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Screening and modes of action of antagonistic bacteria to control two fungal pathogens, Phaeomoniella chlamydospora and Neofusicoccum parvum, involved in grapevine trunk diseases.

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Grapevine trunk diseases (GTDs), such as Esca and Botryosphaeria dieback, markedly impact the worldwide winegrape and tablegrape industry. Detection and development of antagonistic microorganisms, particularly bacteria, to achieve biological control of GTDs, would be of prime importance as a future innovative alternative practice in viticulture.

The antagonistic activity of 46 bacterial strains, isolated from Bordeaux vineyards, were evaluated against *Phaeomoniella chlamydospora* and *Neofusicoccum parvum*, two major pathogens involved in GTDs. Different bioassays, under greenhouse conditions, with foliar grapevine stem cuttings have shown that the protection efficacy depends on the bacterial strain, the targeted pathogen species and, for *N. parvum*, on the application mode of the bacterial strain.

A significant reduction in length of the necrosis due to *P. chlamydospora* and/or *N. parvum*, ranging between 40 and 64% in non-grafted grapevine cuttings, resulted from three bacterial strains: *Pantoea agglomerans* (S1), *Paenibacillus* sp. (S19) and *Bacillus pumilus* (S32). Against *P. chlamydospora*, the bacterial efficacy did not depend on the application method: co-inoculation, preventive inoculation in the soil and preventive inoculation in the wood. Preventive application of the bacteria in the wood was, however, the most efficient method against *N. parvum*. All three strains were subsequently further investigated to determine their major mode(s) of action by

- antibiosis,
- production of antifungal volatile organic compounds, and/or
- induction of grapevine systemic resistance.

The volatile compounds secreted by these strains were identified by gas chromatography/ mass spectroscopy (GC/MS). Finally, the induction of grapevine systemic resistance was studied by quantification associated with the expression of 10 major grapevine defense genes by real-time PCR.