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Draft Genome Sequence for *Ralstonia* sp. Strain OR214, a Bacterium with Potential for Bioremediation

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***Ralstonia* sp. strain OR214 belongs to the class *Betaproteobacteria* and was isolated from subsurface sediments in Oak Ridge, TN. A member of this genus has been described as a potential bioremediation agent. Strain OR214 is tolerant to various heavy metals, such as uranium, nickel, cobalt, and cadmium. We present its draft genome sequence here.**

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Ralstonia spp. are Gram-negative, nonfermentative, rod-shaped bacteria that are ubiquitous in water and soil (1). These bacteria are able to live in oligotrophic environments and thrive under harsh environmental conditions (2). *Ralstonia* spp. have been shown to have the capability to biodegrade multiple organic compounds, including toxic aromatic hydrocarbons (3, 4), carcinogenic groundwater pollutants, chlorophenol compounds from pesticides, nitroaromatics, and quinoline compounds from manufacturing industries (5). *Ralstonia* spp. are candidates for bioremediation, as they offer several advantages, including the ability to break down a variety of organic compounds, and they may have potential for widespread environmental use due to their oligotrophic nature. *Ralstonia* spp. have been used for the remediation of toluene from groundwater in South Carolina (6).

Ralstonia sp. strain OR214 was isolated from subsurface sediments from the Field Research Center (FRC) in Oak Ridge, TN, which were acidic and contaminated with heavy metals and organic pollutants (7). *Microbacterium laevaniformans* strain OR221, another bacterium tolerant to metals, nitrate, and low pH conditions, also isolated from the FRC site, recently had its genome sequence determined (8). Strain OR214 is tolerant to high concentrations of heavy metals, such as up to 500 mM of nitrate, 200 μM of uranium, 500 μM of nickel, 50 μM of cobalt, and 50 μM of cadmium, and to a lowest pH of 3.5 (7). We generated the draft genome sequence of strain OR214 to gain insights into its physiology.

Draft genome sequence data for strain OR214 were generated using a combination of 454 FLX (9) and Illumina MiSeq (10) technologies with single-end and 500-bp paired-end libraries, respectively. The 454 data consisted of 595,223 reads and generated 194,042,698 bp. After quality trimming of Illumina data (CLC Genomics Workbench, version 5.5.1), there were 571,527,000 bp of sequence data, with an average read length of 132 bp. Trimmed Illumina reads were assembled with CLC Genomics Workbench, and consensus sequences were fragmented into 1.5-kbp overlapping fake reads using the fb_dice.pl script from the FragBlast module (http://www.clarkfrancis.com/codes/fb_dice.pl). The Newbler application (version 2.6, 454; Life Sciences) was used to assemble the fragmented Illumina consensus and 454 reads into 46 large (≥500 bp) contigs, with a total genome size of 5.4 Mb. The N_{50} contig size is 321,662 bp, with the largest contig being 632,308 bp, and the genome has an overall estimated G+C content of 63.4%.

The draft genome was annotated at the Joint Genome Institute (JGI) Integrated Microbial Genomes (IMG) database and comparative analysis system (11), which predicted 5,305 candidate protein-encoding gene models for *Ralstonia* sp. OR214. A number of predicted heavy metal-sensing proteins, heavy metal-translocating efflux pumps, and monooxygenase genes potentially involved in the breakdown of aromatic compounds were identified in the genome, which may facilitate its resistance in harsh environments. Genome sequences for *Ralstonia* sp. 12D and 12J, which were resistant to high concentrations of heavy metals, are also available through IMG. The strain OR214 draft genome sequence will allow for the comparison of biodegradation genes across different strains and contribute toward bioremediation research.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. APMQ00000000. The version described in this paper is the first version, accession no. APMQ00000000.

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For strain and DNA requests, please contact A.B.

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