with analysis of: (1) gene regions; (2) SNP; (3) regulatory regions that are important for dietary response or have undergone dietary adaptations.</p>
Bibliography and textbooks	<ul style="list-style-type: none"> - L. Debellis, A. Poli - Alimentazione, Nutrizione e Salute – EdiSES 2019. - Didactic material, distributed during the course, including the slides discussed and the legal references. This material is made available to students of the course on the online educational platform selected at the beginning of the course (eg Edmodo, Teams, etc.).
Notes to textbooks	- None
Teaching methods	- Frontal lessons with PowerPoint slides
Assessment methods	- Written exam
Evaluation criteria	<ul style="list-style-type: none"> - Knowledge of the characteristics of the human genome, of the mechanisms of gene expression regulation and of the epigenetic mechanisms in humans. - Knowledge of the interactions between genome and diet: adaptive changes and evolution of the human genome in relation to diet; effect of diet on the regulation of gene expression and on the proteome - Knowledge of the topics of nutrigenomics, nutri-epigenomics and of the importance of the microbiota for human health.
Further information	