

Draft Genome Sequence for *Pseudomonas aeruginosa* Strain PAO579, a Mucoïd Derivative of PAO381

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***Pseudomonas aeruginosa* is an opportunistic pathogen that establishes a chronic lung infection in individuals afflicted with cystic fibrosis. Here, we announce the draft genome of *P. aeruginosa* strain PAO579, an alginate-overproducing derivative of strain PAO381.**

Pseudomonas aeruginosa is a ubiquitous, opportunistic pathogen and the leading cause of mortality with individuals afflicted with cystic fibrosis (CF). *P. aeruginosa* uses the overproduction of an exopolysaccharide, called alginate, to form mucoïd biofilms. Biofilm formation is responsible for the development of chronic infections, as well as increased resistance to antibiotic treatment (2), and reduced phagocytosis by macrophages (4). *P. aeruginosa* strain PAO579 was first isolated as a mucoïd, alginate-overproducing variant of PAO381, a derivative of the nonmucoïd reference strain PAO1 (3, 5). Both PAO579 and PAO381 have a wild-type *mucA* gene (*mucA*⁺), and both strains are leucine auxotrophic (*leu38*) and streptomycin resistant (*strA2*).

Genomic DNA from *P. aeruginosa* strain PAO579 was isolated using phenol-chloroform extraction and ethanol precipitation; paired-end sequencing libraries were generated using vendor protocols (Illumina, San Diego, CA); and genome sequencing was performed on an Illumina GAIIX with 60-bp-length sequencing generating 54,496,482 raw reads covering a total of 3,269,788,920 bp. Data were generated and assembled using Illumina Pipeline version SCS 2.8.0 paired with OLB 1.8.0 and aligned with the *P. aeruginosa* strain PAO1 reference genome (GenBank accession no. NC_2516.2) using NovoAlign version 2.07.10. All specifics regarding aligner algorithms can be obtained from Novocraft, Selangor, Malaysia. The total number of base pairs aligned with the reference genome is 2,077,041,840 bp, representing an average of 340× per target base pair aligned. The number of bases saturated at or above 8× is 6,016,396 (96.04%), and the number of bases saturated below 8× is 248,008 (3.96%). The total number of reference bases covered is 6,036,589 (96.36%) with the total number of bases missed being 227,815 (3.64%). There are a total of 16 contigs (ALOF01000001 to ALOF01000016). Further analysis of the genome was performed using Samtools version 0.1.16a for the generation of pileup after sorting and removing supuplicate reads and then analysis pipeline software developed by Cofactor Genomics (St. Louis, MO). The genome was annotated and prepared for submission using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; <http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) server at NCBI.

Based upon this analysis, a total of 31 homozygous single nucleotide polymorphisms (SNPs), or point mutations, were called with a high confidence between the sequenced reads and the PAO1 reference genome and were tabulated for each genomic position, as well as the total coverage of bases observed at that

location. Of particular interest is the substitution of thymine for adenine at genome position 4980548 in the DegS-like MucA protease gene, *algW* (PA4446). This alteration results in a change in the primary structure of AlgW, more specifically a substitution of isoleucine for phenylalanine at amino acid position 239. This predicted substitution is thought to affect the proteolytic activity of AlgW (1). Also of note, we observed mutations in *leuA* (PA3792), the 2-isopropylmalate synthase gene, and *rpsL* (PA4268), the 30S ribosomal protein S12 gene. These mutations are contiguously part of the PAO381 lineage and are responsible for leucine auxotrophy and streptomycin resistance, respectively.

Nucleotide sequence accession number. The draft genome sequence of *P. aeruginosa* strain PAO579 has been deposited in GenBank under accession number [ALOF00000000](https://www.ncbi.nlm.nih.gov/nuccore/ALOF00000000).

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