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Draft Genome Sequence of *Cupriavidus* UYMMa02A, a Novel Beta-Rhizobium Species

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We present the draft genome of *Cupriavidus* UYMMa02A, a rhizobium strain isolated from root nodules of *Mimosa magentea*. The assembly has approximately 8.1 million bp with an average G+C of 64.1%. Symbiotic and metal-resistance genes were identified. The study of this genome will contribute to the understanding of rhizobial evolution.

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The *Cupriavidus* genus is comprised of Gram-negative, flagellated, rod-shaped bacteria belonging to the *Burkholderiaceae* family in the beta subclass of *Proteobacteria*. *Cupriavidus* bacteria are model organisms for the study of heavy-metal resistance (1–6), degradation of aromatic compounds (7), and synthesis of polyhydroxybutyrate, making this genus an excellent candidate for biotechnological applications. Additionally, members of the *Betaproteobacteria* class are able to form nitrogen-fixing nodules in symbiotic associations with legumes (8, 9). Beta-rhizobia have been subsequently shown to colonize plant hosts worldwide with preference for the *Mimosoideae* subfamily (8–10). The first genome of beta-rhizobia, *Cupriavidus taiwanensis*, was published in 2008 (10).

Here, we report the draft genome sequence of the rhizobium *Cupriavidus* sp. strain UYMMa02A isolated from root nodules of *Mimosa magentea* naturally occurring in Uruguay. Interestingly, *Cupriavidus* sp. UYMMa02A is not related to the previously described symbiotic species *C. taiwanensis* or *C. necator* (11). The symbiotic bacterial isolation technique has been described elsewhere (11).

The strain was grown to stationary phase in TY media (12), harvested, and genomic DNA was isolated using the ZR fungal/bacterial DNA MiniPrep kit (Zymo Research). Sequences were generated using an Ion Torrent personal genome machine (PGM—Life Technologies), at the sequencing facility of the Institute of Biological, Research "Clemente Estable," Montevideo, Uruguay. Standard procedure and manufacturer's instructions were followed in each step, as described elsewhere (13). In brief, 400 base-pair libraries were prepared using the IonXpress Plus fragment library kit (Life Technologies, Inc.), followed by a Pippin Prep (Sage Science) size selection. Controls were performed by means of a high-sensitivity Bioanalyzer 2100 (Agilent) and Ion Sphere quality control kit (Life Technologies, Inc.). Sequencing was performed using an Ion PGM 400 sequencing kit (Life Technologies, Inc.).

A total of 1,394,358 high-quality reads were produced. *De novo* assembly was performed with SPADES assembler version 3.5.0 (14), using a preassembly approach with Mira version 4.0 (15). More than 98% of the generated reads, with an average length of 285 bp, were used in the assembly resulting in a mean nucleotide coverage of 341×. The final assembly has 8,184,499-bp length, distributed in 310 contigs. The N_{50} is 58,238, with a maximum contig length of 228,874 bp and a G+C content of 64.1%.

The genome was annotated using the RAST server with default search parameters (16, 17). As a result, 8,201 putative protein-coding sequences, 59 transfer RNA genes, and 17 rRNA genes were identified.

The draft genome of this beta-rhizobium strain will allow for testing of different hypotheses about the evolution of symbiosis in the genus as well as the study of the genetic basis of this complex and fundamental ecological process. A comparative genomic analysis will be included in future publications.

Accession number(s). The generated genome sequence has been deposited at GenBank under BioProject PRJNA306671. The version described in this paper is the first version under the accession no. LRMT00000000.

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