

## Complete Genome Sequence of Japanese *Erwinia* Strain Ejp617, a Bacterial Shoot Blight Pathogen of Pear<sup>∇</sup>

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**The Japanese *Erwinia* strain Ejp617 is a plant pathogen that causes bacterial shoot blight of pear in Japan. Here, we report the complete genome sequence of strain Ejp617 isolated from Nashi pears in Japan to provide further valuable insight among related *Erwinia* species.**

The Japanese *Erwinia* strain Ejp617, along with three other strains (Ejp556, Ejp557, and Ejp562), was isolated from Nashi pears in Japan (1). These strains cause bacterial shoot blight of pear (BSBP), which has symptoms similar to those of infection with *Erwinia amylovora*, the causative agent of fire blight (4). Because of the symptom similarities between *E. amylovora* and the isolated Japanese *Erwinia* strains, the latter were tentatively designated *E. amylovora* pv. *pyri* (2). However, the identification of a novel species, *Erwinia pyrifoliae* (3), for the bacterial pathogen of Asian pear in South Korea has stimulated interest in reexamining the identification of Japanese *Erwinia* strains. In this study, we decoded the whole-genome sequences of the Japanese *Erwinia* strain Ejp617 to provide valuable insights into intraspecific genotypic diversity by comparing it with the recently published *E. pyrifoliae* genome sequences (6).

Whole-genome shotgun DNA sequencing of strain Ejp617, including plasmids, was conducted by Roche/454 pyrosequencing on a Genome Sequencer FLX system for totals of 212,569,985 bases and 243,278,193 bases in single reads and paired-end reads, respectively. Genome shotgun sequence data were assembled with Newbler assembler version 2.3 software (454 Life sciences). In total, 141 contigs were produced in 18 scaffolds through the *de novo* assembly. Genome and plasmid sequencing were completed by primer walking using Sanger sequencing. Preliminary prediction for 3,873 and 3,887 genes across the genome was conducted with Rast (<http://rast.nmpdr.org>) and Glimmer (<http://www.cbc.umd.edu/software/glimmer>), respectively. The final set

of genes was selected with high accuracy from among these predicted genes in the entire Ejp617 genome by comparing them with the nr data of the National Center for Biotechnology Information (NCBI).

The genome of strain Ejp617 is a 3,909,168-bp circular chromosome with a G+C content of 53.64% and five plasmids, namely, pJE01 (30,866 bp), pJE02 (5,296 bp), pJE03 (6,417 bp), pJE04 (3,237 bp), and pJE05 (2,691 bp). The coding regions account for 84.68% of the total sequence, with 3,600 annotated coding sequences (CDSs) with an average length of 902 bp. Seven rRNA operons and 76 tRNA sequences were identified in the chromosome. The large plasmid pJE01 is almost identical to pEJ30 of Japanese *Erwinia* Ejp557 (5), which contains 34 predicted CDSs. pJE02 contains 6 CDSs with one mobilization protein A (*mobA*), whereas no blast hits were found in the cases of pJE03, pJE04, and pJE05.

Because this is the first complete genome sequence of the Japanese BSBP pathogen, its availability may help researchers further understand the evolutionary relationships among the related *Erwinia* species, *E. pyrifoliae* and *E. amylovora*.

**Nucleotide sequence accession numbers.** The sequences of the Japanese *Erwinia* strain Ejp617 chromosome and plasmids pJE01, pJE02, pJE03, pJE04, and pJE05 have been deposited in GenBank under accession numbers CP002124, CP002125, CP002126, CP002127, CP002128, and CP002129, respectively.

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