Genome Sequence of *Pseudomonas putida* S12, a Potential Platform Strain for Industrial Production of Valuable Chemicals

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*Pseudomonas putida* strain S12, a well-studied solvent-tolerant bacterium, is considered a platform strain for the production of many chemicals. Here, we present a 6.28-Mb assembly of its genome sequence. We have annotated 32 coding sequences (CDSs) encoding efflux systems of organic compounds and 195 CDSs responsible for the metabolism of aromatic compounds. Some of these CDSs are arranged as a larger gene cluster similar to the reported styrene degradation gene cluster, which is consistent with the degradation ability of the S12 strain (3, 11). Meanwhile, 180 CDSs encoding stress response were annotated, which should be further investigated for their roles in the solvent adaption. We also annotated 53 CDSs related to capsular and extracellular polysaccharides, which are corresponding to the resistance of *Pseudomonas putida* strains.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALNR00000000. The version described in this paper is the first version, ALNR01000000.

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B iocatalysis is a “green” alternative of chemical catalysis for the production of valuable chemicals, especially substituted aromatic compounds (4). Currently, demand for the green production of chemicals is rapidly increasing due to the declining availability of fossil fuels and the urgency to reduce CO2 emissions (4, 13). However, such bioproduction may be hindered by the toxicity of the products of interest to the production host (12, 19). Organic-solvent-tolerant bacteria are remarkable microorganisms capable of surviving with the presence of high concentrations of organic solvents (5, 6). They provide a way to cope with the product toxicity, which is to develop solvent-tolerant microorganisms as biocatalysts (19). In fact, many researchers have successfully developed efficient solvent-tolerant whole-cell catalysts, such as solvent-tolerant biodesulfurizing strains (10, 16, 18, 20).

To take advantage of solvent-tolerant bacteria in enhancing bioproduction, it is necessary to thoroughly understand the molecular mechanisms involved in adaptation to organic solvents (21). However, the solvent-tolerant mechanism of bacteria is not thoroughly known now. Therefore, it is important and urgent to clarify the solvent adaptation of bacteria. Genome sequencing is powerful for discovering molecular mechanisms, especially for seeking functional genes, and would accelerate the studies in such scientific fields (2, 17).

*Pseudomonas putida* S12 (ATCC 700801), with its distinguished solvent-tolerant ability, is considered a good platform for bioconversion of sugars into substituted aromatic compounds (9). It has been used widely in developing many efficient biocatalysts, such as a strain for phenol production (20). Different aspects of the solvent-tolerant mechanism were also studied extensively (8, 21). However, no genomic research about it has been performed until now. Here, we present the draft genome sequence of strain S12, which was obtained using the Illumina GA system. The reads were assembled with VELVET (22), and the sequence was annotated using the RAST annotation server (1).

The sequence contains 6,284,656 bases, 5,635 predicted coding sequences (CDSs), and 90 RNAs and consists of 258 large contigs (>200 bp in size), with a G+C content of 61.5%. We predicted 32 CDSs encoding efflux systems of organic compounds, which are related to the cellular resistance, including solvent tolerance and multiple-drug resistance. Gene cluster *srpRSABC*, an important efflux system in the solvent tolerance of the S12 strain, was also found in the genome (7, 14, 15). Moreover, 53 CDSs encoding biosynthesis of fatty acids were also annotated. There are 195 CDSs annotated for the metabolism of aromatic compounds.