

Genome Announcement

Genome sequence of *Ochrobactrum anthropi* AM3 isolated from compost

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퇴비에서 분리한 *Ochrobactrum anthropi* AM3의 유전체 염기서열

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(Received December 21, 2016; Accepted December 23, 2016)

ABSTRACT: *Ochrobactrum anthropi* AM3 was isolated for the ability to utilize lignin as a sole carbon and energy source from compost in South Korea. Here we report the 5.11 Mb draft genome of strain AM3 with a G+C content of 56.2%, which is helpful for understanding the genetic diversity among *Ochrobactrum* spp. and the mechanism of lignin degradation.

Key words: *Ochrobactrum*, compost, genome

Lignin is a complex aromatic hetero-polymer composed of highly cross-linked phenylpropanoid units, and extremely resistant to microbial breakdown. Taking lignin degradation in consideration, white-rot and brown-rot fungi have been extensively studied, which use oxidative extracellular enzymes (lignin peroxidase, laccase, and manganese peroxidase etc.) to break down it into monomers (Taylor *et al.*, 2012). However, bacteria have been much less studied as degraders of lignin, but there are several bacteria belonging to the genera *Brucella*, *Ochrobactrum*, *Sphingomonas* etc. reported for this capacity (Cheng *et al.*, 2009; Tian *et al.*, 2014).

Compost collected in Iksan, Korea was enriched on minimal salt medium (Chen *et al.*, 2012) containing 1% kraft lignin (Sigma) under aerobic conditions at 37°C for 7 days. Colonies were isolated for the growth on lignin and the isolate was identified by its physiological and phylogenetic properties (i.e., Gram-negative stain, non-spore former, rod-shaped,

mesophilic, production of ligninolytic enzymes and 16S rRNA gene sequencing) (Cheng *et al.*, 2009). The purified isolate was maintained at -80°C in LB with 25% glycerol and publicly available in Korean Culture Center for Microorganisms (KCCM, Seoul, Korea) under KCCM 43248 of accession number.

Genomic DNA of the isolate, *Ochrobactrum anthropi* AM3, was extracted from cells which were grown aerobically at 37°C for 20 h in LB medium using DNA extraction kit (Exgene™ Cell SV, GeneAll Biotechnology Co., Ltd.) and used to construct 20 kb SMRTbell (TM) template libraries. Whole genome sequencing of *Ochrobactrum anthropi* AM3 was performed by PacBio RSII platform (Pacific Biosciences) and the determined 974,551,597 bp filtered subreads with about 190-fold coverage were assembled using hierarchical genome assembly process (HGAP, v3.0) including assembly polishing with Quiver (Chin *et al.*, 2013). This assembly generated 3 contigs (2,754,709 bp, 2,037,532 bp, and 323,461 bp) and revealed that *Ochrobactrum anthropi* AM3 had about 5.11 Mb genome with 56.2% G+C content.

Automatic annotation for *Ochrobactrum anthropi* AM3 genome

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Table 1. Genome features of *Ochrobactrum anthropi* AM3

Contig	Length (bp)	CDS	tRNA	rRNA
Contig 1	2,754,709	2,628	43	6
Contig 2	2,037,532	1,942	17	6
Contig 3	323,461	335	0	0
Total	5,115,702	4,905	60	12

was conducted with Prokka (v1.11, Victorian Bioinformatics Consortium). A total of 4,905 coding sequences (CDSs), 60 tRNA genes, and 12 rRNA genes were identified. Peroxidase, polyphenol oxidase, and oxygenase genes were also identified, which could possibly be involved in lignin degradation (Minogue *et al.*, 2014; Tobias *et al.*, 2015). Information about the genome sequence of *Ochrobactrum anthropi* AM3 offered an opportunity to understand the genetic diversity of *Ochrobactrum* spp. and the mechanism of lignin degradation.

Nucleotide sequence accession number. This whole genome shotgun project has been deposited at EMBL under accession no. PRJEB18454.

적 요

단일 탄소원과 에너지원으로 리그닌을 이용하여 성장할 수 있는 *Ochrobactrum anthropi* AM3 균주를 퇴비로부터 분리하였다. 본 연구에서는 AM3 균주로부터 56.2% G+C 함량의 약 5.11 Mb 크기 유전체 염기서열을 결정하였으며 연구 결과는 *Ochrobactrum* 속의 유전적 다양성과 리그닌 분해기작 연구를 위한 유전체 정보를 제공한다.

Acknowledgements

This research was supported by Advanced Production Technology Development Program (Project No. 316001-03), Ministry of Agriculture, Food and Rural Affairs in Republic of Korea.

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