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GENOME SEQUENCES

Draft Genome Sequence of an Unusually Multidrug-Resistant Strain of *Achromobacter xylosoxidans* from a Blood Isolate

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ABSTRACT *Achromobacter xylosoxidans* strain DN2019 was isolated from blood of a septicemia patient. We describe the draft genome and antibiotic susceptibility of this strain.

Achromobacter xylosoxidans is a Gram-negative, flagellated, motile, and aerobic non-lactose fermenting bacillus first characterized in 1971 (1). This bacterium is an opportunistic human pathogen and often contributes to nosocomial infections (2–6). In general, *A. xylosoxidans* is resistant to a broad range of antibiotics, including aminoglycosides, cephalosporins, and penicillin (4, 7–11).

We sequenced the draft genome of an *A. xylosoxidans* strain DN2019 isolate from a septicemia patient at the Central Texas Veterans Heath Care System. Table 1 shows the resistance pattern of the isolate. The resistance profile was determined using CLSI MIC breakpoints for other non-*Enterobacteriaceae* strains (see Table 2B-5 in reference 12). This strain is a multidrug-resistant organism showing resistance against various classes of antimicrobials, including cephalosporins and quinolones.

One drop of blood was cultured on Trypticase soy agar (TSA) with sheep blood agar (Remel, Inc., San Diego, CA) at 37°C overnight. Strain DN2019 was isolated from the culture. Genomic DNA was extracted using the QIAamp DNA microkit (Qiagen, Hilden, Germany). Libraries were prepared using the Nextera DNA flex library prep kit (Illumina, San Diego, CA), and paired-end reads (2 × 151 bp) were generated using a NextSeq instrument (Illumina, San Diego, CA). The default parameters of the software programs were used for all sequence analyses. The *de novo* assembly was completed using the SPAdes version 3.7.1 assembler (13) in the BioNumerics version 7.6.3 program (Applied Maths NV, Sint-Martens-Latem, Belgium). The final *de novo* assembly consisted of 3,023,655,234 reads. The average quality score of the reads was 30.50 calculated by BioNumerics, based on the Q score generated by Illumina's Sequence Analysis Viewer (SAV) software. In the assembled genome, there were 341 contigs with an N_{50} value of 38,282 bp. The final genome length comprised 6,607,874 bp with a 400-fold average coverage and 67.7% G+C content.

Sequence type 182 (ST 182) was determined using multilocus sequence typing (MLST) analysis (14). *Achromobacter* ST 182 was identified as *Achromobacter xylosoxidans* using the PubMLST database (15, 16). Average nucleotide identity (ANI) analysis (http://enve-omics.ce.gatech.edu/ani/) (17) with the *A. xylosoxidans* type strain genome (NCTC 10807, GenBank accession number NZ_LN831029.1) showed 98.77% mean nucleotide identity with *A. xylosoxidans*. Mean nucleotide identities with other closely related species, *Achromobacter ruhlandii* and *Achromobacter denitrificans*, were 92.46% and 85.71%, respectively. In addition, KmerFinder version 3.1 identified the sequence as *Achromobacter xylosoxidans* (18, 19).

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TABLE 1 MICs of *Achromobacter xylosoxidans* DN2019

Antibiotic	MIC (μg/ml)	CLSI interpretation[a]
Amikacin	≥64	R
Gentamicin	8	I
Tobramycin	8	I
Ampicillin	≥32	R
Ampicillin-sulbactam	8	S
Piperacillin	≤4	S
Piperacillin-tazobactam	≤4	S
Moxifloxacin	≥8	R
Cefotetan	≥64	R
Cefoxitin	≥64	R
Ceftazidime	2	S
Cefuroxime-axetil	≥64	R
Cefuroxime-sodium	≥64	R
Ciprofloxacin	≥4	R
Imipenem	8	I
Norfloxacin	8	I
Trimethoprim-sulfamethoxazole	≤20	S
Ceftriaxone	≥64	R
Amoxicillin-clavulanic acid	8	S
Cefazolin	≥64	R
Aztreonam	≥64	R
Nalidixic acid	≥32	R
Levofloxacin	4	I
Ceftizoxime	≥64	R
Meropenem	1	S

[a] I, intermediate; R, resistant; S, susceptible.

The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (20) predicted 6,175 protein-coding sequences (CDSs), 4 copies of the rRNA, and 58 tRNAs. ResFinder version 3.2 (21) analysis identified the following putative antibiotic resistance genes: β-lactamase class D $bla_{OXA-114a}$, phenicol resistance gene *catB1*, and quinolone resistance gene *oqxB*. Gene annotation revealed various efflux pumps involved in antibiotic resistance (22), multidrug and toxin extrusion (MATE) family efflux pumps *ydhE* and *norM*, macrolide-specific efflux genes *macA* and *macB*, multidrug efflux system *mdtABC-tolC*, RND efflux system *cmeA*, and multidrug efflux system *mexX*. Antibiotic resistance gene *marC* and tetracycline resistance regulatory gene *tetR* (22) were also present.

Data availability. The draft genome sequence described here has been deposited at DDBJ/ENA/GenBank under the accession number WWES00000000. The raw sequence reads are available under the SRA accession number PRJNA591881.

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