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Complete Genome Sequence of *Pseudomonas aeruginosa* Mucoid Strain FRD1, Isolated from a Cystic Fibrosis Patient

Laura A. Silo-Suh,[a] Sang-Jin Suh,[b] Dennis E. Ohman,[c,d] Daniel J. Wozniak,[e] Julia W. Pridgeon[f]

Department of Basic Medical Sciences, Mercer University School of Medicine, Macon, Georgia, USA[a]; Department of Biological Sciences, Auburn University, Auburn, Alabama, USA[b]; Department of Microbiology and Immunology and Virginia Commonwealth University Medical Center, Richmond, Virginia, USA[c]; Hunter Holmes McGuire VA Medical Center, Richmond, Virginia, USA[d]; Center for Microbial Interface Biology, The Ohio State University, Columbus, Ohio, USA[e]; Aquatic Animal Health Research Unit, USDA-ARS, Auburn, Alabama, USA[f]

We announce here the complete genome sequence of the *Pseudomonas aeruginosa* mucoid strain FRD1, isolated from the sputum of a cystic fibrosis patient. The complete genome of *P. aeruginosa* FRD1 is 6,712,339 bp. This genome will allow comparative genomics to be used to identify genes associated with virulence, especially those involved in chronic pulmonary infections.

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Address correspondence to Laura A. Silo-Suh, silo-suh_l@mercer.edu.

The Gram-negative bacterium *Pseudomonas aeruginosa* is the major etiological agent responsible for pulmonary infections in cystic fibrosis (CF) patients leading to morbidity and mortality. CF patients are frequently colonized by environment-borne *P. aeruginosa*, which initially causes intermittent infections (1). Chronic infections are associated with significant genetic changes in the bacterium that appear to facilitate the persistence of the pathogen in this niche (2, 3). One such change is the acquisition of the mucoid phenotype caused by mutations in the *mucA* gene leading to overproduction of the exopolysaccharide alginate (4, 5). Alginate is a major component of the *P. aeruginosa* biofilm matrix responsible for increased tolerance to antibiotics (6). A mucoid strain of *P. aeruginosa*, designated FRD1, was isolated from a sputum sample from a chronically infected CF patient in 1979 by Barbara Iglewski (Portland, OR) and first reported in 1981 as a strain that can be readily manipulated genetically (7). This isolate is arguably the best characterized CF *P. aeruginosa* isolate and has provided the basis for much of the information assembled on alginate biosynthesis and regulation in *P. aeruginosa* (8–11). The complete genome sequence of *P. aeruginosa* FRD1 was determined in this study in order to augment and facilitate a further investigation of the microevolution process of *P. aeruginosa* adaptation in the CF lung.

Genomic DNA was isolated from an overnight broth culture of *P. aeruginosa* FRD1 using the Wizard genomic DNA purification kit (Promega) and sequenced using the Pacific Biosciences RS II platform. HGAP3 was used to *de novo* assemble a total of 117,765 sequence reads, with an average length of 4,559 bp. The whole genome of *P. aeruginosa* FRD1 is 6,712,339 bp, with a G+C content of 66.1% and 6,439 predicted open reading frames. The contigs of the *de novo*-assembled genome of *P. aeruginosa* FRD1 share 99% identity with those of the genome of *P. aeruginosa* strain PA38182 (GenBank accession no. HG530068), a major epidemic strain throughout Europe (12). The annotation of the genome by Manatee detected the following breakdown within subsystems: 91 open reading frames in amino acid biosynthesis, 82 in fatty acid and phospholipid metabolism, 58 in central intermediary metabolism, 320 in energy metabolism, 1,030 in transport and binding proteins, 117 in DNA metabolism, 90 in transcription, and 273 in cell envelope.

Nucleotide sequence accession number. The complete genome sequence of *P. aeruginosa* FRD1 was deposited in GenBank under the accession no. CP010555. The version described in this paper is the first version.

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