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Draft Genome Sequence of the Endophytic Strain *Rhodococcus kyotonensis* KB10, a Potential Biodegrading and Antibacterial Bacterium Isolated from *Arabidopsis thaliana*

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***Rhodococcus kyotonensis* KB10 is an endophytic bacterium isolated from *Arabidopsis thaliana*. The organism showed mild antibacterial activity against the phytopathogen *Pseudomonas syringae* pv. tomato DC3000. This study reports the genome sequence of *R. kyotonensis* KB10. This bacterium contains an ectoine biosynthesis gene cluster and has the potential to degrade nitroaromatic compounds. The identified bacterium may be a suitable biocontrol agent and degrader of environmental pollutants.**

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Rhodococcus species are noted for their metabolic versatility, including degradation of chemically diverse xenobiotics and bioconversion (1, 2). Moreover, they produce indole-3-acetic acid, which is one of the most active auxins that stimulate plant growth (3). *Rhodococcus* species show antagonistic activity against human pathogens and the phytopathogens *Ceratocystis fimbriata* and *Pseudomonas syringae* pv. tomato DC3000 (1, 4, 5). Therefore, *Rhodococcus* may be an attractive genus for the bioremediation of environmental pollutants and for biocontrol in an agricultural setting (6). Endophytic bacteria are beneficial to their host plants in that they provide protection against phytopathogens and other stresses (7). In a previous study, we isolated the leaf-inhabiting endophytic bacterium KB10 from apoplastic fluid extracts from the uninfected upper leaves of *Arabidopsis thaliana* plants infected with *Pseudomonas syringae* pv. tomato DC3000; the bacterium was identified as *Rhodococcus kyotonensis* based on sequence analysis of the 16S rRNA gene (5). *R. kyotonensis* was originally isolated from soil samples in Kyoto city, Japan (8). Phylogenetic analysis using the neighbor-joining method revealed that it is closely related to *Rhodococcus yunnanensis*, a mesophilic actinobacterium (9, 10).

Genome sequencing was performed using the Illumina HiSeq 2500 platform at the National Instrument Center for Environmental Management at Seoul National University (Seoul, Republic of Korea). A total of 1,930,607,782 paired reads (151 cycles) were generated from a library, with an average insert size of approximately 433 bp, which was constructed using the TruSeq Nano LT DNA sample preparation version 2 kit. Adaptor sequence removal, quality trimming, error correction, *de novo* assembly, and scaffolding were all performed using the A5-miseq pipeline (11). The assembly contained 44 scaffolds from 1,467,368,630 reads (average length, 134.4 bp), with a G+C content of 65.2%. The total scaffold length, maximum scaffold length, and N_{50} were 5,472,710 bp, 923,597 bp, and 212,310 bp, respectively. Automatic genome annotation conducted using the RAST server (12) identified 5,152 coding sequences and 63 RNAs, 40% of which were assigned to subsystems.

Potential secondary metabolites were analyzed using analysis with antiSMASH (13) and RAST (12). *R. kyotonensis* KB10 comprised 15 gene clusters, including an ectoine biosynthesis gene cluster. Ectoine is a highly soluble molecule that provides osmoprotection in highly saline environments and has potential industrial applications (14). Furthermore, KB10 may be useful for bioremediation because it harbors genes encoding enzymes that degrade nitroaromatic compounds (15, 16). The information presented herein will enable further study of the genetic and functional characteristics of *R. kyotonensis* KB10 and its potential for biocontrol and biodegradation.

Nucleotide sequence accession numbers. The whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. LVHI00000000. The version described in this paper is version LVHI00000000.1.

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