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Genome Announcements

Draft genome sequence of a caprolactam degrader bacterium: *Pseudomonas taiwanensis* strain SJ9

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ABSTRACT

Pseudomonas taiwanensis strain SJ9 is a caprolactam degrader, isolated from industrial wastewater in South Korea and considered to have the potential for caprolactam bioremediation. The genome of this strain is approximately 6.2 Mb (G + C content, 61.75%) with 6,010 protein-coding sequences (CDS), of which 46% are assigned to recognized functional genes. This draft genome of strain SJ9 will provide insights into the genetic basis of its caprolactam-degradation ability.

Introduction

Members of the genus *Pseudomonas* that have been isolated and characterized so far have mostly been found as innocuous environmental microorganisms. They have great potential for biotechnological applications owing to their metabolic versatility and adaptability.[1,2] *Pseudomonas* spp. can thrive in diverse habitats and are known for their ability to colonize soil and participate in soil biochemical processes.[3,4] The potential of *Pseudomonas* spp. for the degradation and bioremediation of a wide variety of chemicals, including natural and synthetic compounds such as caprolactam,[5] naphthalene,[6] and toluene,[7] has attracted a great research interest. *P. taiwanensis* strain SJ9 was isolated from a wastewater sample collected from a sewage treatment plant in Daegu, South Korea. This work reports the draft genome of *P. taiwanensis* strain SJ9.

The genome of the strain SJ9 was sequenced using an Ion Torrent Personal Genome Machine (PGM) sequencer system.[8] The sequence reads were assembled using Mimicking Intelligent Read Assembly (MIRA) 3.4.0 and CLC Genomics Workbench (version 6.0), with manual processing using SeqMan software to reduce the contig number. The best assembly results comprised 736 contigs (>400 bp). The draft genome consists of 6,253,055 bp covering almost

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whole of the predicted average genome, with a G+C content of 61.75%. The assembled contigs were submitted to the RAST annotation server (http://rast.nmpdr.org/) for subsystem classification and functional annotation.[9] This analysis predicted 6,010 protein-coding sequences (CDS), of which 46% were assigned to recognized functional genes. Furthermore, 71 tRNA and 12 rRNA genes were also predicted.

The genome also harbored a complete gene cluster coding for caprolactam degrading enzymes such as 2,3-dehydroadipyl-CoA hydratase, acyl-CoA dehydrogenase, aldehyde dehydrogenase, and enoyl-CoA hydratase.[10,11] This draft genome sequence of *P. taiwanensis* strain SJ9 will help improve the general understanding of the genetic basis of caprolactam degradation by *Pseudomonas* spp.

Nucleotide sequence accession numbers

The draft sequence of *P. taiwanensis* strain SJ9 obtained in this Whole Genome Shotgun project has been deposited at GenBank under the accession no. AXUP00000000. The version described in this paper is the first version, with accession no. AXUP01000000.

Conflicts of interest

The authors declare no conflicts of interest.

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