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Genome Announcements

Draft genome sequences of five *Pseudomonas syringae* pv. *actinidifoliorum* strains isolated in France

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ABSTRACT

Pseudomonas syringae pv. *actinidifoliorum* causes necrotic spots on the leaves of *Actinidia deliciosa* and *Actinidia chinensis*. *P. syringae* pv. *actinidifoliorum* has been detected in New Zealand, Australia, France and Spain. Four lineages were previously identified within the *P. syringae* pv. *actinidifoliorum* species group. Here, we report the draft genome sequences of five strains of *P. syringae* pv. *actinidifoliorum* representative of lineages 1, 2 and 4, isolated in France. The whole genomes of strains isolated in New Zealand, representative of *P. syringae* pv. *actinidifoliorum* lineages 1 and 3, were previously sequenced. The availability of supplementary *P. syringae* pv. *actinidifoliorum* genome sequences will be useful for developing molecular tools for pathogen detection and for performing comparative genomic analyses to study the relationship between *P. syringae* pv. *actinidifoliorum* and other kiwifruit pathogens, such as *P. syringae* pv. *actinidiae*.

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Introduction

The *Pseudomonas syringae* species group comprises plant-pathogenic bacteria with a vast host range. The multiple strains of this species cause diseases on more than 180 plant species.¹ *P. syringae* is divided into 8 genomospecies^{2,3} and 13 phylogroups.⁴ *P. syringae* is further divided into more than 50 pathovars, according to the disease that the strain causes

on plants. Two pathovars have been described for kiwifruit: *P. syringae* pv. *actinidiae*,⁵ which causes bacterial canker on kiwifruit, and *P. syringae* pv. *actinidifoliorum*^{6–8}, which causes bacterial spots on kiwifruit. Both *P. syringae* pv. *actinidiae* and *P. syringae* pv. *actinidifoliorum* are classified into phylogroup 1 and genomospecies 3. Phylogenetic analysis conducted by MLSA has classified *P. syringae* pv. *actinidifoliorum* strains isolated in Australia, New Zealand and France into four different lineages.⁷ Strain genomes belonging to lineages 1 and 3

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Table 1 – Genome characteristics.

Strain code	Lineage	Accession no.	Genome size (Mb)	No. of contigs	N50 (bp)	No. of protein coding genes	G+C content (%)
CFBP8161	1	LJFL000000000	6.24	206	111,837	5775	58.72
CFBP8180	1	LJFN000000000	6.26	256	98,002	5833	58.69
CFBP8043	2	LJFM000000000	6.05	176	132,698	5630	58.80
CFBP8039	4	LJJM000000000	6.1	204	116,909	5700	58.75
CFBP8160	4	LJLJ000000000	6.09	220	113,613	5679	58.76

of *P. syringae* pv. *actinidifoliorum* (CFBP 7812 and CFBP 7951, respectively), isolated in New Zealand, were sequenced.^{9,10} Here, we briefly describe the genome sequencing of five *P. syringae* pv. *actinidifoliorum* strains representing three different lineages, lineage 1 (CFBP8161 and CFBP8180), lineage 2 (CFBP8043) and lineage 4 (CFBP8039 and CFBP8160), to provide genome sequences for at least one strain of each MLVA lineage described to date.

DNA Libraries were constructed from extracted DNA using the Nextera XT DNA Sample Preparation Kit with average insert sizes of 1200bp. The sequencing was performed on an Illumina Hi-Seq 2500 platform (Genoscreen, Lille, France) using a TruSeq Rapid SBS kit and a TruSeq Rapid paired-end cluster kit v3. The assembly statistics for each genome are reported in Table 1. Reads were assembled in contigs using SOAPdenovo 1.05¹¹ and Velvet.¹² Annotation was performed using EuGene-P (v0.3).¹³ The number of features for each genome are reported in Table 1. Analysis of the five genomes showed that an intact phage was present in the lineage 1 strains only. In all five genomes, in silico analysis confirmed the presence of only one Type III secretion system (hrp 1 type). All specific effector genes (hopO1, hopT1, hopS1, hopAB3, hopF1, hopE1, hopAF1-2) of *P. syringae* pv. *actinidifoliorum* that were previously reported by McCann et al.¹⁰ were present in all 5 genome sequences. No ICE (Integrative and Conjugative Element) was identified in the genome sequences of *P. syringae* pv. *actinidifoliorum*, unlike in *P. syringae* pv. *actinidiae*^{9,10,14}). Regarding nucleotide sequence accession numbers, the genome sequences have been deposited at GenBank under the accession numbers listed in Table 1.

Conflicts of interest

The authors declare no conflicts of interest.

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