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Draft Genome Assembly of *Pseudomonas aeruginosa* Quality Control Reference Strain Boston 41501

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We present the scaffolded genome assembly of *Pseudomonas aeruginosa* Boston 41501, now publicly available in GenBank (JOVK00000000) in 10 contigs placed into a single scaffold. The 6.82-Mbp genome contains 66.1% G+C content and 6,295 coding sequences, including type 4 pilus and type 3 secretion system production genes.

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Pseudomonas aeruginosa is a Gram-negative member of the *Gammaproteobacteria* found in a wide variety of environments (soil water, animals, humans, and hospitals). *P. aeruginosa* Boston 41501 (ATCC 27853) is a quality control strain often used in opportunistic pathogen research and originally isolated from a blood culture. Most human infections are hospital acquired and/or limited to immunocompromised persons. Recently the U.S. Centers for Disease Control and Prevention elevated the risk of antibiotic-resistant *P. aeruginosa* infection to "serious" due to estimates of 6,700 cases and 400 deaths annually (1).

High-quality genomic DNA was extracted from a stationary-phase purified isolate using a Qiagen Genomic-tip 500 at the USARMIID Diagnostic Systems Division (DSD) per the manufacturer's recommendations. Draft sequence data included a 100-bp Illumina library (128-fold genome coverage) and a separate long-insert paired-end library (8,792- ± 2,198-bp insert, 35-fold genome coverage) (Roche 454 Titanium platform). The two data sets 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 (2). Draft data from all platforms were then assembled together with Allpaths and the consensus sequences computationally shredded into 10-kbp overlapping shreds (3). 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 was accomplished with manual editing in Consed (4–6).

Automatic annotation of the *P. aeruginosa* Boston 41501 genome utilized an Ergatis-based workflow at LANL with minor manual curation. The final annotated assembly (6,295 coding sequences, 31 rRNAs, and 66 tRNAs in the 6,819,384-bp genome sequence) is available in GenBank (accession number JOVK00000000), and raw data can be provided upon request. Preliminary review of the annotations finds at least 28% of the virulence genes noted by Feinbaum et al. (7) and both type 4 pilus and type 3 secretion systems (8).

Nucleotide sequence accession number. This genome sequence is available in GenBank under the accession number JOVK00000000.

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