

Genome Sequence of the Multiple- β -Lactam-Antibiotic-Resistant Bacterium *Acidovorax* sp. Strain MR-S7

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***Acidovorax* sp. strain MR-S7 was isolated from activated sludge in a treatment system for wastewater containing β -lactam antibiotic pollutants. Strain MR-S7 demonstrates multidrug resistance for various types of β -lactam antibiotics at high levels of MIC. The draft genome sequence clarified that strain MR-S7 harbors unique β -lactamase genes.**

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Antibiotics are some of the most widely prescribed drugs in modern medicine. Improper use or prolonged use of antibiotics such as in medical treatment and stock farming has led to strains of bacteria that develop resistance to antibiotics (1, 2). In general, four types of antibiotic resistance mechanism are known, i.e., production of antibiotic-degrading or -modifying enzymes (3–5), mutation of active sites (6, 7), presence of antibiotic efflux pumps (8, 9), and formation of biofilm to prevent antibiotics from penetrating (10).

Acidovorax sp. strain MR-S7 was isolated from activated sludge from the treatment of wastewater containing β -lactam antibiotics. According to 16S rRNA gene sequence analysis, we placed strain MR-S7 in the class *Betaproteobacteria*, with 97.4% similarity to the validly described species *A. temperans* strain PHL (11), and located a different clade among the 10 strains with deposited genomic data, *Acidovorax* sp. KKS102 (NC_018708), CF316 (NZ_AKJX01000236), NO1 (EU521706), and JS42 (CP000539); *A. citrulli* AAC00-1 (CP000512); *A. avenae* subsp. *avenae* ATCC 19860 (AF078759) and RS-1 (JN601517); *A. radialis* N35 (HM027578); *A. ebreus* TPSY (CP001392); and *A. delafieldii* 2AN (HM625980).

Strain MR-S7 showed high resistance to a variety of β -lactam antibiotics, for example, MICs for ampicillin, amoxicillin, cephalexin, and cefadroxil in strain MR-S7 were ≥ 500 mg/liter. In this study, the draft genome sequencing of strain MR-S7 was performed, and the genes involved in multiple- β -lactam-antibiotic-resistant activity were identified. The whole genome of strain MR-S7 was sequenced by paired-end sequencing on an Illumina HiSeq2000 sequencing system provided by the Hokkaido System Science Co., Ltd. (Sapporo, Hokkaido, Japan). This sequencing run yielded 21,966,696 high-quality filtered reads with 101-bp paired-end sequencing, providing approximately 440-fold genome coverage. Using the Velvet program with a hash length of 75 bp (12), these reads were assembled into 105 contigs and 12 scaffolds (split into 130 contigs), of which the average length was

42,811 bp. Prediction of protein-coding sequences (CDS) and annotation were performed by the Microbial Genome Annotation Pipeline (<http://www.migap.org/>), which utilizes MetaGeneAnnotator (13), RNAmmer (14), tRNAScan-SE (15), and BLAST (16). The draft genome sequence of strain MR-S7 comprised 5,007,754 bp, with a GC content of 68.3%. The genome contained 4,772 putative CDSs, 51 tRNAs, and 3 rRNAs.

Eighteen putative β -lactamase domain-containing proteins, 12 multidrug efflux pump proteins, and 8 penicillin-binding proteins were found in strain MR-S7. A protein BLAST (BLASTp) search using the NCBI database showed that the average value of the sequence identity of putative β -lactamase proteins was 70%, while the average values of the sequence identities of the multidrug efflux pump proteins and penicillin-binding proteins were 87%. The relatively low sequence identities of putative β -lactamase proteins suggested that the diverse resistance mechanisms in strain MR-S7 have not been acquired by lateral gene transfer in the recent past, but that the acquisition occurred in ancient times, and that the genes responsible for antibiotic resistance have independently evolved into strain MR-S7.

Nucleotide sequences accession numbers. The draft genome sequence of *Acidovorax* sp. strain MR-S7 has been deposited in the DDBJ/EMBL/GenBank database under accession number [BANP00000000](https://www.ncbi.nlm.nih.gov/nuccore/BANP00000000). The version described in this paper is the first version, [BANP01000000](https://www.ncbi.nlm.nih.gov/nuccore/BANP01000000).

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