

Metagenomic analysis of fungal microbiota associated to grapevine trunk diseases in Alentejo region

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Grapevine trunk diseases (GTDs) are considered among the most important problems affecting the longevity and productivity of vineyards in all the major growing regions of the world, causing important economic losses. They are caused by wood inhabiting fungi, namely by 133 species belonging to 9 families and 34 genera, with similar life cycles and epidemiology. Until now, no effective treatments are known. Aiming to gain a better knowledge of these diseases and search alternatives to limit their development, the present work intended to molecularly identify GTDs-associated fungi, grapevine endophytic community and fungi with antagonist ability against GTDs. For this study, two important cultivars from the Alentejo region were selected, ‘Alicante Bouschet’ and ‘Trincadeira’, which demonstrate different levels of susceptibility to GTDs. Samples consisted of cuttings from plants with and without trunk diseases symptoms from both cultivars in a vineyard located in this region. Total DNA was extracted from cortical scrapings and sequenced using a metagenomic approach based on next generation sequence analysis.

Deep sequencing of fungal-directed ITS1 and ITS2 amplicons led to the detection of 215 taxa in grapevine fungal microbiota, with nine fungi previously described as responsible for GTDs. Unexpectedly, symptomatic plants showed a lower relative abundance of GTDs-associated fungi and a higher relative abundance of possible antagonist fungi, in opposition to what was obtained in asymptomatic plants in both cultivars. Nevertheless, symptomatic plants showed greater diversity of GTDs phytopathogenic fungi when compared to asymptomatic plants. These facts corroborate previous reports referring that trunk diseases symptoms are intensified by a set of several associated fungi on the same plant. Some fungal species with biological antagonist characteristics were also identified but their role in GTDs still need further investigation. This study allowed a deeper knowledge of grapevine fungal communities of the selected cultivars and updated the information on the abundance and diversity of GTDs associated fungi and their relationship with the symptomatology in plants. Additional studies are still required to better understand plant-pathogen interactions and contribute to the mitigation and control of GTDs in the Alentejo region.

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