

Draft Genome Sequence of *Sinorhizobium meliloti* CCNWSX0020, a Nitrogen-Fixing Symbiont with Copper Tolerance Capability Isolated from Lead-Zinc Mine Tailings

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***Sinorhizobium meliloti* CCNWSX0020 was isolated from *Medicago lupulina* plants growing in lead-zinc mine tailings, which can establish a symbiotic relationship with *Medicago* species. Also, the genome of this bacterium contains a number of protein-coding sequences related to metal tolerance. We anticipate that the genomic sequence provides valuable information to explore environmental bioremediation.**

Sinorhizobium meliloti is a Gram-negative soil-dwelling bacterium which can interact with *Medicago*, *Melilotus*, and *Trigonella* species by inducing the formation of root nodules, within which *Sinorhizobium meliloti* converts dinitrogen gas into ammonia, a form of nitrogen that can be used by the plant (3, 8). Recent studies reported that rhizobia can tolerate high concentrations of heavy metals (5, 11). Rhizobia can provide nitrogen sources to leguminous plants growing in heavy-metal-polluted soil and increase their biomass. These properties of metal resistance and the ability to promote plant growth in metal-contaminated soils make these microbes one of the most suitable choices for bioremediation studies. Hence, the genetic characterization of *Sinorhizobium meliloti* was studied to elucidate the basis of resistant mechanisms involved in metal stress adaptation. The first published complete genome sequence of a *Sinorhizobium* species was that of *Sinorhizobium meliloti* 1021, which has a 3.65-Mb chromosome, a 1.35-Mb plasmid (pSymA), and a 1.68-Mb plasmid (pSymB) (2, 4, 6). Other complete genome sequences of *Sinorhizobium* were also published in recent years, namely, *Sinorhizobium medicae* WSM419, *Sinorhizobium meliloti* SM11 (10), *Sinorhizobium meliloti* AK83, and *Sinorhizobium meliloti* BL225C (7). However, there is no report that these bacteria contain a heavy-metal-resistant gene. Therefore, we anticipate that the genome sequence of *Sinorhizobium meliloti* CCNWSX0020, isolated from mine tailings, can provide additional valuable insights into environmental remediation and the diversity of *Rhizobium* species.

A highly pure genomic DNA sample of *Sinorhizobium meliloti* CCNWSX0020 was sequenced with the 454 GS FLX sequencer (9), resulting in 7,001,588 bases and representing a 22-fold coverage of the genome. Sequences were assembled using GS De Novo Assembler (Newbler) version 2.5.3, resulting in a total of 233 contigs (length of each sequence was >500 bp; average length, 30,288 bp). All of the assembled contigs were annotated using the RAST Server (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). The metabolic pathways were examined through the use of the Kyoto Encyclopedia of Genes and Genomes (KEGG) database.

The draft genome sequence of *Sinorhizobium meliloti* CCNWSX0020 was approximately 7.001 Mb in length, which is larger than the genome of *Sinorhizobium meliloti* 1021. The ge-

nome of strain CCNWSX0020 has a G+C content of 59.9%. There was a total of 7,086 genes, including 6 rRNA genes, 47 tRNA genes, and 7,033 protein-coding sequences (CDSs), within the genome of *Sinorhizobium meliloti* CCNWSX0020. Of the predicted CDSs, 6,206 are similar to genes found in *Sinorhizobium meliloti* 1021. Moreover, there are 464 subsystems represented in the genome.

Additionally, *Sinorhizobium meliloti* CCNWSX0020 carried a number of predicted protein-coding genes involved in resistance to copper: two operons encoding a putative copper tolerance protein, two encoding a putative multicopper oxidase, one encoding a blue copper oxidase CueO precursor, six coding sequences encoding putative copper-translocating P-type ATPases with a typical cysteine-proline-cysteine (CPx) metal binding motif in the sixth transmembrane helix, one encoding the copper homeostasis protein CutE, and one encoding the cytoplasmic copper homeostasis protein CutC. These unusual features may contribute to the heavy metal resistance of strain CCNWSX0020.

Nucleotide sequence accession numbers. The draft genome sequence shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number **AGVV00000000**. The version described in this paper is the first version, AGVV01000000.

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