

# The Genome Sequence of *Alcaligenes faecalis* NBIB-017 Contains Genes with Potentially High Activities against *Erwinia carotovora*

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***Alcaligenes faecalis* NBIB-017, a Gram-negative bacterium, was isolated from soil in China. Here, we provide the complete genome sequence of this bacterium, which possesses a high number of genes encoding antibacterial factors, including proteins and small molecular peptides.**

Received 21 February 2016 Accepted 24 February 2016 Published 7 April 2016

**Citation** Liu X, Huang D, Wu J, Yu C, Zhou R, Liu C, Zhang W, Yao J, Cheng M, Guo S. 2016. The genome sequence of *Alcaligenes faecalis* NBIB-017 contains genes with potentially high activities against *Erwinia carotovora*. *Genome Announc* 4(2):e00222-16. doi:10.1128/genomeA.00222-16.

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*Alcaligenes faecalis* is a Gram-negative bacterium found in soil and water. Some *A. faecalis* spp. are capable of degrading pesticides such as endosulfan (1, 2) and 2,4-dichlorophenoxyacetic acid (3), as well as other inorganic compounds found in wastewater (4–6), while other strains of this species can produce nonnatural amino acids (7). However, *A. faecalis* strains are widely used in today's agriculture and pharmaceutical industries (8).

Strain NBIB-017 was isolated from a rice paddy field in Hubei Province, China, in 2013. Its 16S rRNA sequence is 99.0% similar to that of *A. faecalis* NBIB-017. Whole-genome sequencing of *A. faecalis* NBIB-017 was performed using a strategy involving Solexa paired-end sequencing technology. Two libraries containing 400-bp and 750-bp inserts were constructed. Sequencing was performed with the paired-end strategy of 500-bp reads to produce 295 Mb and 320 Mb of filtered sequences, representing 147-fold coverage, with an Illumina Solexa Ix genome analyzer (Wuhan Yanxing Biotechnology Co., Ltd., Wuhan, China). The reads were assembled into 20 contigs and 21 scaffolds using the SOAP *de novo* alignment tool (<http://soap.genomics.org.cn/index.html#intro2>). The gaps within and between the scaffolds were filled by sequencing the relevant PCR products by primer walking, with the use of an ABI 3730 capillary sequencer.

The NBIB-017 genome consists of a 4,190,208-bp chromosome with a G+C content of 56.46%. The chromosome consists of 3,900 coding sequences, 5 rRNA operons, and 52 tRNAs. Genome annotation was performed using the NCBI Prokaryotic Genome Automatic Annotation Pipeline, GenBank (nonredundant), Kyoto Encyclopedia of Genes and Genomes (9), and Clusters of Orthologous Groups (10) databases for BLASTp identification (11). Four gene clusters in NBIB-017, covering 2.2% of its whole genome, are involved in antibiotic synthesis, namely, streptomycin, ansamycin, vancomycin, and novobiocin. Several degradation pathways were detected, including those in-

volving benzoate, DDT, bisphenol, fluorobenzoate, dioxin, and xylene.

**Nucleotide sequence accession numbers.** The complete sequence of *A. faecalis* NBIB-017 has been deposited in NCBI under the accession number [LNOL00000000](https://ncbi.nlm.nih.gov/nucl/LNOL00000000). The strain is available from the China Center for Type Culture Collection (Wuhan, China) under the accession number CCTCC M 2015089.

## ACKNOWLEDGMENTS

We thank Wuhan Yanxing Biotechnology Co., Ltd. (Wuhan, China) for sequencing the genome of *A. faecalis* NBIB-017.

This work was financially supported by the National Natural Science Foundation of China (31500428) and the Support Program of the Academy of Agricultural Sciences of Hubei Province (2015jzjxh04).

## FUNDING INFORMATION

This work, including the efforts of Xiaoyan Liu, was funded by the National Natural Science Foundation of China (NSFC) (31500428). This work, including the efforts of Xiaoyan Liu, was funded by the Support Program of the Academy of Agricultural Sciences of Hubei Province (2015jzjxh04).

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