Silencing grapevine methylation-associated genes to improve resilience towards *Plasmopara viticola*

Place of work:
Grapevine Pathogen Systems Lab, C2 building, 4th floor, lab 37, BioISI at Faculdade de Ciências da Universidade de Lisboa

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Grapevine (*Vitis vinifera* L.) has high economic impact worldwide with plantation areas over 7.4 Mha (OIV data, 2021) and it also represents one of the most polluting agronomic industries with many tons of pesticides being used on each growing season. Current disease management practices for grapevine downy mildew rely on the intensive use of pesticides. However, directives from the European Union demand more sustainable agriculture practices, with low pesticide input. To tackle this challenge a deeper knowledge on grapevine defense mechanisms is crucial.

Increasing evidence revealed that epigenetic processes play key roles in the regulation of crop disease resistance and DNA methylation appears as one of the most interesting features of this epigenetic control. We have previously determined the global DNA methylation pattern in tolerant and susceptible grapevine genotypes during their interaction with P. viticola. We have also characterized the grapevine DNA methyltransferases genes family and assessed the expression patterns of its members. With this approach we were able to determine candidates for functional validation.

The aim of this thesis proposal is to develop a gene silencing approach in grapevine leaves to validate the expression of our candidates. In that sense several cloning procedures will be performed as well as transient gene silencing in grapevine leaves through RNAi spray. Genome editing approaches will also be performed. This project will be developed in Portugal and Italy.

Student may apply to a BioISI Junior fellowship (6 months) and to ERASMUS+ program.

The student João Pereira was already selected to develop this project.