Complete Genome Sequence of *Rahnella aquatilis* CIP 78.65

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Rahnella aquatilis CIP 78.65 is a gammaproteobacterium isolated from a drinking water source in Lille, France. Here we report the complete genome sequence of *Rahnella aquatilis* CIP 78.65, the type strain of *R. aquatilis*.

*R*ahnella aquatilis CIP 78.65 (CUETM 77-115, CDC 1327-79, DSM 4594, ATCC 33071) is a gammaproteobacterium isolated from a drinking water source in Lille, France (7, 15). Strains belonging to the genus *Rahnella* have been isolated from soil, freshwater, food, and clinical samples. As a result, members of this genus have been studied in plant biology as they relate to plant growth and nutrient acquisition (13, 16, 18, 26, 27), food sciences (4, 17, 23, 24), medical microbiology (1, 10, 12), and more recently, in studies that demonstrate the potential use of *Rahnella* isolates for bioremediation (2, 8, 19, 21, 25). Therefore, whole-genome sequencing was conducted on *Rahnella aquatilis* CIP 78.65 to support current research that utilizes this strain as well as to support comparative genomics studies.

The complete genome of *Rahnella aquatilis* CIP 78.65 was generated at the DOE Joint Genome Institute (JGI) using a combination of Illumina (3) and 454 technologies (20). For this genome, an Illumina GAII shotgun library (79,438,616 reads totaling 6,037.3 Mb), a 454 Titanium standard library (335,154 reads), and a paired-end 454 library (370,318 reads totaling 202.7 Mb) were generated and sequenced. All general aspects of library construction and sequencing can be found on the JGI website (http://www.jgi.doe.gov/). The initial draft assembly contained 50 contigs in 2 scaffolds. The 454 Titanium standard data and the 454 paired-end data were assembled together with Newbler, version 2.3. Illumina sequencing data were assembled with Velvet, version 1.0.13 (28). We integrated the 454 Newbler consensus shreds, the Illumina Velvet consensus shreds, and the read pairs in the 454 paired-end library using parallel Phrap, version SPS-4.24 (High Performance Software, LLC). The software Consed (5, 6, 9) was used in the following finishing process. Illumina data were used to correct potential base errors and increase consensus quality using the software Polisher, developed at JGI (Alla Lapidus, unpublished). Possible misassemblies were corrected using gapResolution (Cliff Han, unpublished) or Dupfinisher (11) or by sequencing subcloned PCR products. Gaps between contigs were closed by editing in Consed, by PCR, and by Bubble PCR (J.-F. Cheng, unpublished) primer walks. Protein-encoding genes were determined by Prodigal (14) and GenePRIMP (22). The total size of the genome is 5,447,000 bp, and the final assembly is based on 176 Mb of 454 draft data (32.6× coverage) and 5,847 Mb of Illumina draft data (1,083× coverage).

The *Rahnella aquatilis* CIP 78.65 genome consists of a 4,861,101-bp (G+C content, 52.12%) circular chromosome and three plasmids, pRahaq201, pRahaq202, and pRahaq203, of 463,906 bp (G+C content, 52.29%), 115,487 bp (G+C content, 50.69%), and 8,604 bp (paired-end data indicate a circular plas-

mid with a gap spanning a known length of 1,950 bp), respectively. The genome contains 4,970 protein-encoding genes, 104 pseudogenes, 76 tRNA genes, and 7 rRNA gene operons.

Nucleotide sequence accession numbers. The complete genome sequence of *Rahnella aquatilis* CIP 78.65 is available in DDBJ/EMBL/GenBank under the accession number CP003244, in the IMG database under 2506520038, and in the Genomes OnLine Database under Gc02077. The GenBank accession numbers for plasmids pRahaq201, pRahaq202, and pRahaq203 are CP003245, CP003246, and CP003247, respectively.

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