



Functional analysis of candidate resistance genes to oomycete pathogens

Place of work/: Plant Functional Genomics Laboratories (BioISI), FCUL, Edificio C2

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Woody plants are keys to reforestation, carbon dioxide capture, soil erosion prevention, food and global economy. Global warming urges breeding and propagation of improved woody plant species with high level of resistance to biotic stress (pathogens) and abiotic stress (e.g. high temperature, drought). The most destructive pathogens to plant cultures are oomycetes that belong to the *Phytophthora* genus. Knowledge on mechanisms involved in plant-pathogen interaction, namely genomic tools that disclose expressed genes, have the potential to be used in the development of molecular markers to access genetic diversity data and to direct efficient breeding for plant improvement.

Deep transcriptome sequencing on the interaction Chestnut –*Phytophthora cinnamomi* gave us insights on candidate plant resistance genes to oomycete pathogens. Some of these genes are being applied to a functional analysis approach for further gene validation, which recurs to chestnut and cork oak transformation. What we propose for the MSc project is the collaboration in the following tasks of the ongoing project:

1. In vitro culture: maintenance of chestnut transformed lines with resistance genes and obtention of plants.
2. Analyze the expression of genes and estimate copy numbers by qPCR, in transformed material.
3. Cellular localization of chestnut resistance genes: cloning in plant transformation vectors, transient transformation of model plants, confocal microscopy.

The described tasks allow proficiency in the methods, participation in an ongoing research project, contact with the partners of the project and authorship in subsequent publications.

Bibliography:

- **Serrazina, S.**, Santos, C., Machado, H., Pesquita, C., Vicentini, R., Pais, M.S., Sebastiana, M., Costa, R. (2015). *Castanea* root transcriptome in response to *Phytophthora cinnamomi* challenge. *Tree Genetics and Genomes*, 11:6. doi: 10.1007/s11295-014-0829-7
- **Serrazina S**, Machado H, Costa RL, Duque P and Malhó R (2021). Expression of *Castanea crenata* Allene Oxide Synthase in *Arabidopsis* Improves the Defense to *Phytophthora cinnamomi*. *Front. Plant Sci.* 12:628697. doi: 10.3389/fpls.2021.628697
- **Serrazina S**, Martínez M.T., Cano V., Malhó R., Costa R.L., Corredoira E (2022). Genetic Transformation of *Quercus ilex* Somatic Embryos with a Gnk2-like Protein That Reveals a Putative Anti-Oomycete Action. *Plants*, 11, 304. <https://doi.org/10.3390/plants11030304>

Students selected for this project, after thesis registration, are 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.