

Genome Sequence of Pectin-Degrading *Alishewanella agri*, Isolated from Landfill Soil

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Alishewanella agri BL06^T (= KCTC 22400^T = JCM 15597^T) was isolated from landfill soil in Pohang, South Korea. *A. agri* showed the ability to degrade pectin, a structural heteropolysaccharide present in the cell wall of plants. Here we report the genome sequence of *Alishewanella agri* BL06^T, the second sequenced strain in the genus *Alishewanella*.

Pectin is a major component of plant cell walls, and its degradation, which is catalyzed by enzymes in plants, fungi, and bacteria (6, 7), is essential for the ripening of fruits and softening of plant tissues. *Alishewanella agri* BL06^T (= KCTC 22400^T = JCM 15597^T), a novel species, was isolated from landfill soil at an iron manufacturing facility in Pohang, South Korea (5). Similar to *Alishewanella jeotgali* MS1^T, which was the first sequenced *Alishewanella* strain, strain BL06^T also shows the ability to hydrolyze casein, form biofilms, and produce pellicles (3). *Alishewanella aestuarii* (9), *A. jeotgali* MS1^T (4), and *A. agri* BL06^T (unpublished data) can utilize pectin as a sole carbon source.

The *A. agri* BL06^T genome was sequenced by hybridization with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT), which contains an 8-kb paired-end library (231,590 reads) and an Illumina GA IIx genome analyzer (San Diego, CA) with a 100-bp paired-end library (37,583,717 reads). The 454 GS FLX and Illumina reads were assembled using GS assembler 2.6 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 5.0 (CLC Bio, Aarhus, Denmark). The assembled sequences showed three scaffolds that consisted of 30 contigs with 1,099.17-fold coverage. Genome annotation was performed by using the National Center for Biotechnology Information Prokaryotic Genome Automatic Annotation Pipeline (8).

The *A. agri* BL06^T genome contains 3,491,709 bp with a G+C content of 50.6%, 3,223 coding sequences (CDS), 68 tRNA genes, and 3 rRNA genes. Although the genome size of strain BL06^T is smaller than that of *A. jeotgali* MS1^T, *A. agri* BL06^T might have a 74-kb plasmid (the second scaffold containing contigs 27 to 29). The plasmid region contains 68 genes, of which 35 encode hypothetical proteins. Bacterial cells can acquire exogenous genes via horizontal gene transfer, which is essential for survival and adaptation to certain environmental conditions (1). We think *A. agri* BL06^T captured the plasmid for this reason. AGRI_30080, which was annotated as a hypothetical protein, shows 92% amino acid similarity to the pectin methyltransferase (AJE_04921) of *A. jeotgali* MS1^T, which mediates the hydrolysis of methyl ester groups of cell wall pectins (2). AGRI_19170 also shows high amino acid sequence similarity (90%) to the pectate lyase (AJE_07336) of *A. jeotgali* MS1^T. A total of 2,591 CDS were classified by using the Cluster of Orthologous Groups (COG) database (10). The most abundant group was COG category E (involved in amino acid metabolism and transport; 7.60%), followed by COG category M

(involved in cell wall structure and biogenesis and outer membrane; 6.99%). *Alishewanella* species have been isolated from various environments (4, 5, 9, 11), and the two strains whose genomes have been sequenced show differences with respect to genome size, plasmid presence, and protein abundance. The complete genome sequence of *A. agri* BL06^T will be essential in the analyses of genetic evolution and in the early stages of genetic research on *Alishewanella* species.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AKKU00000000. The version described in this paper is the first version, AKKU01000000.

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