Master Thesis Proposal

Supervisor(s): Ana Varela Coelho/Laidson Gomes
Supervisor(s) email address: Varela@itqb.unl.pt
Lab/Institution: Proteomics of non-model organisms – ITQB NOVA
TITLE: Dynamics of circulating proteins during starfish nerve regeneration

BACKGROUND

The potential for tissue, organ and limb regeneration, including the central nervous system, has its maximum expression in echinoderms. Preliminary studies on echinoderms regeneration were based on the morphological, histological and cellular basis of this phenomenon. In the meanwhile, advances have been made in the characterization of the associated molecular processes. Our studies have been focused on the starfish *Marthasterias glacialis, a* species common in the Portuguese coastal areas, that shows strong regeneration capabilities. The coelomic fluid is the main intra-tissue communicating medium in echinoderms for which it is hypothesized a relevant role in the regeneration process. We have recently characterized the proteome of this biological fluid. In fact, several proteins with potential relevance for the regeneration process have been identified, namely glycoproteins involved in cell communication and stem cell biomarkers.

CF Franco et al Proteomics (2011) 11: 1359-1364; CF Franco et al Proteomics (2011) 11: 3587-92; CF Franco et al Electrophoresis (2012), 33, 3764–3778; C Franco et al J Proteomics (2014), 99: 1-25; C Franco et al Proteomics (2013), 13, 686-709 (Review article); Y Ben Khadra Cell and Tissue Research (2017) 370:13-28

OBJECTIVES

To contribute for a deeper knowledge of the molecular factors and biological processes involved in the regeneration of the central nervous system of starfish with potential applications in regenerative medicine. Changes in the proteome of the cell-free coelomic fluid in *M. glacialis* will be characterized during radial nerve regeneration.

PROJECT DESCRIPTION

The process of sea-stars handling, including the induction of regeneration and tissue collection, will be made at the Aquário Vasco da Gama (Dafundo, Oeiras).

Task 1: Extraction and quantification of proteins will be performed according with an already developed protocol.
Task 2: Tryptic digest mixtures obtained before and after cleavage of N-linked oligosaccharides by PNGase F will be analysed by high-resolution LC-MSMS. The detected proteins will be identified and a relative quantification among the several regeneration time-points will be performed using an adequate software.
Task 3: Peptide profiles obtained with and without PNGase F digestion will be compared allowing a characterization of the glycoproteins detected in the coelomic fluid.
Task 4: Quantification date will be evaluated by uni- and multivariate analysis to determine the proteins relevant for the several regeneration steps
Task 5: Pathway analysis will be performed using the proteins identified with expression differences between regeneration time-points
Task 6: Writing of Master Thesis

TIMELINE

	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										
Thesis										