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Preferred type of presentation

Poster presentation

Genetic diversity and population structure of *Pseudomonas syringae* on ground covers in apricot and kiwi orchards

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The phyllosphere is known for hosting a great diversity of fungi, yeasts and bacteria. These microorganisms interact with each other and with the host plant in the form of symbiosis, mutualism, commensalism, parasitism, competition or simply neutralism. *Pseudomonas syringae* is a ubiquitous epiphytic bacterium commonly found in these microbial communities. The phylogeny complex of *P. syringae* comprises 13 phylogroups, containing strains that are well-known pathogens and strains that apparently have limited capacity as pathogens. Emblematic among the pathogens are *P. syringae* pv. *syringae* (Pss) and *P. syringae* pv. *actinidiae* (Psa) belonging respectively to phylogroups 2 and 1. Bacterial blights of fruit trees caused by *P. syringae* lead to significant economic losses worldwide. With the expansion of bacterial blight of kiwifruit caused by *P. syringae* pv. *actinidiae* and bacterial blight of apricot caused by *P. syringae* pv. *syringae*, the identification of reservoirs of these pathogenic strains and an understanding of the role of the accompanying diversity of *P. syringae* in disease epidemiology are needed. Here we describe the structure of *P. syringae* populations on orchard ground covers based on a series of PCR that specifically identify most of the phylogroups of this species. This efficient technique allows us to link population structure on ground covers to those associated with trees and to the botanical diversity and location of the ground cover reservoirs. The overall goal of these analyses are to identify microbiological contexts that are unfavorable for disease and to conceive management strategies of ground covers to foster these microbiological contexts.