Estudo Orientado em Biologia Celular e Biotecnologia

Estudo Orientado em Biologia Molecular e Genética

Título: Spread of antimicrobial resistant bacteria in multi-host systems: integrated phenotypic and molecular analyses within a landscape framework

Enquadramento: Antimicrobial resistance (AMR) is often referred to as the "silent pandemic" and has contributed to an estimated 1.27 million deaths in 2019, with this number expected to rise to 10 million deaths by 2050. In the European Union, the economic losses associated with human infections due to AMR are in the region of one billion euros per year and the proportion of antibiotics with more than 50% resistance has increased from 12-15% in 2000 to 34-41% in 2018. Despite a large and growing literature on AMR, integrated approaches on a One Health perspective remain lacking.

Plano e Métodos: This project aims to characterise antimicrobial resistance in selected isolates of *E. coli, Salmonella, S. aureus* obtained from cattle, wildlife and the environment in Portugal, in a One Health Approach, and to identify at the molecular level bacterial isolates which tested negative for the above mentioned taxa. The isolates will be characterised by PCR, antimicrobial susceptibility testing and, in a restricted group, whole-genome sequencing analyses. A large dataset of genomes generated by our group and complete genomes from GenBank may be included to extend context.

[TASK 1] Molecular identification of bacterial isolates by PCR.

[TASK 2] Antimicrobial susceptibility testing of bacterial isolates against critically important antimicrobials by disk agar diffusion and/ or microdilution following EUCAST guidelines.

[TASK 3] Whole-genome sequencing analyses (WGS) of selected isolates aiming the characterization of the resistomes, virulomes and plasmidomes.

[TASK 4] Integrated data analyses.

[TASK 5] Preparation of final report.

The project provides the student with an opportunity to work in a cross-disciplinary topic (microbiology, genomics, bioinformatics, surveillance, epidemiology, public health) with opportunities to generate unique knowledge on the drivers of antimicrobial resistance and cross-species bacterial transmission.

Nº de alunos: 3

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