Which proteins help *Listeria* to survive harsh environments?

My name is Tiago Santos, I am 25. I carried out my studies in Portugal, at the University of Trás-os-Montes and Alto Douro (UTAD), where I received, in 2012, my Bachelor of Science degree in Genetics and Biotechnology. There, I acquired my first research experience with emphasis in molecular microbiology and my will to prosecute my career on general proteomics. I continued my academic training in the same institution, with a Master Degree in Molecular, Comparative and Technological Genetics. In July 2014 I won a one-year MSc research fellow in the INNOFOOD project (CGB-UTAD). Research work I developed up to date was focused on the use of genomics and proteomics in microbial species and plant varieties.

Currently I am an Early-Stage Researcher in INRA, as well as a PhD student in Clermont-Ferrand at the University Blaise Pascal and working on understanding which proteins play a role in the adaptation of a pathogenic bacterium (*Listeria monocytogenes*) in different conditions (temperature, humidity,…).

Overview

Listeria monocytogenes associated infections (listeriosis) have high mortality rate and at first glance this bacteria is generally regarded as a pathogen but it should primarily be considered as a saprophytic bacterium well adapted for survival in the environment and to different stresses. In combination with its ability of growing to biofilm state (microbial cells sticked to each other on a surface), *Listeria monocytogenes* can persist in several conditions (low temperature and high relative humidity) and places, including food producing factories and our fridges. So, the knowledge of which proteins have a connection to the survival and persistence of *L. monocytogenes* to harsh conditions is of a major importance.

Objectives

My sub-project 5 of the List_Maps network will connect the role of secreted proteins, particularly the cell surface-associated proteins during biofilm formation and adaptation to controlled environments. To explore the molecular response of *L. monocytogenes* I will use a combination of classical and innovative proteomic approaches by using different protein extraction methods and protein separation/mass spectrometry analysis. I expect to identify proteins with major relevant connection with the survival capacity of *Listeria monocytogenes* to harsh environments and to better understand the molecular response of this pathogenic bacterium.

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