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Note (Genome Announcement)

Complete genome sequence of *Bacillus aryabhattai* K13 isolated from compost

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퇴비에서 분리한 *Bacillus aryabhattai* K13의 유전체 염기서열

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Bacillus aryabhattai K13 was originated from enriched culture of compost using 1% kraft lignin as a sole carbon and energy source. The complete genome of strain K13 consists of one 5.0 Mb chromosome and two circular plasmids with 139 kb and 78 kb, respectively. Analysis of the genome determined in this study may contribute to identify the genes responsible for degradation of lignin.

Keywords: *Bacillus aryabhattai*, compost, genome

Lignin is one of the most abundant natural polymers on the earth and mostly originated from plants which contain at significant quantities ranging between 15% and 40% of dry weight (Ragauskas *et al*., 2014). Its complex aromatic heteropolymer structure comprising phenylpropanoid aryl-C_3 units joined via a variety of ether and carbon-carbon linkages (Bugg *et al*., 2011). The chemical structure makes it more recalcitrant in the environment causing a major challenging task towards chemical and biological degradation. To date, microbial degradation of lignin has been comprehensively studied, especially in fungi as they secret significantly higher levels of ligninolytic enzymes (Wan and Li, 2012). However, another concern has focused on investigating the role of bacteria in lignin degradation (Prabhakaran *et al*., 2015). Bacteria showed tolerance towards extreme environmental conditions and versatility in substrate utilization. Thus, they are considered as useful candidates to develop efficient pretreatment technologies (Kumar *et al*., 2015).

Bacillus aryabhattai K13 was isolated from compost sample collected from Iksan, South Korea after enrichment on minimal salt medium (Chen *et al*., 2012) containing 1% kraft lignin (Sigma) as a source of carbon and energy at 30ºC for 7 days under aerobic condition. The purified isolate was deposited in Korean Culture Center for Microorganisms (KCCM) under KCCM 43272 of accession number.

Genomic DNA of strain K13 was extracted from cells which were grown aerobically at 30ºC for 20 h in LB medium and used to construct 20 kb SMRTbell™ template libraries. The whole genome sequencing was performed at ChunLab, Inc. using PacBio RSII platform (Pacific Biosciences). The determined filtered subreads with about 124-fold coverage were assembled using hierarchical genome assembly process (HGAP, v3.0)

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Table 1. Genome features of *Bacillus aryabhattai* K13

Contig	Length (bp)	CDS	tRNA	rRNA	G + C ratio
Contig 1 (Chromosome)	5,035,815	5,097	112	39	38.33
Contig 2 (plasmid)	139,863	161	1	0	33.53
Contig 3 (plasmid)	78,572	62	16	3	36.02
Total	5,254,250	5,320	129	42	38.17

including assembly polishing with Quiver (Chin *et al*., 2013). *De novo* assembly generated three circularized contigs of 5,035,815, 139,863 and 78,572 bp indicating that the assembled contigs were completed. Automatic annotation for the genome was conducted with Prokka (v1.11, Victorian Bioinformatics Consortium). A total of 5,320 coding sequences (CDSs), 129 tRNA genes, and 42 rRNA genes were identified as described in Table 1. Interestingly, rRNA genes were detected in contig 3. Although most of plasmids do not contain rRNA genes, the rRNA operon has been reported to locate on plasmids in the genus *Aureimonas* (Anda *et al*., 2015).

The genome revealed the presence of potent genes responsible for the degradation of lignin and lignin-derived aromatic compounds such as peroxidases, laccase, esterases, methyltransferases, cytochrome P450, glyoxal oxidase, vanillate *O*-demethylase, dioxygenases, and oxidoreductases. These findings suggest that *Bacillus aryabhattai* K13 contributes to lignin degradation during a composting process.

Nucleotide sequence accession number

The genome sequence of *Bacillus aryabhattai* K13 has been deposited in NCBI GenBank under accession nos. CP024035-CP024037.

적 요

단일 탄소원과 에너지원으로 1% 리그닌을 사용하여 퇴비를 농축배양한 시료로부터 *Bacillus aryabhattai* K13 균주를 분리하였다. K13 균주의 유전체는 약 5.0 Mb 크기의 염색체와 139 kb와 78 kb 크기의 2개 플라스미드로 구성되어 있다. 본 연구에서 결정된 유전체의 분석은 리그닌 분해에 관여하는 유전자를 규명할 수 있는 정보를 제공할 것으로 판단된다.

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