

Complete Genome Sequence of *N*-Acylhomoserine Lactone-Producing *Pseudomonas* sp. Strain StFLB209, Isolated from Potato Phyllosphere

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***Pseudomonas* sp. strain StFLB209 is isolated from the potato leaf and produces *N*-acylhomoserine lactone quorum-sensing signal compounds. Here, we present the 6,332,373-bp complete genome sequence of StFLB209, with a G+C content of 60.7%, which carries 5,598 protein-coding genes, 6 rRNA operons, and 69 tRNA genes.**

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In many Gram-negative bacteria, *N*-acylhomoserine lactones (AHLs) have been identified as signal compounds involved in quorum sensing (1). Several *Pseudomonas* species produce AHLs that regulate the expression of many genes and are responsible for pathogenicity, biofilm development, rhizosphere colonization, production of antibiotics, and other processes (2). Fluorescent pseudomonads are widely known to be beneficial to plants as biological control agents of plant diseases or as plant growth-promoting agents (3). In previous work, we reported the community structure of AHL-producing fluorescent pseudomonads in the potato rhizosphere and phyllosphere (3, 4). Based on the results of the phylogenetic analysis, 16S rRNA sequence of the most dominant phyllosphere species showed a certain degree of similarity to the opportunistic plant pathogen *Pseudomonas cichorii* (4). These dominant strains caused leaf necrosis and putrefaction of tuber slices as well as *P. cichorii* (4). The complete genome sequence of *P. cichorii* JBC1 has been deposited in DDBJ/ENA/GenBank databases (accession number CP007039) in the previous study (5). Here, we report the complete genome sequence of one of the dominant strains in the potato phyllosphere, *Pseudomonas* sp. StFLB209.

Single- and paired-end whole-genome shotgun sequencing of StFLB209 was performed using Roche Genome Sequencer FLX Titanium pyrosequencing technology (6) by Eurofins Genomics (Tokyo, Japan). We produced 1,026,084 reads with an average read length of 210 bases. The total number of sequenced bases is 216,076,150, representing a sequencing depth of 34×. Using the Celera Assembler version 5.3, these reads were assembled into one large scaffold including 31 large contigs (>1,000 bp). Gap closure was attempted using gap-spanning clones and PCR products. Prediction of putative coding sequences and gene annotation were done using the Microbial Genome Annotation Pipeline (<http://www.migap.org/>). Briefly, protein-coding sequences (CDSs) were predicted by the combined use of MetaGeneAnnotator (7), RNAmmer (8), tRNAScan (9), and BLAST (10). The complete genomic information of *Pseudomonas* sp. StFLB209 is contained

on a single circular chromosome of 6,332,373 bp with an average G+C content of 60.7%. The genome contains 5,598 protein-coding genes, 6 rRNA operons, and 69 tRNA genes. We searched for homologs of the reported AHL synthase gene in the complete genome sequence of StFLB209. One predicted coding sequence (PSCI_0294), which encoded 197 amino acids, showed 85.8% identity with PpuI from *Pseudomonas putida* IsoF (11). On the other hand, any AHL synthase gene homologs were not identified in the complete genome sequence of *P. cichorii* JBC1. Further studies on AHL-mediated quorum-sensing-regulated gene expression are needed to understand the mechanisms underlying the pathogenicity of StFLB209.

Nucleotide sequence accession number. The complete genome sequence of *Pseudomonas* sp. strain StFLB209 has been deposited in the DDBJ/ENA/GenBank databases under accession number AP014637.

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