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Emergence of *Pseudomonas syringae* pv. *actinidiae* (Takikawa, 1989) in France: methods of characterization

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Pseudomonas syringae pv *actinidiae* (Psa), causal agent of Kiwi canker, has been known since recent outbreaks in Italy in 2007 (Balestra, 2009) as an aggressive pathogen on Kiwi fruit, spreading rapidly in orchards and the environment. The first recordings of Psa were in 1984 in Japan (Takikawa *et al.*, 1989, Serizawa *et al.* 1989), then in 1992 in Korea (Lee & Koh, 1994) and Italy (Scortichini, 1994) where outbreaks had been eradicated.

This bacterium was first detected in France in July 2010 by isolation on nutrient agar media and identification. Its spread has been rapid since then, to Portugal (Balestra, 2010), New Zealand (2010, MAF Biosecurity Website) it was then reported in 2011 in Chile, Australia, Switzerland and Spain. The bacterial canker poses a serious threat to the cultivation of the yellow-fleshed kiwifruit in Italy (*Actinidia chinensis*), but also to green-fleshed kiwifruit (*Actinidia deliciosa* cv. Hayward). In France, this variety comprises about 95% of orchards.

The French strains isolated in 2010 were shown to belong to the same population as the strains from recent outbreaks in Italy. These genetics profiles were confirmed for most of the strains isolated during 2011 by using different biomolecular tools. The genetic structure of the population of strains isolated from French Kiwifruit is under investigation.

Gilles Cellier

Story of an array based technology designed to grasp and detect the complex plant pathogen *Ralstonia solanacearum*

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The ancient soil borne plant vascular pathogen *Ralstonia solanacearum* evolved and adapted to cause severe damage on an unusually wide range of plants. Based on the phylotype classification, it was questioned how genetically and phenotypically diverse strains of *Ralstonia solanacearum* may be, in an attempt to produce adapted diagnostic tools. A pangenomic microarray was first used to better describe and understand the phylogeny of *R. solanacearum*, especially three particular ecotypes in the phylotype II: (i) Brown rot strains from sequevars IIB-1 and IIB-2, historically known as race 3 biovar 2 and clonal; (ii) new pathogenic variants from sequevar IIB-4NPB that lack pathogenicity to Cavendish banana but can infect many other plant species; and (iii) Moko disease-causing strains from sequevars IIB-3, IIB-4, and IIA-6, historically known as race 2, that cause wilt on banana, plantain, and Heliconia. Results revealed a phylogeographic structure within Brown rot strains, allowing European outbreak strains of Andean and African origins to be distinguished, and also showed a close but distinct relationship between Moko ecotype IIB-4 and the emerging IIB-4NPB strains. Based on those results, it is proposed to develop new DNA-based diagnostic tools, including array and routine PCR, to ensure better detection of this complex plant pathogen.