



Draft Genome Sequences of the 1,2-Dichloropropane-Respiring *Dehalococcoides mccartyi* Strains RC and KS

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ABSTRACT *Dehalococcoides mccartyi* strains RC and KS respire toxic 1,2-dichloropropane to environmentally benign propene. Their genomes were sequenced with Ion Torrent technology, assembled, and annotated. The draft genomes of strains RC and KS were 1.50 and 1.49 Mb in size and carried 1,653 and 1,671 genes, respectively.

D*ehalococcoides mccartyi* strains RC and KS conserve energy and produce innocuous propene and inorganic chloride from the dichloroelimination of 1,2-dichloropropane (1,2-D), a chlorinated aliphatic hydrocarbon regulated to less than 5 ppb in groundwater (1). The 1,2-D dechlorinating *D. mccartyi* strains RC and KS possess a 1,2-D reductive dehalogenase (RDase) gene, *dcpA* (2), yet share >99% 16S rRNA gene sequence identity with *D. mccartyi* strains that cannot grow on 1,2-D. To support comparative genome and trait analyses of *D. mccartyi* strains, we prepared draft genome sequences of strains RC and KS, which were identified as the key 1,2-D dechlorinators in enrichment cultures comprising strains RC and KS, respectively.

Cultures of RC and KS were derived from sediment samples collected from the Red Cedar River in Okemos, Michigan, and the King Salmon River in Alaska, respectively (3). Antibiotic treatment and continuous transfers to completely synthetic, defined mineral salts medium amended with 1,2-D as the electron acceptor and hydrogen as the electron donor resulted in highly enriched bacterial communities dominated by *D. mccartyi* (1–3). DNA was extracted from 10⁹ *D. mccartyi* cells by using a PowerWater kit (Mo Bio, Qiagen, Venlo, Netherlands) and treated with RNase I (Sigma-Aldrich, St. Louis, MO, USA). Sequencing libraries were prepared using an Ion Xpress Plus fragment library kit and an Ion Xpress Template 200 kit (Thermo Fisher Scientific, Waltham, MA, USA) and sequenced using an Ion 316 chip kit on the Ion Torrent PGM sequencer (1 × 200-bp libraries). A total of 3,640,282 and 4,501,960 reads passed quality control (average Phred score, ≥20; minimum read length, 50 nucleotides [nt]) with average read lengths of 148.0 ± 79.4 and 176.4 ± 65.2 nt for strains KS and RC, respectively. A random subsample of 600,000 reads from each consortium metagenome was assembled using Newbler v2.6 (default settings). Totals of 45 and 23 contigs were generated for strains RC and KS, respectively. Contigs failing to align to genomes of representative *Dehalococcoidia* strains were excluded, and remaining contigs were scaffolded with SIS software (default settings) (4) using the genome of *D. mccartyi* strain DCMB5 as a reference (99.0 and 99.6% genomic average nucleotide identity against strains RC and KS, respectively). The final draft genomes of strains RC and KS were assembled into 25 and 23 contigs totaling 1,502,842 and 1,485,739 bp, with *N*₅₀ values of 210,101 and 268,024 bp and G+C contents of 47.17% and 47.23%, respectively.

Genome annotation using the RAST server (5) identified 1,653 and 1,671 gene

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sequences for strains RC and KS, respectively. A total of 46 tRNA genes were detected, along with single copies of the 5S, 16S, and 23S rRNA genes, which shared 99 to 100% nucleotide identity to rRNA genes in other *D. mccartyi* strains. The 16S rRNA genes were detected within a distinct contig separate from the colocated 23S and 5S rRNA genes. The draft genomes of strains RC and KS contained 38 and 31 putative RDase genes, respectively, 25 of which possessed cognate RDase B genes. With the exception of *dcpA*, all RDase genes were determined to be orthologs of known *D. mccartyi* genes, including *pcbA4*, implicated in reductive dechlorination of polychlorinated biphenyls (6). The genomes of strains RC and KS expand the sequence space of organohalide-respiring *Chloroflexi* spp. and knowledge of the genetics underlying 1,2-D dechlorination.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession numbers [QGLD00000000](#) and [QGLC00000000](#). The versions described in this paper are versions QGLD01000000 and QGLC01000000. The raw sequence data are available within the Sequence Read Archive under the accession numbers [SRR7653600](#) and [SRR7653601](#).

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