

Draft Genome Sequence of Caprolactam-Degrading *Pseudomonas putida* Strain SJ3

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***Pseudomonas putida* strain SJ3, which possesses caprolactam-degrading ability, was isolated from dyeing industry wastewater in Daegu, Republic of Korea. Here, we describe the draft genome sequence and annotation of the strain. The 5,596,765-bp-long genome contains 4,293 protein-coding genes and 68 RNA genes with 61.70% G+C content.**

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Most of the *Pseudomonas putida* strains that have been isolated and characterized so far are usually found as innocuous environmental microorganisms with a great potential for biotechnological applications because of their metabolic versatility and adaptability (1). *P. putida* strains are metabolically versatile and thrive in diverse habitats. Strains of this species are known for their ability to colonize soil and strongly participate in bioremediation and degradation of a wide variety of chemicals, including natural and man-made compounds such as ϵ -caprolactam, naphthalene, and toluene (2–4). ϵ -caprolactam is synthesized synthetically from benzene and used almost exclusively for nylon-6 production. Nylon-6, a man-made polymer, has wide applications in the manufacturing of fabrics, automobiles parts, car tires, ropes, etc. (5). Because of its mass production, vast quantities of wastewater are generated during the manufacturing process, which is mostly discharged into natural water reservoirs without treatment (6).

To isolate caprolactam-degrading microorganisms, wastewater samples were spread on NB agar plates containing 50 mM caprolactam. From the initial caprolactam-tolerant screening, seven isolates showed varying degrees of tolerance. Subsequently, these strains were further screened for caprolactam degradation potential, and strain SJ3 showed the best degradation rate.

Microbial whole-genome sequencing was done using an Ion Torrent personal genome machine with a 200-bp single-end library and a 5 kb mate pair library, which generated 2,685,794 fragment reads (61 \times coverage of genome) and 1,097,427 mate pair reads (55 \times coverage of genome). The fragment reads were assembled with Mira Assembler version 3.4.0 and CLC Genomics Workbench 6.0. Assembly produced 424 contigs (400 bp or more), with an N_{50} contig length of 19,018 bp. For mate pair data, DNASTar version 11.0 was applied and generated 279 final contigs and an N_{50} contig length of 32,019 bp. The draft genome sequence consisted of 5,596,765 nucleotides with 61.70% G+C content. Subsequent to the assembly, the contigs were submitted to the

RAST annotation server (<http://rast.nmpdr.org/>) for subsystem classification and functional annotation (7). The annotation results revealed 4,293 predicted coding sequences, including 60 tRNAs, 5 rRNAs, and 3 noncoding RNAs.

We looked for genes involved in caprolactam degradation using next-generation sequencing (NGS) as in previous studies (8, 9). Polycyclic aromatic hydrocarbons (PAHs) and dioxin-like compounds have been widely identified in the environment and in industrial production waste (10). Many of these contaminated habitats are also characterized by high concentrations of organic solvents (11). The versatile metabolic capacity of the pseudomonads enables efficient degradation of these compounds (12, 13). Several of the genes found in strain SJ3 were mapped to the degradation pathways of aminobenzoate, benzoate, bisphenol, and dioxin within the KEGG orthology database, similar to previous NGS studies. The genome sequencing of this strain will provide great insight into its genetic variability and the biodegradation of a diverse range of chemical compounds. In a future study, we will investigate the application of degradation in strain SJ3 to environmental contamination.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AXDX00000000](https://www.ncbi.nlm.nih.gov/nuccore/AXDX00000000). This version of the second project is AXDX02000000. The 279 contigs have been deposited under the accession numbers [AXDX02000001](https://www.ncbi.nlm.nih.gov/nuccore/AXDX02000001) to [AXDX02000279](https://www.ncbi.nlm.nih.gov/nuccore/AXDX02000279).

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