

Draft Genome Sequence of Antagonistic Agent *Lysobacter antibioticus* 13-6

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***Lysobacter antibioticus* 13-6, isolated from the roots of Chinese cabbage, effectively controls the pathogens *Plasmidiophora brassicae*, *Xanthomonas oryzae* pv. *oryzicola*, *X. oryzae* pv. *oryzae*, *Xanthomonas axonopodis* pv. *dieffenbachiae*, and *Pseudomonas syringae* pv. *tabaci*. We report the first draft genome sequence of the *L. antibioticus* species in China.**

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The genus *Lysobacter* represents a source of biocontrol agents, which consisted of 16 species (1, 2). Recently, we reported that application of *L. antibioticus* 13-6 can control *brassicae* clubroot (3). Due to its tremendous potential application value, we analyzed the draft genome sequence of *L. antibioticus* 13-6.

13-6 genomic DNA was extracted from cell grown at 28°C in Luria-Bertani agar (LB) liquid cultures by using a genomic-tip 100/G kit (Qiagen GmbH, Hilden, Germany). DNA shotguns libraries were constructed using 1-kb fragments which were break-interrupted by Fisher. A TruSeq™ DNA sample prep kit—Set A (Illumina, USA), TruSeq PE cluster kit, and Illumina HiSeq2500 were used for the construction of libraries, amplification, and sequencing, respectively. A total of 11,524,134 filtered reads for the 13-6 genome were assembled into 162 contigs (N_{50} length, 60,432), with an average coverage of 40.0×, using the A5 pipeline. The genome has a G+C content of 67.14%, which is similar to the content of the strain of *L. capsici* AZ78 (4); 4,056 genes belong to homologous sequences in the NCBI nr database, in which 2,674 genes were assigned functions by using the NCBI Prokaryotic Genomes Annotation Pipeline utilizing Gene-MarkS.

The analysis showed that the genome contains genes involved in phenylalanine, lipoic acid, laurine, and hypotaurine metabolism. Betalain synthetic genes were also found in the 13-6 genome. As expected, the 13-6 genome contains a high number of genes coding for antibiotics, a property that explains its resistance to plant pathogens, specifically, tetracycline, vancomycin, β-lactam, streptomycin, novobiocin, penicillin, cephalosporin, butirosin, and neomycin.

The availability of the draft genome of *L. antibioticus* 13-6 will help elucidate the mechanism of disease prevention and will provide background knowledge for its production and application.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at GenBank under the accession no. [JMTZ00000000](https://www.ncbi.nlm.nih.gov/nuclink/JMTZ00000000).

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