MSc in Biochemistry for Health

Dissertation Project – 2nd Cycle

Student´s Name:
Student email address : No.
Supervisor(s) (max. one supervisor and one co-supervisor): Ana Varela Coelho (ORCID: 0000-0002-6143-4203)
Co-supervisor: Maria Miragaia (ORCID: 0000-0002-1323-7184)
Supervisor(s) email address: varela@itqb.unl.pt
Lab/Institution: Proteomics of Non-model Organisms Lab – ITQB NOVA
TITLE: Identification of cell wall-specific targets for antimicrobials against *Staphylococcus epidermidis* pathogenic strains

BACKGROUND

Staphylococcus epidermidis include the skin microbiota and contribute to homeostasis and protection against pathogens. However, they are the most frequent cause of medical device-associated infections. Skin isolates belonging to clonal complex 2 (CC2) lineage are the major colonizers and the more frequent strains in infection, but they share their ecological niche with other minor genetic backgrounds (non-CC2). Discovery of biological processes and/or metabolic pathways that discriminate strains from these two lineages will have potential application on the development of additives to supplement general use disinfectants during clinical practice. Comparative genomics and proteomics analyses previously performed by us for two selected *S. epidermidis* strains belonging to the two lineages, showed that they display different metabolic and phenotypic profiles. Enrichment on the cell wall proteome will complement the data previously obtained from the whole cell with more accessible protein targets.

OBJECTIVES

Identification of proteins/biological processes that can be used as specific targets for antimicrobial activity against *S. epidermidis* pathogenic strains colonizing the skin.

PROJECT DESCRIPTION

- Task 1: Two *S. epidermidis* strains belonging to CC2 and non-CC2 lineages, will be grown in TSA medium at the skin pH (pH 5.5). Protein extracts will be prepared for the cell wall and membrane fractions from recovered colonies.
- Task 2: Tryptic digest mixtures will be analysed by high-resolution LC-MSMS. Proteins of each strain will be identified and the obtained MS/MS data used for reannotation of strain´s genomes using proteogenomic approaches.
- Task 3: A relative quantification of the levels of the identified proteins between the two strains will be performed using adequate software and the re-annotated genomes
- Task 4: Uni- and muitivariate statistical analysis of the differential proteomic data followed by String network analysis will be used to select the more specific biological processes/metabolic pathways to be targeted by antimicrobials.
- Task 5: Functional analysis of the common and differential biological events between the two *S. epidermidis* strains to better understand the skin colonisation processes.
- Task 6: Writing of master thesis

	Month 1	Month 2	Month 3	Month 4	Month 5	Month 6	Month 7	Month 8	Month 9	Month 10
Task 1										
Task 2										
Task 3										
Task 4										
Task 5										
Task 6										

Disponibilidade do aluno: Total