Pseudomonas syringae diversity and population structure in Kiwifruit orchards
Christelle Lacroix, Benoît Borschinger, Luciana Parisi, Odile Berge, Charlotte Chandeysson, Caroline Guilbaud, Jean-François Bourgeay, Cindy E. Morris

To cite this version:

HAL Id: hal-02788277
https://hal.inrae.fr/hal-02788277
Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Pseudomonas syringae diversity and population structure in Kiwifruit orchards

Christelle Lacroix, Benoit Borschinger, Luciana Parisi, Odile Berge, C. Chandeysson, C. Guilbaud, J.-F. Bourgeay, Cindy E. Morris

INRA, UR0407 Plant Pathology, F-84143 Montfavet, France

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