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Draft Genome Sequence of *Pseudomonas syringae* Pathovar *Syringae* Strain FF5, Causal Agent of Stem Tip Dieback Disease on Ornamental Pear

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***Pseudomonas syringae* FF5 causes stem tip dieback disease on ornamental pear (*Pyrus calleryana*). Its genome encodes a complete type III secretion system (T3SS) and HopAC1, HopM1, AvrE1, HopI1, HopAA1, HopJ1, HopAH2, HopAH1, HopAG1, and HopAZ1. Lacking detectable homologues of other T3SS effectors, it may encode novel, undiscovered effectors.**

Pseudomonas syringae is a Gram-negative bacterial pathogen that causes disease on a broad range of important crops and uncultivated plants, but individual strains show a high degree of host specificity. The species *P. syringae* is subdivided into about 50 pathovars, with each defined primarily by its host range (3, 6). A major determinant of ability to evade the host's defenses is the bacterium's type III secretion system (T3SS) and its substrates, the T3SS effector proteins (2, 8, 9).

Pseudomonas syringae pv. *syringae* strain FF5 was originally isolated (15) in Oklahoma, where it was causing stem tip dieback disease on ornamental pear (*Pyrus calleryana*). It is a common laboratory strain used in molecular studies (1, 4, 7, 10–12, 14–19).

The draft genome sequence assembly of *P. syringae* pv. *syringae* FF5 contains 79 supercontigs consisting of 4,578 contigs assembled from 100× deep genome-wide sequencing with Illumina GAI1 paired reads. The *de novo* assembly was performed using Velvet 0.7.48 (20).

Strain FF5 belongs to clade 2b in the phylogeny of Sarkar and Guttman (13) based on multilocus sequence analysis. A complete closed genome sequence is available for *P. syringae* pv. *syringae* B728a (5), which is also a member of clade 2c. Approximately 83% of the B728a genome is conserved in FF5; the two genomes share 95.3% nucleotide sequence identity in this conserved portion of their genomes. The remaining 17% of their genomes share no detectable nucleotide sequence similarity. *P. syringae* pv. *syringae* FF5 encodes a complete T3SS and homologues of the effectors HopAC1, HopM1, AvrE1, HopI1, HopAA1, HopJ1, HopAH2, HopAH1, HopAG1, and HopAZ1. However, it lacks detectable homologues of any other T3SS effectors found in *P. syringae* pv. *syringae* B728a and other sequenced strains of this species. This suggests that either *P. syringae* pv. *syringae* FF5 has an unusually small repertoire of T3SS effectors or, more likely, it encodes several as-yet-unidentified novel effectors.

Nucleotide sequence accession numbers. Sequence data from this whole-genome shotgun project have been deposited at GenBank under the accession number ACXZ00000000. The version described in this paper is the first version, ACXZ00000000.1. The genome project was also deposited in the Genomes OnLine Database as project number Gi04242, and the NCBI taxonomy identification number is 591153.

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