

Genome Sequence of the Urethral Isolate *Pseudomonas aeruginosa* RN21

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***Pseudomonas aeruginosa* is known to cause complicated urinary tract infections (UTI). The improved 7.0-Mb draft genome sequence of *P. aeruginosa* RN21, isolated from a patient with an acute UTI, was determined. It carries three (pro)phage genomes, genes for two restriction/modification systems, and a clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated (Cas) system.**

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Pseudomonas aeruginosa is one of most frequently occurring Gram-negative nosocomial pathogens and is known as one of the major agents causing complicated urinary tract infections (UTIs) (1, 2). These infections are predominantly biofilm-related phenomena, influenced by the action of lytic bacteriophages (3, 4). Here, we report the draft genome sequence of *P. aeruginosa* RN21 isolated from a patient with an acute UTI (5). The strain was urease negative and had a moderately virulent phenotype without remarkable antibiotic resistances. In order to obtain the draft genome sequence, we extracted genomic DNA from this isolate to construct a paired-end library for shotgun sequencing on a genome sequencer FLX (GS FLX) system using Titanium technology (Roche) as described recently (6, 7, 8). Standard protocols were applied per the manufacturer's instructions. The sequencing run yielded 216,518,852 bases from 958,125 aligned individual reads, among them 345,167 paired-end reads. The assembly obtained by applying the GS Assembly software resulted in 216 contigs (>500 bp), of which 160 were organized into 9 scaffolds. An *in silico* gap closure approach (9, 10) was performed, which reduced the number of contigs to 83. The improved draft genome had a total size of 6,970,506 bp with an average coverage of 31.1×. The G+C content of the genome was 65.88%. Automated genome annotation was carried out by means of the GenDB platform (11). This resulted in the prediction of 6,422 protein-coding sequences (CDSs). Three copies of the rRNA operons and 60 tRNAs were predicted. Identification of RN21 singletons in comparison to the *P. aeruginosa* core genome was established using the platform EDGAR (12). Most of the unique genes were related to three (pro)phage genomes and to multiple protection systems against phages and other foreign DNA. In detail, a complete D3112-like virus genome

(PARN21_0994 to PARN21_1037), a novel phage genome containing multiple genes with strong homology to phage D3 genes (PARN21_3655 to PARN21_3727), and a leukocidin-like cytotoxin gene containing (pro)phages (PARN21_6249 to PARN21_6290) were found (13, 14). A genomic island (PARN21_2458 to PARN21_2502) encoded type II and III restriction/modification systems, a glutathione S-transferase, and a filamentous hemagglutinin-like protein with corresponding labile enterotoxin output protein (15, 16). Similarly, the unique genomic region PARN21_2633 to PARN21_2669 encoded various DNA methylases, endonucleases, RecT, LexA-type regulators, an FlsK homologue, and structural maintenance of chromosomes (SMC) domain proteins, possibly involved in chromosome assembly (17). These observations were completed by the detection of a set of genes encoding the proteins recognizing clustered regularly interspaced short palindromic repeats (CRISPR), a complete CRISPR-associated (Cas) system (PARN21_4342 to PARN21_4350) (18). Finally, CDSs for lipopolysaccharide (LPS)-modifying enzymes (PARN21_1897 to PARN21_1899 and PARN21_2688), a capsule biosynthesis enzyme (PARN21_4510), a type IV secretion system (PARN21_6231 to PARN21_6236), an antitoxin (PARN21_5028/59), and multiple potential transcriptional regulators were found (19–21). A more detailed and comparative analysis of this genome will contribute to a deeper understanding of urinary tract infections caused by *P. aeruginosa* and may advance our conception of its phage interactions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession numbers [CGFY01000001](https://www.ncbi.nlm.nih.gov/nuccore/CGFY01000001) to [CGFY01000083](https://www.ncbi.nlm.nih.gov/nuccore/CGFY01000083). The version described in this paper is the first version, CGFY01000000.1.

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