



# Complete Genome Sequence of Hydrocarbon-Degrading Halotolerant *Acinetobacter radioresistens* DD78, Isolated from the Aconcagua River Mouth in Central Chile

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**ABSTRACT** *Acinetobacter radioresistens* strain DD78 (= CCUG 69565) is a soil hydrocarbon-degrading and biosurfactant-producing bacterium isolated from chronically crude oil-polluted soil of the Aconcagua River mouth in Chile. The 3.25-Mb *A. radioresistens* DD78 genome (41.8% GC content) was completely sequenced, with 4 replicons, 2,970 coding sequences, and 77 tRNAs.

**A** *Acinetobacter* species are aerobic Gram-negative coccobacilli present in soil, freshwater, sediment, polluted environments, and clinical samples (1, 2). *A. baumannii*, *A. venetianus*, and *A. oleivorans* degrade crude oil and alkanes (3, 4). *A. radioresistens* and *A. calcoaceticus* synthesize biosurfactants (e.g., alasan), improving hydrocarbon bioavailability (5, 6). Here, we report the complete genome sequence of *A. radioresistens* DD78 (CCUG\_69565), a soil hydrocarbon-degrading and biosurfactant-producing bacterium from crude oil-polluted soil of the Aconcagua River mouth in Central Chile, which was isolated using enrichment in diesel (0.1% [vol/vol]) in Bushnell Hass mineral medium (7). Strain DD78 grew on *n*-hexadecane and diesel (7). DNA was extracted from Trypticase soy broth (TSB)-grown cells as described (8) and was purified using a Zymo Research DNA Clean & Concentrator-100 kit. Next-generation sequencing was performed using a PacBio Sequel v3 platform (Uppsala Genome Center, Sweden) with a SMRTbell library (average 20-kb insert library), obtaining 100,261 reads with an average length of 17,616 bp (raw read  $N_{50}$ , 24,564 bp). The PacBio reads were trimmed and assembled into 5 contigs using SMRTLink v5 and the Hierarchical Genome Assembly Process v4.0 (HGAP4.0) with default parameters (9) and an expected 3.2-Mb genome size based on *Acinetobacter* genome sizes (10). The 5 contigs were reduced to 4 contigs with dotplot analysis using Gepard v1.40 with default settings (11). The DD78 genome (41.8% GC content, 246 $\times$  coverage) consists of a 3,009,347-bp circular chromosome and three putative circular plasmids, pAr1 (88,584 bp), pAr2 (80,103 bp), and pAr3 (69,207 bp). Gene functional annotation using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.6 (12) identified 2,970 coding sequences, 77 tRNAs, 7 rRNA operons, 4 noncoding RNAs (ncRNAs), and 1 CRISPR array. The Comprehensive Antibiotic Resistance Database (CARD) v3.0.0 (13) identified one antibiotic resistance gene (E3H47\_05270), possessing 96.7% identity with oxacillinase OXA-239, from a clinical *A. baumannii* isolate (14). Genes encoding alasan protein components (*alnA*, *alnB*, and *alnC*: E3H47\_11220, E3H47\_09040, and

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E3H47\_05485, respectively), proteins for osmoprotectant glycine betaine synthesis (*betIBA*: E3H47\_10580, E3H47\_10585, and E3H47\_10590), and the osmoprotectant transporters osmo-dependent choline transporter, sodium/proline symporter, and aspartate/alanine antiporter (E3H47\_06620, E3H47\_06825, and E3H47\_10585, respectively) were identified (>30% identity) with BLASTP using the Uniprot-KB/Swiss-Prot database. Arsenic and heavy metal (copper, cobalt, and cadmium) resistance genes are in pAr1. Catabolic genes encoding an alkane monooxygenase (*alkM*, E3H47\_10210), a rubredoxin NAD(H) reductase/rubredoxin system (E3H47\_10395 and E3H47\_10400), and the catechol (*catBCA*: E3H47\_07710, E3H47\_07715, and E3H47\_07720) and benzoate catabolic pathways (*benABCDE*: E3H47\_07725, E3H47\_07730, E3H47\_07735, E3H47\_07740, and E3H47\_07745) are chromosomal. Comparative complete 16S rRNA gene sequence analysis showed a close relationship (99.7% identity) with *A. radioresistens* FO-1<sup>T</sup> (CIP 103788<sup>T</sup>; GenBank accession number [X81666](#)) and <97.5% identity with other *Acinetobacter* species (15). Genome sequence analysis using average nucleotide identity based on BLAST (ANIb) (16) and using JSpeciesWS v3.0.2 (17) with *A. radioresistens* CIP 103788<sup>T</sup>, *A. Iwoffii* ATCC 9957<sup>T</sup>, and *A. tandonii* CIP 107469<sup>T</sup> showed ANIb values of 98.9%, 74.1%, and 73.6%, respectively, indicating that strain DD78 most likely belongs to the species *A. radioresistens*. The genome sequence of *A. radioresistens* DD78 provides essential data on alkane degradation, salt resistance, and biosurfactant production.

**Data availability.** The *Acinetobacter radioresistens* DD78 genome sequences have been deposited in DDBJ/ENA/GenBank under the accession number [GCA\\_005519305](#) and the SRA accession number [SRX5548971](#). The version discussed here is the first version. The BioProject number for the publicly available raw data is [PRJNA528312](#).

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