UCLouvain

wmds1229

2019

In view of the health context linked to the spread of the coronavirus, the methods of organisation and evaluation of the learning units could be adapted in different situations; these possible new methods have been - or will be - communicated by the teachers to the students.

2 credits	20.0 h	Q2

Teacher(s)	Vikkula Miikka ;
Language :	French
Place of the course	Bruxelles Woluwe
Prerequisites	*The prerequisite(s) for this Teaching Unit (Unité d'enseignement – UE) for the programmes/courses that offer this Teaching Unit are specified at the end of this sheet.*
Aims	*The contribution of this Teaching Unit to the development and command of the skills and learning outcomes of the programme(s) can be accessed at the end of this sheet, in the section entitled "Programmes/courses offering this Teaching Unit".*
Evaluation methods	**Due to the COVID-19 crisis, the information in this section is particularly likely to change.** The student should show his-her acquired knowledge in following situations : During the exam (multiple choice questions, open questions with short response, true/false questions). The book Pasternak conteins questions and the book Thompson & Thompson questions and answers for self-learning after each chapter.
Teaching methods	**Due to the COVID-19 crisis, the information in this section is particularly likely to change.** Teaching is based on lectures (total 20 hours). It relies on the development of theoretical concepts, but also on the description of concrete examples of genetic diseases and genetic analyses.
Content	**1. DNA - carrier of genetic information** **2. Cytogenetics: low-resolution genome analysis** 2.1. Normal karyotype 2.2. Abnormal karyotype **3. Types of polymorphisms** 3.1. Vocabulary: polymorphism, gene, allele, homozygous, heterozygous 3.2. Genome in a single (<10) copy (haploid genome) 3.3. Genome moderetly repetitive 3.4. Genome strongly repetitive 3.5. Other polymorphisms 3.6. Calculation of heterozygosity **4. Methods to detect genetic markers** (polymorphisms) 4.1. Southern blot 4.2. PCR amplification 4.3. Molecualr karyotyping (DNA arrays) 4.4. Sequencing 4.5. Next Generation Sequencing (NGS) **5. Transmission of hereditary characters (Laws of Mendel)** 5.1. How to draw a genealogic tree in genetics - symbols 5.2. Types of heredity 5.3. Independent and non-independent segregation **6. Use of polymorphisms** 6.1. Genetic maps 6.2. Identification of an individual 6.3. Linkage analysis 6.4. Autozygosity analysis 6.5. Association studies 6.6. Loss-of-heterozygosity analyses **7. Other parameters of heredity** 7.1. *de novo* mutations

	7.2. Factors to modify the phenotype 7.3. Law of Hardy-Weinberg 7.4. eQTL 7.5. Personalised medecine
Bibliography	Jack Pasternak : Génétique moléculaire humaine : une introduction aux mécanismes des maladies héréditaires Editeur: De Boek (2003) **Chapitres: 1-3(p.3-80), 5.1, 5.4, 5.6, 5.7, 6 (p.161-183)** et Robert L. Nussbaum, Roderick R. McInnes, Huntington F. Willard. Genetics in Medicine Editeur: Thompson & Thompson, 7e édition (2007) - Syllabus (Notes de cours vérifié)(iCampus) - Dias du cours (iCampus)
Faculty or entity in charge	MED

Programmes containing this learning unit (UE)				
Program title	Acronym	Credits	Prerequisite	Aims
Bachelor in Medecine	MD1BA	2	WMEDE1112 AND WMDS1109 AND WMDS1111	