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GENOME SEQUENCES

Draft Genome Sequence of *Enterobacter asburiae* NCR1, a Plant Growth-Promoting Rhizobacterium Isolated from a Cadmium-Contaminated Environment

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ABSTRACT *Enterobacter asburiae* NCR1 is a plant growth-promoting rhizobacterium isolated from the rhizosphere of *Carpobrotus rossii*. We report the draft genome sequence of *E. asburiae* strain NCR1, which revealed many genes facilitating beneficial interactions with plant hosts.

The genus *Enterobacter* comprises more than 20 species that are widely distributed through various environments. Some species of *Enterobacter* can enhance plant growth by increasing the availability of nutrients and water and synthesizing plant growth-promoting hormones (1, 2). *Enterobacter asburiae* NCR1 was previously isolated from the rhizosphere of *Carpobrotus rossii* grown in a cadmium-contaminated environment (3).

E. asburiae NCR1 was grown at 27°C for 16 h in Luria-Bertani broth, and total genomic DNA was extracted using the Bioline Isolate II genomic DNA kit and converted to sequencing libraries using the Nextera XT DNA library prep kit (Illumina) with 1 ng of input DNA, according to the manufacturer's instructions. The quality and concentration of the genomic DNA were assessed using an Invitrogen Qubit 3.0 fluorometer. The libraries were sequenced on an Illumina MiSeq instrument using a MiSeq v.3 reagent kit (600 cycles), which generated 919,623 reads of 300-bp paired-end reads. The sequence reads were trimmed to a Phred threshold quality score of 20 using Trimmomatic v.0.36.6 (4), and assembly was performed using SPAdes v.3.12.0 (5), both on Galaxy Australia (6). The total length of the genome sequence of *E. asburiae* NCR1 was 4,546,475 bp, with a G+C content of 56.08%. The final number of contigs was 15, with an N_{50} value of 2,597,842 bp, and the final genome coverage was 50×. Default parameters were used unless otherwise stated.

The annotation of the assembled genomic sequence was performed using the Prokaryotic Genome Annotation Pipeline (PGAP) v.4.10 of the National Center for Biotechnology Information (NCBI) (7). The genome sequence of *E. asburiae* NCR1 was closely related to that of *E. asburiae* GN04222 with an average nucleotide identity (ANI) of 98.06%, as calculated by a JSpeciesWS v.3.8.2 analysis (8). A total of 4,237 genes were identified, with 4,240 coding sequences (CDS), including 87 RNA genes. The RNA genes comprised 4 5S rRNAs, 1 partial 16S rRNA, 1 partial 23S rRNA, and 73 tRNA genes.

The annotated genome sequence revealed several genes pertinent to plant-microbe interactions, including those involved in auxin synthesis (*iaa* and *ipdC*) and phosphorus metabolism (*phoP*). Bacterially derived auxin can enhance the growth of plants, while the catabolism of phosphates may improve phosphate availability to the host plants (9).

Heavy metal resistance to Zn, Cd, and Pb is conferred through *zntA*, which acts as a P-type ATPase pump (10) and is suggestive of this strain's ability to survive in challenging environments. This draft genome sequence of *E. asburiae* NCR1 could provide

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valuable information regarding the plant growth-promotive properties and heavy metal resistance and tolerance of this strain.

Data availability. The *E. asburiae* NCR1 whole-genome sequencing project has been deposited at GenBank under accession number JAAAJX000000000, BioProject accession number PRJNA600757, and BioSample accession number SAMN13831070. The raw sequences were deposited in the Sequence Read Archive under accession number SRR14460571.

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