ASM | Microbiology Resource Announcements

| Applied and Industrial Microbiology | Announcement

Complete genome sequence of *Rhodococcus erythropolis* strain ICBD2, isolated from hydrocarbon-polluted coastal sediments in Central Chile

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ABSTRACT *Rhodococcus erythropolis* strain ICBD2 (=CCUG 74281) is a hydrocarbon-degrading bacterium isolated from chronically hydrocarbon-polluted saline coastal sediments from the Valparaíso Region, Central Chile. The complete genome sequence of *R. erythropolis* ICBD2 (62.3% GC content) comprises a 6.35 Mb circular chromosome and a 387 kb linear plasmid, with 6,196 coding sequences.

KEYWORDS *Rhodococcus erythropolis*, genome, hydrocarbon, Central Chile

Rhodococcus genus (*Actinomycetota* phylum) comprises aerobic, non-motile, metabolically versatile Gram-positive bacteria that degrade persistent organic pollutants and synthesize antimicrobial molecules (1–4). Environmental bacteria possess diverse adaptation mechanisms to oxidative and saline stress (5–7). This study presents the complete genome sequence of the hydrocarbon-degrading bacterium *Rhodococcus erythropolis* ICBD2 (=CCUG 74281), isolated from a chronically hydrocarbon-polluted saline coastal sediment at the Las Salinas site (33.0011° S, 71.5469° W) in Viña del Mar (Valparaíso Region, Central Chile). Strain ICBD2 was isolated in 2016 after two successive enrichments of a sediment sample (1 g, 4 m depth) in Bushnell–Haas (BH) mineral medium (20 mL) using diesel (1% vol/vol) and acetate (10 mM) as sole carbon/energy sources without agitation. Thereafter, the enrichment culture without prior dilution (100 µL) was plated onto BH agar containing acetate (10 mM) as sole carbon/energy sources; a single colony was isolated and characterized. Strain ICBD2 grew in BH or low-phosphate Tris-buffered mineral salt media on *n*-dodecane, *n*-tetradecane, *n*-hexadecane, *n*-eicosane, and diesel as sole carbon/energy sources (30°C).

Genomic DNA was extracted from a single colony grown on tryptic soy agar using a modified Marmur procedure (8). An Illumina standard genomic paired-end library, prepared from DNA using an optimized protocol (Eurofins Genomics, Konstanz, Germany) with standard Illumina adapters, was Illumina-sequenced (NovaSeq-6000-platform/flow-cell S2), achieving 22,030,486 paired-end reads/151 bp average length (3,326 Mb). Quality was assessed using FastQC (v0.11.9) (9). DNA was complementary sequenced using the Oxford Nanopore Technologies MinION Mk101B sequencer. The library was prepared with DNA without pre-treatment and Rapid-Barcoding-Kit (vR9) (SQK-RBK004) and Nanopore-sequenced (48 h) using a flow cell FLO-MIN106 (vR9.4). Base calling was done (Guppy, v4.0.14), obtaining 157,563 long reads/10,937 bp average length. The hybrid assembly using SPAdes (v3.13.1) with read error correction (10) yielded a single circular chromosome (6,351,314 bp/62.3% GC) and a linear plasmid (387,366 bp/61.1% GC), containing inverted repeats at the ends. The overlaps were identified by BLASTN analysis of the ends against the genome sequence. The overlap of one of the chromosome ends was trimmed manually using UGENE (v36). The *dnaA* gene

Editor Silvia T. Cardona, University of Manitoba, Winnipeg, Manitoba, Canada

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The authors declare no conflict of interest.

See the funding table on p. 3.

Received 31 March 2026
Accepted 11 May 2026
Published 29 May 2026

located by TBLASTN analysis of the Unicycler (v0.4.8) start gene database was chosen as the start gene to re-orient the chromosome (UGENE v36). Genome completeness (CheckM2, v1.0.2) was assessed (11). Genes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (v6.10) (12). All software was utilized with default parameters unless otherwise noted. The ICBD2 genome (100% completeness) contains 6,196 coding sequences, 54 tRNA genes, and 15 rRNA genes.

Comparative whole-genome sequence analyses with the Type Strain Genome Server platform (13) and Pyani-plus (v.1.0.0) (14) identified strain ICBD2 as *Rhodococcus erythropolis*; 16S rRNA gene identity (100%), digital DNA–DNA hybridization ($d4 = 89.3\%$), and average nucleotide identity (ANIb = 98.5%) with *Rhodococcus erythropolis* NBRC 15567^T.

BLAST gene function analyses using the UniProt-KB/Swiss-Prot database (>30% identity) identified genes associated with alkane degradation and oxidative stress response, including five *alkB* genes encoding alkane monooxygenase (≥69% identity with *Rhodococcus* spp. *alkB* genes, ACV96D_03880/ACV96D_10690/ACV96D_26645/ACV96D_11635/ACV96D_31060), *katG* gene encoding catalase-peroxidase (ACV96D_05890), *katA* (ACV96D_02200), and *katE* (ACV96D_28135) genes encoding catalases, and *sod* genes encoding superoxide dismutase ([Mn]SodA/ACV96D_00775, [Fe]SodB/ACV96D_23855, [Cu-Zn]SodC/ACV96D_07375). The *Rhodococcus erythropolis* ICBD2 genetic repertoire highlights its potential for hydrocarbon biodegradation.

ACKNOWLEDGMENTS

The authors acknowledge Timur Tunovic for DNA extraction and Las Salinas S.A. for providing access to the Las Salinas site and facilitating sediment sampling in the frame of a collaborative agreement between Las Salinas S.A. and Universidad Técnica Federico Santa María, aimed at promoting scientific research on environmental remediation and the sustainable management of impacted industrial sites.

This study was supported by ANID PhD scholarships (numbers 21211723 [X.B.-M.] and 21242707 [R.E.D.], PUCV [X.B.-M.], USM [X.B.-M.], and PIIC 055/2021 [X.B.-M.]); PhD scholarships; ANID Master scholarship (2230193 [T.E.-C.]); and Agencia Nacional de Investigación y Desarrollo ANID-Milenio-NCN2023_054 (M.S., X.B.-M., R.E.D., T.E.-C., and R.O.), Fondo Nacional de Desarrollo Científico y Tecnológico Fondecyt (1250809 and 1200756 [M.S., X.B.-M., R.E.D., and T.E.-C.]) (http://www.anid.cl), Las Salinas S.A. (M.S., R.O., X.B.-M., R.E.D., and T.E.-C.), and USM (M.S., X.B.-M., and R.E.D.) (http://www.usm.cl) grants. F.S.-S., D.J.-L., and E.R.B.M. were supported by the "Genomics and Proteomics Research on Bacterial Diversity" Culture Collection University of Gothenburg (CCUG) grant. The authors acknowledge the support of the National Genomics Infrastructure/Uppsala Genome Center and UPPMAX for providing assistance in massive parallel sequencing and computational infrastructure, funded by RFI/VR and Science for Life Laboratory, Sweden. This research was supported by the supercomputing infrastructure of the NLHPC (CCSS210001). The CCUG (www.ccug.se) is supported by the Department of Clinical Microbiology, Sahlgrenska University Hospital, and the Sahlgrenska Academy of the University of Gothenburg.

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FUNDING

Funder	Grant(s)	Author(s)
Agencia Nacional de Investigación y Desarrollo	ANID-Milenio-NCN2023_054	Ximena Báez-Matus Roberto E. Durán Roberto Orellana Teresa Esparza-Correa Michael Seeger
Fondo Nacional de Desarrollo Científico y Tecnológico	Fondecyt 1250809	Ximena Báez-Matus Roberto E. Durán Teresa Esparza-Correa Michael Seeger
Fondo Nacional de Desarrollo Científico y Tecnológico	Fondecyt 1200756	Ximena Báez-Matus Roberto E. Durán Teresa Esparza-Correa Michael Seeger
LAS SALINAS S.A.	Bioremediation Studies	Ximena Báez-Matus Roberto E. Durán Roberto Orellana Teresa Esparza-Correa Michael Seeger
CCUG	Genomics and Proteomics Research on Bacterial Diversity	Francisco Salvà-Serra Daniel Jaén-Luchoro Edward R. B. Moore

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Daniel Jaén-Luchoro, Data curation, Investigation, Methodology, Validation, Writing – review and editing | Edward R. B. Moore, Conceptualization, Data curation, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Writing – review and editing | Michael Seeger, Conceptualization, Formal analysis, Funding acquisition, Investigation, Project administration, Resources, Supervision, Validation, Visualization, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

The complete genome sequence of *Rhodococcus erythropolis* ICBD2 has been deposited in DDBJ/ENA/GenBank under accession number JBSDZJ000000000. The genome sequence described in this paper is the first version, BioProject PRJNA1309126. The raw sequencing reads are deposited and publicly available at the Sequence Read Archive, under accession numbers SRR35078506 (MiniON) and SRR35078507 (Illumina).

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