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Genome announcement

Complete genome sequence of the crude oil-degrading thermophilic bacterium *Geobacillus* sp. JS12

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ABSTRACT

Here, we report the complete genome sequence of *Geobacillus* sp. JS12, isolated from composts located in Namhae, Korea, which shows extracellular lipolytic activities at high temperatures. An array of genes related to the utilization of lipids was identified by whole genome analysis. The genome sequence of the strain JS12 provides basic information for wider exploitation of thermostable industrial lipases.

Lipolytic enzymes comprising carboxylesterases and lipases represent a highly diverse group of hydrolases. They occur widely in animals, plants, and microorganisms. Presently, about 900 of these enzymes are identified to originate from bacteria (Hausmann and Jaeger, 2010). Because microbial lipolytic enzymes are usually more thermostable than animal or plant lipolytic enzymes, they have received much attention for their potential use in industry and diagnostics (Nielsen, 1985). *Geobacillus* sp. JS12 was isolated from composts located in Namhae, Korea, and it can use crude oil as its sole carbon source at high temperatures. To identify the lipolytic enzyme activity of this strain, we performed genome sequencing and hereby present the complete genome sequence of *Geobacillus* sp. JS12.

Genomic DNA from *Geobacillus* sp. JS12 was extracted using standard genomic DNA isolation methods. Sequencing was performed using the PacBio RS II (Pacific Biosciences, USA) by constructing a 20 kb insert library at MACROGEN (Seoul, Korea), and 1,685,557,476 bp were generated from 300,584 subreads. The N50 subread sequence length was 14,693 bp. For sequence assemblies, PBcR pipeline in Celera assembler (Ver. 8.3) was used (Berlin et al., 2015; Koren et al., 2012). One complete circular chromosome was generated. Genome annotation was performed using the Rapid Annotation using Subsystems Technology (RAST) server (Aziz et al., 2008).

The complete genome comprises 3,721,489 nucleotides, with 51.95% GC content (Table 1). The count of predicted protein-coding sequences is 4274, and the genome contains 87 tRNA genes and 8 rRNA operons (Table 1). A total of 1932 (40.89%) proteins were assigned to 459 RAST subsystem categories. As a result, we identified nine genes encoding enzymes involved in oil degradation, namely two acylhydrolase, three lipase, three carboxylesterase, and one lysophospholipase gene. The strains of the genus *Geobacillus* are facultative thermophiles, and grow optimally at 55–60 °C (Nazina et al., 2001). To date, several thermostable lipases isolated from the genus *Geobacillus* have been reported (Abdel-Fattah and Gaballa, 2008; Balan et al., 2012; Li and Zhang, 2005). The thermostability of lipases is an important factor for their usage in industry (Nielsen, 1985), because higher temperature increases conversion rates and substrate solubility, and reduces the viscosity of the reaction medium. The optimal growth temperature of *Geobacillus* sp. JS12 is 58 °C, so the genes relating to the lipolytic activity of this strain were enough to evaluate its usage for industrial applications.

The complete genome sequence of *Geobacillus* sp. JS12 will enrich the sources of thermostable enzymes and provide basic information for wider exploitation of thermostable industrial lipases.

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Table 1
Genomic features of *Geobacillus* sp. JS12.

	Chromosome
Genome size (bps)	3,721,489
GC content (%)	51.95
CDSs	4274
rRNA operons	8
tRNA genes	87

Nucleotide sequence accession numbers

The complete genome sequence of *Geobacillus* sp. JS12 has been deposited at DDBJ/EMBL/GenBank under the accession numbers CP014749. This strain is available from Korean Collection for Type Cultures (KCTC) with the accession number KCTC 33799.

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