Draft Genome Sequence of *Leucobacter chromiiresistens*, an Extremely Chromium-Tolerant Strain

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Here we present the draft genome of *Leucobacter chromiiresistens*. This is the first genome sequence of an organism belonging to the genus *Leucobacter*. *L. chromiiresistens* was sequenced due to its capability to tolerate up to 300 mM Cr(VI) in the medium, which is so far a unique feature for microorganisms.

Organisms belonging to the genus *Leucobacter* are Gram-positive bacteria. *Leucobacter* species have been isolated from various habitats, including activated sludge from chromium-contaminated wastewater, uncontaminated soil, nematodes, food, and air (3, 6–8, 10, 11). *Leucobacter chromiiresistens* was isolated from a soil sample during a series of experiments with the ultimate goal of isolating chromate-resistant bacteria. Within the genus *Leucobacter*, there are several strains reported to be resistant against moderate chromate concentrations of up to 18 mM. *L. chromiiresistens* established a higher resistance than every other species of the genus and is so far the only organism described as being able to resist Cr(VI) concentrations of up to 300 mM (12; G. Sturm et al., unpublished data). Further investigation of the strain revealed a multitude of resistance mechanisms, including Cr(VI) reduction and chromate stress-induced biofilm formation. Since there is no genetic information available and no genetic system established for *Leucobacter*, the elucidation of the genome sequence will provide deeper insights into the molecular mechanisms that establish high-level chromium tolerance of *L. chromiiresistens*. Furthermore, it might provide a basis for the biotechnological usage of the organism or its resistance mechanisms for remediation of chromium-contaminated field sites.

DNA preparation, genome sequencing, and draft assembly. Genomic DNA from *Leucobacter chromiiresistens* was isolated using standard techniques based on the method of Marmur (5). Sequencing was performed using a combination of Illumina and 454 technologies (2, 4). In total, the Illumina data set contained 29 million paired-end reads with an insert length of 300 bp. Initial assembly of the Illumina reads was performed using Velvet (14) with a k-mer length of 29, resulting in an L50 of 8,470 bp. In an approach similar to that of Wurm et al. (13), the assembled Illumina contigs were split into fragments of 300 bp length with a 200-bp overlap with EMBOSS Splitter (9). These virtual reads were combined with the 454 raw data and assembled using Newbler 2.5.3 (Roche; minimum overlap identity [mi], 90; minimum overlap length [ml], 40). 454 data consisted of 255,378 sequences with 161,077 (true) paired-end reads and an average read length of 361 nucleotides. The assembled sequence resulted in 29 scaffolds with a total length of 3,373,426 bp, of which 97.2% were contained in the longest scaffold (GC content, 64.23%). In total, 228 gaps remained, 66% of them falling into the range below 1,000 bp and accounting for 8.8% of the total amount of bases. Automated annotation was performed using the RAST annotation server (1) and Geneious v5.4 software. The draft genome harbors 2,639 protein-coding sequences and contains 41 tRNA genes.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AGCW00000000. The version described in this paper is the first version, AGCW01000000.

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REFERENCES