

Molecular basis of resistance/susceptibility of *Vitis vinifera* L. to wood infection by fungal trunk pathogens in Alentejo region

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Grapevine (*Vitis vinifera* L.) is one of the most cultivated crops around the globe and has a high commercial value for fresh table grape, dried fruit and wine production. Grapevine is affected by several diseases among which grapevine trunk diseases (GTDs) are the most spread. These diseases are caused by several species of fungi that infect and damage the wood, causing chronic infections, affecting the longevity and productivity of grapevines in all major growing regions worldwide. Until now, no effective treatments are known. The recent increase of GTDs incidence is believed to be the consequence of several factors such as the grapevine planting 'boom' as occurred in Alentejo region, which increased the circulation of potentially contaminated propagating material, the drastic changes in production methods that greatly favor fungal infection, and finally because of the European laws concerning pesticide restrictions which have banned the use of effective chemical products available against GTDs fungi.

The recently accepted PhD project that will be here presented intends to exploit the natural phenotypic expression of plants' resistance/susceptibility to GTDs and to identify the gene(s) involved in these processes. Firstly, a preliminary study on the fungal community present will be performed in plants from selected cultivars from different vineyards in Alentejo region, with and without trunk diseases symptoms, using a strategy based on next generation sequence analysis (NGS). This study will give a better knowledge of the endophytic and pathogenic fungal communities and update the information on the diversity and abundance of the fungi responsible for trunk diseases. The antagonistic capacity of the identified endophytic fungi against the most frequently GTDs will also be tested. The information obtained on fungal communities, together with natural phenotypic expression of resistance/susceptibility to these diseases, will be the basis for the selection of plants for all transcriptome analyses. The comprehensive transcriptome data set will provide molecular insights into gene network responsible for activation of antifungal responses to trunk diseases, in resistant and susceptible grapevine cultivars, indicating novel candidates to be latter tested in strategies involving gene knockout and overexpression and contribute to the development of effective protective methods against these diseases.

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