S
oil microbial diversity is shaped in part by bacterial secondary metabolite production (1). A well-characterized example comes from Janthinobacterium (Betaproteobacteria, Oxalobacter-
aceae), a purple-pigmented chemoorganoheterotroph that is commonly found in soils (2). The characteristic pigmentation of Janthinobacterium is due to the production of violacein, an anti-
microbial compound that affects predator-prey interactions (3) and microbial-host symbioses (4). To date, only a few Janthino-
bacterium spp. have been sequenced. Despite a recent genome from lake sediments (5), most sequenced isolates come from ei-
ther extremely cold or synthetic habitats (6–8). Here, we present the draft genome of Janthinobacterium sp. KBS0711, which was enriched from never-plowed soil at the Kellogg Biological Station Long-Term Ecological Research site (9, 10).

DNA purified from a single colony was prepared with the Illumina TruSeq DNA sample prep kit using an insert size of 250 bp and sequenced on an Illumina HiSeq 2500 using 100-bp pair-end reads (Illumina, San Diego, CA). Raw FASTQ reads were pro-
cessed by removing Illumina TruSeq adaptors and the first 10 bp using Cutadapt (version 1.7.1) (11), interleaving reads using Khmer (version 1.3) (12), and quality-filtering with an average Phred score of 30 using the FASTX-toolkit (version 0.0.13, Hannon Lab [http://hannonlab.cshl.edu/fastx_toolkit/]). Coverage was normalized to 25 based on a k-mer size of 25 bp using Khmer. We removed NCBI-flagged coding regions using BWA (version 0.7.10) (13).

A total of 3,130,492 unmapped reads remained after quality filtering. We assembled the genome using Velvet (version 1.2.03) (14) with the following parameters: a k-mer size of 55, expected coverage of 18, and a coverage cutoff of 2.29. Contigs larger than 200 bp were annotated using Prokka (version 1.10) (15), and we predicted meta-

The draft assembly of Janthinobacterium sp. KBS0711 is 6.08 Mbp. It consists of 25 contigs with an N50 of 882 kbp, and a G+C content of 62.7%. Annotation detected 5,386 coding sequences, 1 rRNA, 69 tRNAs, and 1 transfer-messenger RNA (tmRNA). The 16S rRNA has 99% sequence identity to a Janthinobacterium livi-
dum isolate (NCBI accession no. NR_026365.1).

In addition to the pathway for violacein production (Vio-A-VioD), we detected genes encoding traits that are associated with violacein production, including quorum sensing (QseC-QseB) and biofilm production (BdcA, KinB-AlgB) (17–19). The genome also contains genes that may allow the isolate to contend with nutrient starvation (PhoR-PhoB) and osmotic stress (EnvZ-OmpR). Last, Janthinobacterium sp. KBS0711 contains genes related to nitrogen (urea transport, dissimilatory nitrate reduction), phosphorus (phosphonate transport), and sulfur (sulfonate transport, assimilatory sulfate reduction) metabolism, which are im-
portant for soil functioning.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. LBCO00000000. The version described in this paper is the first version, LBCO00000000.1. The code used for assembly is available online (https://github.com/LennonLab/JanthinobacteriumKBS0711/).

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