Genome Announcements

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

Amandine Cunty\(^a,b\), Sophie Cesbron\(^a\), Martial Briand\(^a\), Sébastien Carrère\(^c,d\), Françoise Poliakoff\(^b\), Marie-Agnès Jacques\(^a\), Charles Manceau\(^b,\ast\)

\(^a\) Institut National de la Recherche Agronomique, IRHS, Beaucouzé, France
\(^b\) Agence Nationale de la Sécurité sanitaire, de l’alimentation, de l’environnement et du travail, Plant Health Laboratory, Angers, France
\(^c\) INRA, LIPM, Castanet-Tolosan, France
\(^d\) Centre National de la Recherche Scientifique, LIPM, Castanet-Tolosan, France

**A R T I C L E   I N F O**

Article history:
Received 18 January 2016
Accepted 17 February 2016
Available online 22 April 2016
Associate Editor: John Anthony McCulloch

Keywords:
*Pseudomonas syringae*
Actinia
Kiwifruit pathogen
Leaf necrotic spots

**A B S T R A C T**

*Pseudomonas syringae* pv. *actinidifoliorum* causes necrotic spots on the leaves of *Actinia delicosa* and *Actinia 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*.

\(\ast\) 2016 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

**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 genospecies\(^2,3\) 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*,\(^6,7\), which causes bacterial spots on kiwifruit. Both *P. syringae* pv. *actinidiae* and *P. syringae* pv. *actinidifoliorum* are classified into phylogroup 1 and genospecies 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

\(^\ast\) Corresponding author.
E-mail: charles.manceau@anses.fr (C. Manceau).

http://dx.doi.org/10.1016/j.bjm.2016.04.023
1517-8382/\(\copyright\) 2016 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).
of P. syringae pv. actinidifoliorum (CFBP 7812 and CFBP 7951, respectively), isolated in New Zealand, were sequenced.\(^3\,10\)

Here, we briefly describe the genome sequencing of five P. syringae pv. actinidifoliorum strains representing three different lineages, lineage 1 (CFBP8161 and CFBP1810), lineage 2 (CFBP8043) and lineage 4 (CFBP8039 and CFBF8160), 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 1200 bp. The sequencing was performed on an Illumina Hi-Seq 2500 platform (Genoscreen, Lille, France) using a TruSeq Rapid SBS kit and a TrueSeq Rapid paired-end cluster kit v3. The assembly statistics for each genome are reported in Table 1. Reads were assembled in contigs using SOAPdenovo 1.05\(^13\) 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 plasmid 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 (hhr 1 type). All specific effector genes (hopO1, hopT1, hopS1, hopAB3, hopF1, hopE1, hopAF1-2) of P. syringae pv. actinidifo- liorum 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.\(^3\,10\,11\) Regarding nucleotide sequence accession numbers, the genome sequences have been deposited at GenBank under the accession numbers listed in Table 1.

<table>
<thead>
<tr>
<th>Table 1 – Genome characteristics.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Strain code</strong></td>
</tr>
<tr>
<td>------------------</td>
</tr>
<tr>
<td>CFBP8161</td>
</tr>
<tr>
<td>CFBP1810</td>
</tr>
<tr>
<td>CFBP8043</td>
</tr>
<tr>
<td>CFBP8039</td>
</tr>
<tr>
<td>CFBP8160</td>
</tr>
</tbody>
</table>

**Conflicts of interest**

The authors declare no conflicts of interest.

**Acknowledgements**

Support for this work came from in-house funding of the EmerSys team at IRHS. We thank Jerome Gouzy (LIPM-INRA SPE platform, Toulouse) for performing automatic annotation of the genomes. We thank Corinne Audusseau and Sandrine Paillard for the isolation of the P. syringae pv. actinidiae and P. syringae pv. actinidifoliorum strains and Perrine Portier and Géraldine Taghouti at the International Centre for Microbial Resources and Plant-associated Bacteria (CIHM-CFPB) for providing strains and extracted DNAs, respectively. A. Cuny is supported by a fellowship provided by Anses and the Region Pays de la Loire, France.

**REFERENCES**