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Kiwifruit trees and ground covers host diverse *Pseudomonas syringae* communities.

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Abstract

Infectious diseases are known as significant stressors of plant fitness, yet predicting their emergence and mitigating their impacts remains challenging. Kiwifruit crop has been cultivated commercially worldwide for 50 years but has already experienced at least 4 independent emergences of bacterial canker caused by strains of *Pseudomonas syringae*. *P. syringae* is a ubiquitous bacterium that can grow on a wide range of angiosperms in temperate regions. This bacterium is currently considered to be the main pathogen affecting kiwifruit yield through different types of tissue alterations including wood canker, bud necrosis and leaf die-back. The recent and global kiwifruit canker epidemic is attributed to a rather homogeneous population of *P. syringae* pv. *actinidiae* (Psa). Other strains in the genetically diverse *P. syringae* species complex are also known to colonize kiwifruit leaves and flowers. In addition, herbaceous plants in orchard ground covers could constitute potential reservoirs of inoculum. Yet, whether Psa strains can be found in single and/or mixed populations in both Kiwifruit trees and nearby ground covers has not been studied. To assess *P. syringae* genetic diversity in orchards, we determined its population structure in tissue samples from Kiwifruit trees in four orchards in the Drôme region (a main production region in France with high Psa disease incidence) and in bulk leaf samples of ground cover plants in close proximity of each tree. In contrast to previous descriptions, a high diversity of *P. syringae* strains from at least five genetic groups were detected both in Kiwifruit trees and in plant ground covers. In addition, *P. syringae* population sizes and structure in Kiwifruit buds were affected by ground cover management. The relative effects of various biotic (e.g. ground cover plant community composition) and abiotic (e.g. pedo-climatic conditions) parameters on *P. syringae* diversity and population sizes will be discussed.

Keywords: population structure, *Pseudomonas syringae*, *Actinidia deliciosa*, ground covers