


Complete Genome Assembly of Reference Strain *Ochrobactrum anthropi* ATCC 49687

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***Ochrobactrum anthropi* is an occasional cause of nosocomial infections; however, interest in the organism lies in its phylogenetic proximity to the genus *Brucella*. Here, we present the 4.9-Mb finished genome of *Ochrobactrum anthropi* ATCC 49687, most commonly used as an exclusionary reference organism.**

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Ochrobactrum anthropi ATCC 49687 causes sporadic nosocomial human infection but is commonly found in environmental samples (1). The ATCC 49687 strain is most commonly used as a reference organism in phenotypic kits. Important in its own right, *O. anthropi* is largely used in phylogenomics and diagnostics as it is the closest relative to *Brucella* based on both DNA and protein analyses (2–4).

High-quality genomic DNA was extracted from a purified isolate using a QIAgen Genome Tip-500 at USAMRIID-DSD by growing a 100-ml culture to stationary phase and extracting nucleic acid as per manufacturer's recommendations. Sequence data for the draft genome includes a combination of Illumina and 454 technologies (5, 6). For this genome assembly, we constructed and sequenced an Illumina library of 100-bp reads to high coverage (301-fold genome-coverage) and a separate long-insert paired-end library (average insert size, 7,704 ± 1,926-bp, run on Roche 454 Titanium platform to 30-fold genome-coverage). The two datasets were assembled together in Newbler (Roche) and the consensus sequences computationally shredded into 2-kbp overlapping fake reads (shreds). The raw reads were also assembled in Velvet and those consensus sequences computationally shredded into 1.5-kbp overlapping shreds (7). Draft data from all platforms was then assembled together with Allpaths and the consensus sequences computationally shredded into 10-kbp overlapping shreds (8). We then integrated the Newbler consensus shreds, Velvet consensus shreds, Allpaths consensus shreds, and a subset of the long-insert read-pairs using parallel Phrap (High Performance Software, LLC). Possible misassemblies were corrected and some gap closure accomplished with manual editing in Consed (9–11).

Automatic annotation for the *O. anthropi* ATCC 49687 genome utilized an Ergatis based workflow at Los Alamos National Laboratory (LANL) with minor manual curation. Annotation located 4,630 coding genes, 57 tRNAs, and 12 rRNAs. The final

4,901,165-bp assembly has 56.1% G+C content. To our knowledge, there is only one other complete genome of *O. anthropi* publicly available (strain ATCC 49118^T); however, further investigation is warranted to understand the genetic relationship between the two strains (12).

Nucleotide sequence accession numbers. The final sequence has been deposited to GenBank under four accession numbers: CP008820 (Chr I), CP008819 (Chr II), CP008817 (pOAB1), and CP008818 (pOAB2).

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