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Complete genome sequence of a multidrug-resistant *Proteus mirabilis* clinical isolate harboring 22 antimicrobial resistance genes including *bla*$_{CTX-M-15}$

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ABSTRACT *Proteus mirabilis* causes urinary tract infections and wound infections and frequently exhibits multidrug resistance, complicating patient treatment. Here, we describe the complete genome sequence of a multidrug-resistant *P. mirabilis* wound isolate from 2025, providing insight into the repertoire of antimicrobial resistance genes in a recent *P. mirabilis* clinical isolate.

KEYWORDS *Proteus mirabilis*, antimicrobial resistance, wound infection, clinical

Proteus mirabilis is a gram-negative bacterium that can be found in soil, water, and wastewater, as well as colonizing the gastrointestinal tract of animals and humans (1). *P. mirabilis* is also a versatile opportunistic pathogen that causes human urinary tract infections, wound infections, and bacteremia (2, 3). Prior studies reported an increase of drug-resistant *P. mirabilis* among hospitalized patients (4, 5).

P. mirabilis isolate Pm879 was obtained in April 2025 from a right leg soft tissue wound of a hospitalized patient who presented with gangrene. A deep wound sample was collected using a swab and cultured on MacConkey agar and blood agar. The isolate was stored at −80°C. Species identification was performed using VitekMS (Biomérieux). Antimicrobial susceptibilities were determined using MicroScan WalkAway panel NM56 (Beckman Coulter) and interpreted with Clinical and Laboratory Standards Institute breakpoints (6). Multidrug resistance was determined as resistance to three or more antimicrobial categories (7). Pm879 was grown on blood agar overnight at 37°C, and genomic DNA was extracted using the Nanobind CBB kit (Pacific Biosciences). The quantity and sizing of the genomic DNA were determined by fluorometric detection and Femto Pulse electrophoresis (Agilent). Sequencing libraries were generated without size selection using the Rapid Barcoding Kit (SQK-RBK114.24) (Oxford Nanopore Technologies). The genome of Pm879 was sequenced on a MinION MK1D (Oxford Nanopore Technologies) using R10.4.1 flow cells, generating 324,737 total reads with an N50 of 20,985 bp, yielding 585× sequence coverage. Basecalling, adapter trimming, and index trimming were performed using MinKNOW v.25.05.14 with the Dorado basecall server v.7.9.8 (https://nanoporetech.com/software/other/dorado-basecall-server) and the dna_r10.4.1_e8.2_400bps_sup@v5.2.0 model. Reads that passed QC (Q > 10) were assembled using Autocycler v.0.5.2 (8) with default settings. This generated a resolved consensus assembly with a single circular chromosome and two circular plasmids, which had 100% completeness and <1% contamination determined using CheckM2 v.1.1.0 (9). Sequences were not reoriented. Taxonomic classification was performed using GTDB-Tk v.2.5.2 (10, 11). Annotation by PGAP v.6.10 (12) predicted 4,129 total genes, including 3,932 protein-coding sequences and 108 RNA genes.

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TABLE 1 Antimicrobial susceptibilities and resistance determinants of Pm879[a]

Antibiotic	Drug class	Resistance genes	MIC (µg/mL)	Interpretation
Amikacin	Aminoglycosides	*aadA1, aph(3′)-Ia, aph(3″)-Ib, aph(6)-Id, aac(3)-IIe, ant(2″)-Ia, aac(6′)-Ib, aac(6′)-Ib-cr5*	≤16	S
Gentamicin			>8	R
Tobramycin			>8	R
Ampicillin	Beta-lactams	bla_{TEM-1}, bla_{OXA-1}, $bla_{CTX-M-15}$	>16	R
Aztreonam			>16	R
Ampicillin-sulbactam	Beta-lactams + beta-lactamase inhibitors	$bla_{CTX-M-15}$, bla_{OXA-1}	16/8	I
Pipercillin-tazobactam			≤8	S
Cefazolin	Cephalosporins	$bla_{CTX-M-15}$	>16	R
Cefepime			>16	R
Ceftriaxone			>32	R
Ertapenem	Carbapenems	None	≤0.5	S
Meropenem			≤1	S
Trimethoprim-sulfamethoxazole	Dihydrofolate reductase inhibitor-sulfonamide	*dfrA1, sul1, sul2*	>2/38	R
Levofloxacin	Fluoroquinolones	*qnrB1, aac(6′)-Ib-cr5*	4	R
Ciprofloxacin			>2	R
Tetracycline	Tetracyclines	*tet(A), tet(J)*	>8	R

[a]Additional resistance determinants harbored by Pm879 for which susceptibilities were not determined: *sat2, catA1, catB3, catA*, and *qacEdelta1*.

The genome of Pm879 contains a single chromosome with a sequence length of 4,340,484 bp and G + C content of 39.5%. The average nucleotide identity of Pm879 compared to the RefSeq reference genome of *P. mirabilis* (GCF_000069965.1) was 98.74%, which is greater than the ≥95% threshold for species-level classification (13). Pm879 also contains two plasmids with sequence lengths of 35,988 bp (GC 34.3%) and 25,868 bp (GC 40.2%), identified using MOB-suite v.3.1.9 (14). Multilocus sequence typing using PubMLST (15) identified Pm879 as sequence type (ST) 446. Previous ST446 clinical isolates have been described with acquired carbapenem resistance (16) and aztreonam-avibactam resistance (17). AMRFinderPlus v.4.2.7 (18) identified 22 resistance genes in the chromosome of Pm879 (Table 1). A prior study demonstrated *P. mirabilis* isolates in a widespread global lineage contained, on average, 17 antimicrobial resistance genes, while other lineages had ~8 to 12 resistance genes per isolate (19). The large number of antimicrobial resistance genes of Pm879 (>22) highlights the importance of genomic surveillance to monitor acquired drug resistance mechanisms among pathogens infecting and colonizing hospitalized patients.

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DATA AVAILABILITY

The sequence data from *P. mirabilis* isolate 879 are deposited under BioProject PRJNA1445273 and BioSample SAMN56782725. The raw sequence reads are deposited in SRA under SRS28915757 and the genome assembly is deposited in GenBank under JBWQEX000000000.

ETHICS APPROVAL

Genome sequencing of Pm879 was performed under an Institutional Review Board approved study (HP-00112564) at the University of Maryland, Baltimore, for investigating isolates of interest for hospital infection control.

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