

Complete Genome Sequence of the Type Strain *Pseudomonas stutzeri* CGMCC 1.1803

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Here we report the complete genome sequence of *Pseudomonas stutzeri* strain CGMCC 1.1803 (equivalent to ATCC 17588), the type strain of *P. stutzeri*, which encodes 4,138 open reading frames on a 4,547,930-bp circular chromosome. The CGMCC 1.1803 genome contains genes involved in denitrification, benzoate/catechol degradation, chemotaxis, and other functions.

Pseudomonas stutzeri is a Gram-negative, nonfluorescent member of the genus *Pseudomonas* with exceptional genetic (1, 6) and physiological (7) diversity. These bacteria have received attention for their ability to oxidize a large variety of organic compounds, and some members of this species have been shown to be involved in nitrification and denitrification, degradation of aromatic compounds, and nitrogen fixation (5). *P. stutzeri* CGMCC 1.1803 (= ATCC 17588) was isolated from a clinical specimen (9) and is the type strain of *P. stutzeri* (8).

Whole-genome sequencing of *P. stutzeri* CGMCC 1.1803 was performed by a combination of the Roche/454 GS FLX system and the Illumina (Solexa) genome analyzer. Genomic libraries containing 8-kb inserts were constructed, and 392,575 reads were generated using the GS FLX system, achieving 16.68-fold coverage of the genome. A total of 94% of the reads were assembled into 114 contigs, using a 454 Newbler assembler. A total of 3,903,548 reads were generated to reach a depth of 85.83-fold coverage with an Illumina Ix genome analyzer. Newbler-generated contigs and ABI reads were assembled using the Phred/Phrap/Consed software package (3). Sequence gaps were filled through sequencing of PCR products. Prediction and annotation of protein-coding genes were performed as described previously (2).

The genome of *P. stutzeri* CGMCC 1.1803 consisted of a single circular chromosome of 4,547,930 bp in length with an average GC content of 63.9%, and no plasmid was detected. The genome is predicted to contain 4,217 protein-encoding genes, 58 tRNA-encoding genes, and 12 rRNA-encoding genes. The genome is a little smaller than those reported for two other *P. stutzeri* strains (A1501 and DSM 4166) sequenced to date. Comparative genome analyses indicated that CGMCC 1.1803 exhibited high overall similarity to A1501 and DSM 4166 at the gene and genome level. The three *P. stutzeri* strains share 3,186 genes, which form the core genome of each. CGMCC 1.1803 shares 3,255 genes with A1501 and 3,472 genes with DSM 4166. A total of 614 (14.6% of 4,217) genes are present only in the *P. stutzeri* CGMCC 1.1803 genome. More than half of these genes (325) encode proteins of unknown

function, implying that horizontal gene transfer might confer on CGMCC 1.1803 evolutionary adaptation to clinical environments through genomic plasticity. The organization of the genes involved in denitrification, benzoate/catechol degradation, chemotaxis, and other functions in CGMCC 1.1803 is close to that for *P. stutzeri* A1501 and DSM 4166. Although the nitrogen fixation island present in both *P. stutzeri* A1501 and DSM 4166 (4, 10) is absent in the CGMCC 1.1803 genome, the conserved adjacent genes (PSTAB_1294 and PSTAB_1301) outside the *nif* island are also found in CGMCC 1.1803. Instead of the *nif* island, there are six genes, including a *modABC* operon, located in this region. Overall, comparative genome analysis of *P. stutzeri* strains will help us elucidate evolutionary adaptation among the members of this species, and our findings also offer perspectives for future investigation into the genomic dynamics of this organism.

Nucleotide sequence accession number. The complete nucleotide genome sequence of *P. stutzeri* CGMCC 1.1803 has been deposited in GenBank under accession number CP002881.

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