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The effect of olive knot disease in bacterial communities associated to olive phyllosphere

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Abstract

The interactions between microorganisms sharing the same phyllosphere environment can be highly relevant for plant health. Although such interactions are ubiquitous in nature, the possible interaction between the incoming pathogen and the resident microbial flora, as well as the impact of these interactions on disease development/suppression, are unknown and not understood. To assess this, we will use in this study the olive knot disease as a model system. This disease is caused by the bacterium *Pseudomonas savastanoi* pv. *savastanoi* (Psv), that produced knots, mainly on olive tree twigs and young branches.

Endophytic and epiphytic bacterial were isolated from asymptomatic twigs and knots of olive trees from two cultivars with different susceptibilities to olive knot (cv. Verdeal-Transmontana - susceptible; cv. Cobrançosa - tolerant). Bacterial isolates obtained were molecularly identified through sequencing of V1 - V4 regions from 16S rDNA. Overall, 73 species belonging to 37 genera were identified. The composition of bacterial community colonizing asymptomatic twigs changed drastically when becomes diseased. A set of bacterial was showed to be highly associated with either asymptomatic twigs or knot of each cultivar, suggesting that they might have an important role as “pathogen antagonist” or “pathogen facilitator”, respectively. Bacterial community composition of the tumors showed also to be extremely different between cultivars, suggesting an effect of the cultivar in bacterial community assemblage. Future research should be carried out in order to identify it these bacterial-bacterial and bacterial-plant interactions can be really part of host defense against olive knot disease.

Keywords: *Olea europaea*, bacterial-bacterial interaction, plant-bacterial interaction, *Pseudomonas savastanoi* pv. *savastanoi*

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