EMERGING AND REEMERGING VIRAL INFECTIONS

CU characterization:

    CU name:

    Emerging and Reemerging Viral Infections

    Duration:

    Semiannual

    Working hours:

    168h

    Contact hours:

    44h

    ECTS:

    6

    Observations:

    Opcional

Teacher in charge and respective teaching load in the CU:

Ricardo Manuel Soares Parreira (ricardo@ihmt.unl.pt)

Other teachers and respective teaching load in the CU:

João Piedade
Carla A. Sousa
Maria Teresa Novo
Paulo Gouveia de Almeida

Intended learning outcomes (knowledge, skills and competences to be developed by the students):

1. To describe the taxonomic position, structure and replication cycle of emerging and reemerging viruses.
2. To understand the characteristics of the natural maintenance cycles of emerging and reemerging viruses, and to describe the respective ranges of potential hosts, including assessment of their zoonotic potential including the factors that can contribute to their amplification and transmission to humans.
3. To recognize, at the molecular level, the mechanisms that account for the generation of viral genetic variability, and how they can contribute to promote immune escape or the breakdown of the species (host) barrier.

4. To characterize infections associated with emerging and reemerging viruses, including recognition of their major clinical manifestations, laboratory diagnosis and therapeutic/prophylactic options available/under development for their control.

5. To assess the impact of emerging and reemerging viruses on human and animal health.

6. To identify the main morphological characteristics, the main determinants of bioecology, and the geographic distribution of mosquitoes and ticks emerging from arboviruses.

7. To understand, execute and critically analyze results resulting from the use of multiple experimental approaches, including (i) the detection of viruses with RNA genome in environmental samples, and (ii) the use of bioinformatics tools in order to characterize (annotation) of viral genomes.

Syllabus:

The syllabus will include a theoretical training component where the topics (1) emerging arboviruses transmitted by hematophagous arthropods, (2) emerging coronaviruses, (3) filoviruses causing hemorrhagic fevers, (4) arenavirus and hantavirus, (5) bat lissaviruses, (6) and the emergence of the human immunodeficiency virus will be addressed. This curricular unit will also include a practical training component, based on laboratory (including on-hand bioinformatics) practice sessions which will include (1) the detection of RNA viruses in mosquito macerates, (2) assembly in a unique sequence (sequence assembly) , annotation and characterization of viral genomes from fragmented sequences and (3) the detection of viral genomes: construction of datasets (presentation of the NCBI-virus platform), and the planning (in silico) of primers and definition of PCR conditions. In a Theoretical-Practical session, the identification of mosquitoes and ticks vectors of arboviruses will be addressed and in a Discussion session, challenges presented to the detection and characterization of viruses and their genomes will be addressed.

Evidence of the syllabus coherence with the CU intended learning outcomes:

The theoretical training component will allow objectives 1 to 5 to be achieved. Objective 6 will be achieved through a medical entomology-based session, which will also allow students to contact with study models and analysis approaches different from those normally used in the field of medical microbiology. Finally, the two sub-objectives (i and ii) of objective 7 will be achieved through the realization of practical classes, either involving laboratory manipulation (i), or involving the use of bioinformatic analysis of viral genomic sequences available in access databases public (ii).

Teaching/learning methodologies articulated with pedagogical model:
Theoretical/theoretical-practical classes will be taught using the aid of expository methodologies, while at the same time encouraging the participation of students. The practical classes will take place in a BSL1 (basic biosafety level) laboratory facility, or will involve the use of tools from the field of bioinformatics, that will take place in a room equipped with individual computers, and which will involve the use of computer applications for unrestricted use

(freeware). Gamification (Kahoot) sessions will be carried out to allow students to revise all theoretical topics presented. A discussion session addressing the general challenges of virus detection and identification will also be promoted.

Assessment:

A formal/theoretical assessment in the form of a written exam, consisting of a set of statements that must be graded True/False, a group (n=2 students) oral presentation (or seminar) on a topic selected by the students from a list provided at the beginning of the course, and, finally, a continuous assessment component (i.e. assessment of each student's daily performance).

Evidence of the teaching methodologies coherence with the CU intended learning outcomes:

The teaching of the theoretical component will be carried using an expository approach, interspersed with the execution of laboratory-based and bioinformatics work (in independent sessions), will allow the integration of the acquisition of theoretical knowledge with the execution of experimental protocols. The students will be encouraged to critically analyse the results obtained, and to exploration of the potential of in silico analysis, aiming at the characterization of viral genomes through their annotation. The diversity of teaching strategies that will be used, and their complementation with a gamification session, will allow students to carry out an objective and critical analysis of the different themes presented.

References for consultation / mandatory existence:

- Banyard AC, Evans JS, Luo TR, Fooks AR (2014). Lyssaviruses and bats: emergence and zoonotic threat. Viruses 6, 2974-2990; doi:10.3390/v6082974.
- Coltart C.E., Lindsey B., Ghinai I., Johnson A.M., Heymann D.L. (2017). The Ebola outbreak, 2013-2016: old lessons for new epidemics. Philos. Trans. R. Soc. Lond. B. Biol. Sci. 372(1721). pii: 20160297. doi: 10.1098/rstb.2016.0297.
- de Wit E., van Doremalen N., Falzarano D., Munster V.J. (2016). SARS and MERS: recent insights into emerging coronaviruses. Nat. Rev. Microbiol. 14(8):523-534. doi: 10.1038/nrmicro.2016.81.
- Huang Y.S., Higgs S., Vanlandingham D.L. (2019). Emergence and re-emergence of mosquito-borne arboviruses. Curr. Opin. Virol. 34:104-109. doi: 10.1016/j.coviro.2019.01.001.
- Kirtipal N., Bharadwaj S., Kang S.G. (2020). From SARS to SARS-CoV-2, insights on structure, pathogenicity and immunity aspects of pandemic human coronaviruses. Infect. Genet. Evol. 85:104502. doi: 10.1016/j.meegid.2020.104502.
- Marston HD, Folkers GK, Morens DM, Fauci AS (2014). Emerging viral diseases: confronting threats with new technologies. Sci. Transl. Med. 6. doi: 10.1126/scitranslmed.3009872.
- Sharp PM, Hahn BH (2011). Origins of HIV and the AIDS pandemic. Cold Spring Harb Perspect Med; doi: 10.1101/cshperspect.a006841.
- Wang L.F., Anderson D.E. (2019). Viruses in bats and potential spillover to animals and humans. Curr. Opin. Virol. 34:79-89. doi: 10.1016/j.coviro.2018.12.007.