



Analysis of histone modifications in potato periderm development

Place of work: *ForGen Lab – Forest Genomics and Molecular Genetics Laboratory - Faculdade de Ciências da Universidade de Lisboa (FCUL)*

<https://forgen.rd.ciencias.ulisboa.pt/>

Supervisors: Vera Inácio (vlinacio@fc.ul.pt), Célia Miguel (cmmiguel@fc.ul.pt FCUL)

Abstract / MSc thesis project proposal

The periderm is the outermost line of defense against external stresses in plants with secondary growth and it is formed by three tissues: a secondary meristem, the phellogen; suberized phellem or cork produced by the phellogen; and the phelloderm also produced by the phellogen. The potato tuber periderm is widely used as a model to study periderm development. Early in the development of potato tuber periderm, the phellogen is activated and produces the immature skin, while during tuber maturation, the phellogen becomes inactive and the skin adheres to the tuber flesh.

Previous findings established that key regulatory networks of secondary meristems involve histone post-translational modifications (HPTMs). These modifications are critical for plant development being involved in gene activity control at the chromatin level, cell-cycle regulation, cell differentiation, and tissue specification.

Our main goal is to investigate the role and dynamics of antagonist H3K27me3 (chromatin mark of developmentally repressed genes) and H3K27ac (a chromatin mark associated with actively transcribed genes) chromatin marks in potato periderm formation and phellogen activity.

The plan includes:

- 1) Isolation of phellogen nuclei at distinct periderm developmental stages (active vs inactive phellogen) by fluorescence-activated nuclei sorting (FANS);
- 2) Chromatin extraction of sorted phellogen nuclei and immunoprecipitation with antibodies against antagonist HPTMs (H3K27me3/H3K27ac);
- 3) Analysis of regions of interest of candidate genes (gene regulatory regions of genes known/likely to be associated with H3K27me3/H3K27ac marks) in the immunoprecipitated samples by qPCR.

This innovative project will contribute to elucidating the role of these two antagonist chromatin marks in potato periderm development and contribute to advancing the knowledge of chromatin regulatory mechanisms underlying periderm formation and phellogen activity.

The student will be integrated into a multidisciplinary team of researchers and will develop his/her knowledge of experimental tools and techniques and teamwork ability, autonomy, organization, and critical thinking, essential in any professional area. Specifically, the student will acquire skills in molecular biology (DNA/RNA/chromatin extraction and immunoprecipitation, qPCR), flow cytometry, and bioinformatics, transversal to research areas. The student selected for this project, after thesis registration, is eligible to apply to the BioISI Junior Programme (supporting 8 students with a 6-month Scholarship(BII), being the selection criterium the academic merit of the candidates.