Data in Brief 57 (2024) 111040

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Genomics sequence data of a drug-resistant *Pseudomonas aeruginosa* producing Tripoli Metallo-β-lactamase 1 isolated from Sudan

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ARTICLE INFO

Article history:
Received 5 September 2024
Revised 8 October 2024
Accepted 9 October 2024
Available online 16 October 2024

Dataset link: Pseudomonas aeruginosa strain PANU108, whole genome shotgun sequencing project (Original data)

ABSTRACT

We whole-genome sequence a drug-resistant *Pseudomonas aeruginosa* strain (PANU108) isolated in 2020 from an elderly male patient admitted to an intensive care unit with bloodstream infection in Khartoum, Sudan. The analysis of the sequenced data revealed that the strain is sequence type 319 (ST319) and carrying 11 acquired resistance genes belonging to 5 drug classes. Interestingly, we found that PANU108 strain harbouring $bla_{\text{TMB-1}}$ resistance gene. To the best of our knowledge,

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https://doi.org/10.1016/j.dib.2024.111040

Keywords:
blaTMB-1
Extensively drug-resistant
ST319
Pseudomonas aeruginosa
Carbapenem resistance
Sudan

this the first report of a *P. aeruginosa* producing Tripoli Metallo-β-lactamase 1 (TMB-1) resistance determinant.

Specifications Table

Subject	Microbiology
Specific subject area	Pathogenic genome
Type of data	Genome sequence data, Raw, Filtered and assembled genome
Data collection	*Pseudomonas aeruginosa* strain PANU108 was isolated and identified phenotypically from an ICU patient in Khartoum, Sudan. Genomic DNA was extracted from a pure colony using DNA QIAamp DNA Mini Kit (Qiagen). The whole-genome sequencing and analysis were performed using the Illumina NextSeq platform (Illumina, Inc., USA), and JEKESA pipeline (https://github.com/jekesa), respectively.
Data source location	-Bahri Hospital, Khartoum, Sudan -Faculty of Medical Laboratory Sciences, National University, Khartoum, Sudan
Data accessibility	Repository name: GenBank (at National Center for Biotechnology Information, NCBI) Data identification number: JAPQXL000000000 Direct URL to data: https://www.ncbi.nlm.nih.gov/nuccore/JAPQXL000000000
Related research article	Prevalence of Multidrug-Resistant, Extensively Drug-Resistant and Pandrug-Resistant *Pseudomonas aeruginosa* Clinical Isolates in Khartoum, Sudan https://pubs.sciepub.com/ajidm/11/1/1/index.html

1. Value of the Data

- This whole-genome data presents the first genomic description of a clinical *Pseudomonas aeruginosa* carrying $bla_{\text{TMB-1}}$ carbapenemase-encoding gene.
- Characterization of carbapenemase-producing *Pseudomonas aeruginosa* is crucial for the implementation of proper infection control measures.
- The sequence data of this isolate may serve as a source to develop diagnostic and therapeutic approaches to combat drug resistance *Pseudomonas aeruginosa* infections among hospitalized patients with bloodstream infections.

2. Background

Pseudomonas aeruginosa (P. aeruginosa) is a versatile bacterium capable of causing a wide range of intensive care unit (ICU) infections and particularly in immunocompromised individuals [1]. *P. aeruginosa* possesses a large and adaptable genome, allowing it to thrive in different environments and exhibit high nutritional versatility. Beside the inherent resistance encoded within the bacterium's core genome. *P. aeruginosa* possesses natural defense mechanisms such as low outer membrane permeability, efflux pumps, and production of β-lactamases that limit the effectiveness of antimicrobial agents [2,3]. One significant concern in the context of *P. aeruginosa* resistance is the global dissemination of Metallo-β-lactamases genes. The emergence and spread of Metallo-β-lactamases genes particularly those encoding such as bla_{IMP}, bla_{VIM} followed by bla_{NDM}, bla_{SPM}, and bla_{GIM} classes in *P. aeruginosa* strains have significantly reduced the efficacy of all β-lactam antibiotics [3]

3. Data Description

The whole-genome sequence data for strain PANU108 was recovered from blood culture of a 69-years old male patient in April 2020. The patient was admitted to the intensive care unit

Table 1
Assembly details and annotated genome features for *P. aeruginosa* PANU108.

Item	Value
Genome length (bp.)	7,480,081
Number of contigs	3777
GC content (%)	65.24
N50 (bp.)	3432
Smallest contig	315
Largest contig (bp.)	54,782
Coverage (X)	80X
Total No. of CDS	10,301
tRNA	46
rRNA	3
Sequence type	ST319
BioProject accession number	PRJNA837467
BioSample accession number	SAMN32024321
Assembly accession number	JAPQXL000000000

Table 2
Acquired antimicrobial genes predicted in *P. aeruginosa* PANU108 strain.

Gene	Drug class	Identity (%)	Alignment/ Gene Length	Coverage	Contig	Position in contig
catB7	amphenicol	98.75	639/639	100	JAPQXL010000001.1	8075..8713
blaOXA-488	beta-lactam	99.87	789/789	100	JAPQXL010000155.1	1871..2659
crpP	quinolone	94.95	198/198	100	JAPQXL010000215.1	3544..3741
blaPAO	beta-lactam	99.33	1194/1194	100	JAPQXL010000386.1	1158..2351
cmx	amphenicol	99.91	1176/1176	100	JAPQXL010000895.1	984..2159
blaOXA-4	**beta-lactam**	**100**	**831/831**	**100**	**JAPQXL010000919.1**	**96..926**
aac(6′)-IIa	**aminoglycoside**	**99.82**	**555/555**	**100**	**JAPQXL010000919.1**	**1045..1599**
blaTMB-1	**beta-lactam**	**100**	**738/738**	**100**	**JAPQXL010000919.1**	**1645..2382**
sul1	folate pathway antagonist	100	840/840	100	JAPQXL010001214.1	547..1386
aph(6)-Id	aminoglycoside	100	837/837	100	JAPQXL010001501.1	22..858
aac(6′)-Ib3	aminoglycoside	99.64	555/555	100	JAPQXL010002737.1	53..607

in Bahri Hospital in Khartoum, Sudan with symptoms of chronic obstructive pulmonary disease and bloodstream infection. He stayed in the hospital for three weeks with intravenous meropenem chemotherapy required for 7 days. Following the isolation and the identification of *P. aeruginosa*, the phenotypic susceptibility test showed that the isolate was resistant to gentamycin, tobramycin, amikacin, impenem, meropenem, ceftazidime, cefepime, ticarcillin-clavulanic acid, aztreonam, fosfomycin and colistin but sensitive to ciprofloxacin, levofloxacin, and piperacillin-tazobactam. The paired-end sequencing of PANU108 resulted 3,628,354 high-quality reads which assembled to 3777 contiguous sequences (the average contig length was 1,980 bp., and N50 value of 3,432 bp) with 80X genome coverage and 65.24 % G+C content. The genome of PANU108 was found to harbor 10,301 protein coding sequences (CDS), 46 transfer RNA (tRNA) genes, and 3 ribosomal RNA (rRNA) genes. Multilocus sequence typing (MLST) indicated ST319. The assembly details and annotated genome features of strain PANU108 were summarized in (Table 1). PANU108 found to be extensively drug-resistant strain as it carried 11 acquired resistant genes including $bla_{\text{TMB-1}}$ gene which located in a class 1 integron (contig JAPQXL010000919.1). Interestingly, the integron also contained genes encoding resistance to aminoglycosides (aac(6′)-IIa), and β-lactams ($bla_{\text{OXA-4}}$) (Table 2).

4. Experimental Design, Materials and Methods

The procedure for collecting, isolating, and identifying PANU108 has been described previously [4]. Moreover, antibiotic susceptibility profiles were determined according to the Clinical and Laboratory Standards Institute guidelines and interpretative criteria [5]. *P. aeruginosa* PANU108 strain DNA was extracted using a QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. The paired-end libraries were prepared using the Nextera DNA Flex library kit, followed by $2 \times$ 150 bp. sequencing on a NextSeq machine (Illumina, Inc., USA). For the genomic analysis and MLST typing, the JEKESA pipeline (https://github.com/stanikae/jekesa) was used. Briefly, Trim Galore v0.6.2 (https://github.com/FelixKrueger/TrimGalore) was used to filter the sequence reads (Q, $\geq$ 20; length, $\geq$ 50), de novo assembly was performed using SPAdes v3.15.4 (https://github.com/ablab/spades), and sequence typing was done using the MLST tool v2.16.4 (https://github.com/tseemann/mlst). All resultant contiguous sequences were annotated using the NCBI Prokaryotic Genome Annotation Pipeline [6]. Furthermore, the assembled genome was uploaded to the Center for Genomic Epidemiology web server to determine acquired antimicrobial resistance genes using ResFinder v4.6.0 [7–9].

Limitations

None

Ethics Statement

Ethical approval was obtained in 2020 from the Faculty of Graduate Studies and Scientific Research of the National University in Sudan, as well as the Khartoum State Ministry of Health in Sudan.

CRediT Author Statement

Sara E Mohammed: Conceptualization, Methodology, Validation, Formal analysis, Investigation, Resources, Data Curation, Writing - Original Draft. **Omnia Hamid:** Conceptualization, Methodology, Validation, Formal analysis, Investigation, Resources, Data Curation, Writing - Review & Editing. **Mohammed Abdelrahim:** Conceptualization, Supervision. **Arshad Ismail:** Methodology, Formal analysis, Data Curation. **Anthony M Smith:** Funding acquisition. **Mushal Allam:** Conceptualization, Methodology, Software, Formal analysis, Investigation, Resources, Data Curation, Writing - Review & Editing, Supervision, Project administration.

Data Availability

Pseudomonas aeruginosa strain PANU108, whole genome shotgun sequencing project (Original data) (Genbank).

Acknowledgments

We would like to thank the National Institute for Communicable Disease in South Africa for providing the sequencing of this strain. Also, we would like to extend our thanks to the National University in Sudan for support.

Funding

Whole genome sequencing was supported by the SEQAFRICA project which is funded by the Department of Health and Social Care's Fleming Fund using UK aid. The views expressed in this publication are those of the authors and not necessarily those of the UK Department of Health and Social Care or its Management Agent, Mott MacDonald.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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