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GENOME ANNOUNCEMENT

Heavy-Metal Resistance of a France Vineyard Soil Bacterium, *Pseudomonas mendocina* Strain S5.2, Revealed by Whole-Genome Sequencing

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Here we present the draft genome of *Pseudomonas mendocina* strain S5.2, possessing tolerance to a high concentration of copper. In addition to being copper resistant, the genome of *P. mendocina* strain S5.2 contains a number of heavy-metal-resistant genes known to confer resistance to multiple heavy-metal ions.

Heavy metal ions, such as Fe, Co, Ni, Zn, and Cd, are essential micronutrients that can lead to toxicity when present in excessive amounts (7). Heavy-metal pollution caused by a discharge of various toxic metals from anthropogenic activities poses significant threats to wildlife and human health (6). Throughout the years, bacterial bioremediation of heavy-metal pollutions was implemented due to various metal resistance mechanisms present in bacteria. Mechanisms, including sequestration of metal in complexes and direct efflux of the metal from the cell to counteract toxicity, are well documented (9). Here we report the draft genome sequence of the copper-resistant *Pseudomonas mendocina* strain S5.2, isolated from vineyard soil in Riquewihr, France.

The genome of *P. mendocina* strain S5.2 was sequenced by an Illumina HiSeq 2000 platform, and the DNA library was prepared using the TruSeq DNA sample preparation kit (Illumina, Inc., CA). The acquired raw data were trimmed and assembled with CLC Genomic Workbench (version 5.1). Sequence reads with low quality (<Q20), ambiguous nucleotides, and sequence lengths less than 50 nucleotides were dropped from assembly. In total, 13,730,506 paired-end reads were obtained, amounting to 1,092,724,306 bases, with an average length of 79.58 bp. The draft genome size was 5,351,183 bases. The G+C content was 62.4%. The assembly generated 52 contigs (>500 bp), with average coverage of 202.5-fold. The average length of the contigs was 102,907 bp, and the largest contig was 655,445 bp, with an N_{50} contig size at 285,505 bp. Gene prediction using Prodigal version 2.60 (3) revealed a total of 5,023 open reading frames (ORFs). Subsequently, 54 tRNAs and one complete rRNA operon were identified using tRNAscan-SE (5) and RNAmmer (4), respectively. The predicted ORFs were further annotated by comparison with NCBI-NR using BLAST.

Results from the annotation revealed the presence of numerous ORFs encoding proteins predicted to be involved in heavy-metal resistance in *P. mendocina* strain S5.2. For instance, three heavy-metal-translocating P-type ATPases, known for their role in ion homeostasis and biotolerance of heavy-metal ions, such as Cu^{2+}, Cd^{2+}, Zn^{2+}, and Ag^{+}, were found (1). This study also identified two determinants of heavy-metal transport/detoxification proteins and a series of metal ABC-type transporter permeases. Interestingly, the annotation also led to the identification of genes coding for several putative MerR-like metalloregulator proteins known to regulate the bacterial mercury resistance (*mer*) operon (2, 8). With the demonstration of heavy-metal resistance potential through *in silico* analysis, the draft genome of *P. mendocina* strain S5.2 has provided more insight on the potential development of engineered, heavy-metal sequestering systems aimed at bioremediation processes in various heavy-metal contaminated sites.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AMCD00000000. The version described in this paper is the first version, AMCD01000000.

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