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Identification of the reservoirs of *Pseudomonas syringae* in *Prunus armeniaca* orchards

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Bacterial cankers of perennial trees caused by *Pseudomonas syringae* provoke serious economic losses all around the world, and also affect tree species in the genus *Prunus*. When pedo-climatic conditions are favorable, the disease can severely affect apricot (*Prunus armeniaca*). The epidemiology of this complex disease is not completely understood. Based on recent work on the presence of *P. syringae* in very diverse non-agricultural habitats, the complexity of the phylogeny of *P. syringae*, and the existence of phylogroups containing more aggressive strains than others, the scope of this work was the identification of the potential reservoirs of pathogenic strains of *P. syringae* in *Prunus* orchards. We addressed the following questions: What is the structure of the *P. syringae* population in the ground-cover, in the soil, in the irrigation water, and in the plant (epiphytic and endogenous)? What are the relationships between these populations and the populations in non-agricultural habitats? What are the factors that trigger disease when pathogenic populations are present? To answer these questions, a specific molecular detection method, by PCR, allowing rapid and accurate identification of the different phylogroups of *P. syringae* was developed. With this method, the different potential reservoirs: plants (buds, leaves, twigs), cover-grass, soil, and water, were investigated in 2014 in 3 different French orchards of apricot, at 3 different periods of the plant's vegetative development. Leaf litter was collected and analyzed during winter. Preliminary results showed different structuration of the populations according to their origin. For example, in March, the abundance of isolates of phylogroup 1 (including *P. syringae morsprunorum* race 2) and phylogroup 2 (including *P. syringae* pv *syringae*) was different in plant, soil and ground-cover populations.