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
TITLE: *Staphylococcus epidermidis* cell wall proteome remodeling induced by skin-to-blood pH shift in commensal vs 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). Disruption of the skin barrier allows *S. epidermidis* to access the bloodstream, which can lead to infection. During the passage from skin to blood, *S. epidermidis* needs to cope with drastically different environmental conditions, namely a change of 2 pH units (from pH 5.5 to pH 7.4). Comparative genomics and proteomics analyses previously performed by us for two selected *S. epidermidis* strains belonging to each of the two lineages, showed different metabolic and phenotypic profiles when grown at the skin or blood pH. Discovery of differential biological processes undergone by the strains of each lineage will provide knowledge on the adjustments suffered by them during the infection process. Enrichment on the cell wall proteome will complement the data previously obtained from the whole cell.

OBJECTIVES

Contribute to explain S. epidermidis infection based on the diversity of the biological processes and/or metabolic pathways associated to each genomic lineage when submitted to a skin-to-blood pH shift.

PROJECT DESCRIPTION

- Task 1: Two *S. epidermidis* strains belonging to CC2 and non-CC2 lineages, inoculated at skin pH (pH 5.5) will be grown in TSB medium at the blood pH (pH 7.4) till middle exponential phase. Protein extracts will be prepared for the cell wall and membrane fractions from the recovered cellular pellet.
- 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 identify the biological processes/metabolic pathways involved in *S. epidermidis* infection.
- Task 5: Results from Task 4 will be complemented with the proteomic and metabolomic data previously obtained in our group to characterize the *S. epidermidis* adaptation to the blood pH and contribute to explain its transition from a colonizer to an infectious state.
- 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