The psychrophilic bacterium *Pseudomonas syringae* strain Lz4W was isolated from soil samples from Antarctica to decipher the mechanisms of low-temperature adaptation. We report here the 4.982-Mb draft genome sequence of *P. syringae* Lz4W. This sequence will provide insights into the genomic basis of the psychrophilicity of this bacterium.

Antarctic psychrophilic bacteria grow at and around 0°C (1, 2). The molecular mechanisms by which these bacteria overcome barriers for growth at low temperatures are not well understood. To investigate these mechanisms, we have been using *Pseudomonas syringae* strain Lz4W as a model system (3, 4, 5). This Gram-negative nonfluorescent pseudomonad was isolated from soil samples from the Schirmacher Oasis and Antarctica (6). Our studies have yielded novel insights into various mechanisms of psychrophilic adaptation that include modifications in lipopolysaccharides (7, 8), the RecBCD complex (9, 10, 11), RNA polymerase (12, 13), and a novel RNA degradosome with exoribonuclease RNase R (14, 15, 16). We and others have generated a transposon-mutagenized library of cold-sensitive mutants which have determined the genome sequence of the bacterium.

We sequenced the genomes of the wild type (WT) and a suppressor of the *recBCD* mutant (LCBD) of *P. syringae* Lz4W (11). Genomic DNAs were sequenced using the Illumina GAIIx sequencing platform and for collection of data.

The genome sequence was annotated using RAST (19) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (20). The annotation predicted 4,450 protein-encoding genes, 62 tRNA-encoding genes, and 6 genes for three rRNAs (16S, 23S, and 5S) on two separate contigs. The sequence analysis suggests that *P. syringae* Lz4W is more closely related to *P. fluorescens* than to plant-pathogenic *P. syringae* species and therefore should be classified as a distinct new species under the genus *Pseudomonas*, which will be reported separately.

**Nucleotide sequence accession numbers.** This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AOGS0000000. The version described in this paper is the first version, number AOGS01000000.

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