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GENOME SEQUENCES

Draft Genome Sequence of *Enterobacter* sp. Strain AD2-3, Isolated from a Postmining Site in Benguet, Philippines

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ABSTRACT The novel strain *Enterobacter* sp. strain AD2-3 was isolated from postmining soil samples collected from Antamok mine in Benguet, Philippines. Here, we report a draft of its whole-genome sequence, with predicted gene inventories supporting metal tolerance, nitrogen fixation, phosphate solubilization, and indole acetic acid production.

Various *Enterobacter* species with plant probiotic properties have been isolated (1), including those from the rhizosphere of economically important crops (2). Here, we report the draft genome sequence of *Enterobacter* sp. strain AD2-3, isolated from soil samples collected at a post-gold mine site (Antamok) in Benguet, Philippines. AD2-3 was sequenced because it is one of the components of a microbial inoculum under the trademark Anfer (Antamok biofertilizer) being developed as part of the MykoPlus biofertilizer technology (http://www.pcaarrd.dost.gov.ph/home/portal/index.php/quick-information-dispatch/2435-beneficial-microorganisms-makes-soil-healthier-and-increases-yield) for the revegetation of post-gold mine sites in the Philippines (3, 4). The soil sample was collected at 16°23′58″N, 120°39′45″E at a depth of 5 to 10 cm along the road and not attached to any plant or root system.

AD2-3 was isolated by spreading 0.1 ml of diluted soil solution on Ashby-sucrose agar (5), mannitol agar (6), and Burk's medium (7), and each was incubated at 28 to 30°C for 2 to 3 days. The colonies of bacteria that grew on all media were purified on Dobereiner's medium (8, 9), followed by National Botanical Research Institute Phosphate growth medium (10) for 2 to 3 days of incubation each at 28°C. Single-colony isolates were streaked for at least 5 rounds of purification, generating isolate AD2-3. AD2-3 was grown in 3 ml nutrient broth at 28°C with shaking at 120 rpm for 16 h, and genomic DNA (gDNA) was purified using the KingFisher cell and tissue DNA kit (Thermo Fisher Scientific, Waltham, MA), according to the manufacturer's protocol. The DNA library was prepared using a Nextera XT library kit (Illumina, San Diego, CA) and sequenced on the MiSeq platform using the 600-cycle V3 reagent kit at the Philippine Genome Center. Quality checking was performed with FastQC version 0.11.7 and adapter trimming with Trimmomatic version 0.36.5 (11). The trimmed reads were *de novo* assembled using SPAdes version 3.13.0 (12). Gene prediction was performed using Prokka version 1.13 (13) and the NCBI PGAP version 4.8 (14). Genus identity was determined by BLAST (15) alignment of the predicted 16S rRNA gene sequence against the SILVA database (16). The genome-wide average nucleotide identity (gANI) and alignment fraction (AF) using the Microbial Species Identifier (MiSI) calculator employed in IMG/M-ER (17) were used to determine the relatedness of AD2-3 to the endophytic *Enterobacter* sp. strain DC3 (18), the most similar genome identified by LASTZ version 1.3.2 (19). Strain novelty was verified by the digital DNA-DNA hybridization (dDDH)

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score using the Genome-to-Genome Distance Calculator version 2.1 (20). All programs were run with default parameters, unless otherwise noted.

The AD2-3 genome has an ANI of 94.27% (AF, 0.89) and dDDH of <70% with the DC3 genome, whereas the most closely related type strain, *E. asburiae* ATCC 35953, has an ANI of 94% (AF, 0.58). Paired-end sequencing yielded 627,045 reads (22× coverage). The draft genome is 4,639,072 bp in 16 contigs (N_{50}, 574,736 bp) and has a G+C content of 55%. Genome annotation detected 4,293 coding sequences, 13 rRNA genes, 65 pseudogenes, and 74 tRNAs. The genome contains gene inventories supporting rhizosphere processes and having plant growth-promoting properties (21–23). An aryl polyene cluster for protection against reactive oxygen species (24), a homoserine lactone cluster for quorum sensing (25), and genes for Fe(II/III) (*efe*) acquisition (26) were identified. Genes were also detected for indole acetic acid production (*iaa* and *ipdC*), phosphate solubilization (*bgl* and *ybg*), and nodulation and atmospheric nitrogen fixation (*nif* and *nod*) (1).

Data availability. The raw reads were deposited at the NCBI Sequence Read Archive with accession number SRR8723068. The assembled draft genome sequence was deposited in DDBJ/ENA/GenBank under accession number SOPQ00000000. The version described in this paper is the first version.

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