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The use of three biocontrol agents alone or in combination to control Neofusicoccum parvum, a Grapevine Trunk Disease pathogenic fungus.

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Neofusicoccum parvum is one of the most virulent fungal pathogens involved in Grapevine Trunk Diseases (GTDs). Using biocontrol agents (BCAs) may a promising method to limit the extension of this pathogen, and one of the strategies for enhancing plant protection is to combine BCAs. Previous studies showed that some microorganisms such as the oomycete, P. oligandrum, and bacteria, Pantoea agglomerans and Brevibacillus reuszeri, applied individually on young vines, reduced necrosis caused by GTD pathogens. In the present experiment, P. oligandrum, P. agglomerans and B. reuszeri (inoculated at trunk or root levels) were applied individually or in combination to evaluate their effectiveness against N. parvum (inoculated at the trunk level). Results showed that 5 months after N. parvum inoculation, necrosis size was reduced by about 60 % in most treatments. Efficacy was very similar when BCA were applied individually or in combination. However, for two modes of BCA combinations, the efficacy had decreased. These results suggest that there was no synergistic effect between these BCAs to control N. parvum attacks. In order to develop an adapted control strategy, the molecular events occurring during the tripartite interaction: grapevine/BCAs/N. parvum have been investigated. Wood samples have been collected 0 and 14 days post-inoculation and the expression of a set of 96 genes ("NeoViGen96"chip) implicated in Vitis vinifera defense mechanisms were analyzed. Gene expressions were quantified by real-time-PCR. Studied genes include 26 genes encoding PR proteins; 18 and 3 genes involved, respectively, in secondary metabolites and indole biosyntheses; 14 genes involved in wall thickness enhancement; 15 and 4 genes involved, respectively, in signaling and oxylipine pathways. Preliminary results will be presented.