IDENTIFICATION OF FUNGI RESPONSIBLE FOR GRAPEVINE TRUNK DISEASE IN ALENTEJO REGION

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Grapevine trunk diseases (GTDs) are one of the most important fungal diseases affecting grapevine plants in all the major growing regions of the world (Pintos et al, 2018)[1] with up to 133 fungal species belonging to 34 genera associated to this disease (Gemaje et al, 2018)[2]. Management of GTDs is difficult and its complete eradication is not possible. For these reasons, its control is meanly focused on disease prevention and mitigation (U´rbez-Torres 2011)[3].The work here presented had the aim to identify molecularly the endophytic fungi present in different tissues of grapevines, and among them the fungi responsible for GTDs. Pure fungal cultures were isolated from diseased grapevines plants belonging to two cultivars of Alentejo region (‘Trincadeira’ and ‘Alicante Bouchet’). Mycelium was then harvested, gDNA was extracted (Doyle and Doyle, 1987), and for fungal genetic classification the ribosomal internal transcribed spacer (ITS) region of nuclear rDNA was amplified through PCR by using ITS1 and ITS4 primers (White et al. 1990)[4]. All the fungi sequences that showed resemblance of 98% were used to classify the fungus analysed. The most prevalent grapevine trunk disease fungi identified were *Hormonema viticola, Stereum armeniaccum, Philophorafastigiata, Diaporthe, Truncatella angustata, Cytospora acaciae, Diplodia pseudoseriata, Neofusicocum parvum, and Pestalotiopsis sp.*

Palavras chave: Grapevine trunk disease, *Vitis vinifera*; fungal genetic classification, internal transcribed spacer (ITS).

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