Complete Genome Sequence of *Enterobacter aerogenes* KCTC 2190

Sang Heum Shin,^a Sewhan Kim,^a Jae Young Kim,^a Soojin Lee,^b Youngsoon Um,^c Min-Kyu Oh,^d Young-Rok Kim,^e Jinwon Lee,^b and Kap-Seok Yang^a

MacroGen Inc., Gasan-dong, Seoul, Republic of Korea^a; Department of Chemical and Biomolecular Engineering, Sogang University, Seoul, Republic of Korea^b; Clean Energy Research Center, Korea Institute of Science and Technology, Seongbuk-gu, Seoul, Republic of Korea^c; Department of Chemical and Biological Engineering, Korea University, Seoul, Republic of Korea^d; and Institute of Life Sciences and Resources & Department of Food Science and Biotechnology, Kyung Hee University, Yongin, Republic of Korea^e

This is the first complete genome sequence of the *Enterobacter aerogenes* species. Here we present the genome sequence of *E. aerogenes* KCTC 2190, which contains 5,280,350 bp with a G + C content of 54.8 mol%, 4,912 protein-coding genes, and 109 structural RNAs.

2,3-Butanediol is a very important chemical because of its wide commercial applications in the manufacture of butadiene (6) and butan-2-ol, aviation fuels, fumigants, moistening agents, and plasticizers and its use as an antifreeze agent and in liquid fuel (2, 4) and as an octane booster (1). 2,3-Butanediol can be produced from both hexose and pentose by several microorganisms, among them *Klebsiella oxytoca*, *Bacillus polymyxa*, *Bacillus licheniformis*, *Bacillus subtilis*, *Aeromonas hydrophila*, *Serratia marcescens* (3, 4), and *Bacillus amyloliquefaciens* (1). *Enterobacter aerogenes*, a facultative anaerobic bacterium, preferentially produces hydrogen under strictly anaerobic conditions (7) and becomes a butanediol producer with properties very similar to those of *K. oxytoca* when fermentation is stimulated by microaeration (9, 10). *E. aerogenes* KCTC 2190 was obtained from the Korean Collection for Type Culture (Daejun, South Korea).

Genomic DNA isolated from an overnight culture of *E. aerogenes* strain KCTC 2190 by the use of a DNeasy blood and tissue kit (Qiagen) was sequenced by 454 GS FLX Titanium pyrosequencing (Roche), following the manufacturer's instructions, with 25× coverage (5). Then, the 541,712 reads generated, with a length of 133,195,988 bp, were assembled using GS De Novo assembler (version 2.3; Roche). The N50 contig was 294,108 bp, and the largest contig assembled was 542,263 bp. This assembly generated 55 large (>500 bp) contigs, with a length of 5,243,714 bp. The 517,103 reads (95.45% of the total) were assembled into 11 scaffolds composed of 88 contigs, with a length of 5,243,714 bp. The N50 scaffold was 2,741,105 bp, and the average length of the scaffolds was 476,701 bp.

The order of scaffolds was determined by a similarity search among published references and confirmed by a PCR size check. Gaps both within and between scaffolds can be closed by long-range PCR (using MG Taq-HF DNA polymerase; MacroGen, Seoul, South Korea) and subsequent Sanger sequencing using an ABI 3730 capillary sequencer. The sequences from ABI 3730XL sequencing and scaffolds were completely assembled into one circular genome using Phred/Phrap/Consed software and annotated with Prokaryote Genomes Automatic Annotation Pipeline (PGAAP) software (8).

The complete genome is composed of a circular chromosome of 5,280,350 bp (54.8% G + C content), including 4,912 coding genes, 84 tRNAs, and 25 rRNAs. A total of 3,824 coding genes (77.85% of the total) have putative functions assigned on the basis of annotation.

We found the genes acetoin dehydrogenase (*budC*), acetolactate synthase (*budB*), and alpha-acetolactate decarboxylase (*budA*), a putative transcriptional regulator (*budR*), and a putative 3-hydroxybutyrate dehydrogenase (*budH*), which is involved in the production of 2,3-butanediol in the genome.

This is the first report of the genome sequence of the *E. aerogenes* species, which should provide the basis for a better understanding of its genetic background for further study. A more detailed analysis of full-genome comparisons of this and other available *Enterobacter* strains is to be included in a further publication on transcriptome analysis.

Nucleotide sequence accession number. The genome sequence of *E. aerogenes* KCTC 2190 has been deposited in NCBI GenBank under accession number [CP002824](#).

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Address correspondence to Kap-Seok Yang, ksyang@macrogen.com.

S.H.S. and S.K. contributed equally to this article.

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