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Draft Genome Assembly of *Delftia acidovorans* Type Strain 2167

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The *Delftia acidovorans* 2167 (ATCC 15668, *Delftia* type strain) genome was sequenced into a 6-contig scaffolded assembly of 6.78-Mb. This environmental microbe, previously named to both the *Comamonas* and *Pseudomonas* genera, is an opportunistic pathogen and often the subject of phylogenetic placement debates.

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A common microbe of soils and freshwater and originally isolated in Delft, Netherlands, *Delftia acidovorans* is an opportunistic pathogen of immunocompromised individuals (1–4). Infections are rare, but rapid identification is imperative as many are resistant to aminoglycosides (5). We sequenced the genome of *Delftia acidovorans* 2167 (ATCC 15668, *Delftia* type strain), isolated in 1926 from acetamide-enriched soil.

High-quality genomic DNA was extracted from a purified isolate using a Qiagen Genomic-tip 500 at USARMIID-DSD. Specifically, a 100-mL bacterial culture was grown to stationary phase and nucleic acid extracted per the manufacturer's recommendations. Sequence data for the draft genome include a combination of Illumina and 454 technologies (6, 7). We constructed and sequenced an Illumina library of 100-bp reads to 448-fold genome coverage and a separate long-insert paired-end library (21-fold genome coverage, 6,961 ± 1,741-bp insert) (Roche 454 Titanium platform). The two datasets were assembled together in Newbler (Roche) and the consensus sequences were computationally shredded into 2-kbp overlapping fake reads (shreds). Raw reads were also assembled in Velvet and those consensus sequences were computationally shredded into 1.5-kbp overlapping shreds (8). All draft data were then assembled together with Allpaths and the consensus sequences computationally shredded into 10-kbp overlapping shreds (9). Finally, we used parallel Phrap (High Performance Software, LLC) to integrate the Newbler consensus shreds, Velvet consensus shreds, Allpaths consensus shreds, and a subset of the long-insert read-pairs . Possible misassemblies were corrected and some gap closure accomplished with manual editing in Consed (10–12).

Automatic annotation for the *D. acidovorans* 2167 genome utilized an Ergatis-based workflow at LANL with minor manual curation. The 6,777,458-bp annotated genome contains 66.6% G+C and 6,043 coding sequences. The final scaffolded assembly (6 contigs) is available in NCBI and raw data files are available upon request.

Nucleotide sequence accession number. This genome is available in GenBank under accession number JOUB00000000.

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