Vol. 5 No. 1 (2026)

Pakistan Journal of Medical & Cardiological Review

https://pakjmcr.com/index.php/1/about

Online ISSN 3007-2387

Print ISSN 3007-2379

Sumbal et al., 2026

Uncovering the Genomic Architecture of Pseudomonas Aeruginosa in Urinary Tract Infections Cases Using Whole Genome Sequencing

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Received on 02 March, 2026
Accepted on 25 March, 2026
Published on 29 March, 2026

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Abstract

Pseudomonas aeruginosa is a major opportunistic pathogen responsible for urinary tract infections and is increasingly associated with multidrug resistance (MDR), limiting treatment options. This study aimed to characterize the phenotypic and genomic antimicrobial resistance profile of an MDR *P. aeruginosa* isolate from a clinical urine sample. A clinical isolate was identified using conventional microbiological and biochemical methods. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method following CLSI guidelines. Whole-genome sequencing was conducted using the Illumina platform, followed by bioinformatics analysis for antimicrobial resistance gene identification and SNP/indel characterization. The isolate exhibited resistance to β-lactams, fluoroquinolones, aminoglycosides, and imipenem, while remaining susceptible to meropenem and colistin. Whole-genome sequencing identified multiple resistance genes, including blaOXA-488, blaPAO, aac(3)-Id, aac(6')-Il, crpP, qnrVC1, fosA, dfrB5, and sul2, consistent with the phenotypic resistance profile. Genome analysis also revealed substantial SNP and indel variations, indicating considerable genomic diversity. The findings demonstrate a strong correlation between phenotypic antimicrobial resistance and genomic determinants, highlighting the utility of whole-genome sequencing for

antimicrobial resistance surveillance and improving the understanding of MDR *P. aeruginosa*.

Keywords: Antibiotics microbiome resistance, whole genome sequence, UTI

INTRODUCTION

Pseudomonas aeruginosa is the commonly spread Gram negative bacteria, and belongs to the family of *Pseudomonas aeruginosa*, and also may exist under various circumstances (1). The *P. aeruginosa* genome's improved coding capacity enables a high degree of metabolic adaptation and environmental change resistance (2). Metagenomics is a promising technique for unbiased pathogen detection in clinical diagnostics. however, its use for urinary tract infection identification is just being realized (3). It has been determined that *Pseudomonas aeruginosa*, the most prevalent bacterium linked to nosocomial infections and ventilator-associated pneumonia, is an opportunistic pathogen (4).

Antibiotic resistance is a serious public health issue with substantial effects on the treatment of infections. Invasion by multidrug-resistant bacteria has increased over the past decade (MDROs). As a result, social and economic growth has been harmed in poor countries like Pakistan (5). (6) Reported that more than 150 million people are affected globally every year by urinary tract infections. In the routine diagnosis of UTI, conventional methods, such as culture and sensitivity, are time-consuming. *Escherichia coli* is a common resistant bacterium in UTI and *Escherichia coli (E. Coli), Pseudomonas, Proteus,* and *Klebsiella* have frequently been detected in urine tract infection (7). *P. aeruginosa* is highly pathogenic due to its high degree of genetic flexibility and phenotypic plasticity. This bacterium produces more virulence factors and becomes more pathogenic. When *P. aeruginosa* is subjected to stressors, modifications to its growth mode take place, leading to the formation of biofilms. The genome of *P. aeruginosa* is unusually big, containing 5567 genes at 6.3 million base pairs (Mbp). In comparison, the genomes of *Escherichia coli* K12 (4.64 Mbp; 4279 genes), *Staphylococcus aureus* N315 (2.81 Mbp; 2594 genes), and *Haemophilus influenza* Rd. (1.83 Mbp; 1714 genes). Furthermore, compared to all other sequenced bacterial genomes, *P. aeruginosa's* genome has a higher fraction of anticipated regulatory genes. (8) UTI prevalence differed among regions. Meta-analysis Males had a UTI prevalence of 15%, which was greater than the 16% incidence in females. 10% in comparison to youngsters (9). Overexploitation of anti-microbial agents, plasmid mediated transfer of genes and formation of biofilms contribute towards antibiotic resistance in *Pseudomonas aeruginosa* UTIs. The other contributing factors of multidrug resistance, including the carbapenems, such as NDM-1, OXA, KPC, CTX-M are the resistance genes.

The resistance and persistence is further augmented by the use of catheters which develop Biofilm. (10). All *Pseudomonas aeruginosa* strains showed 95.2% resistance to amoxicillin-clavulanic acid and 71.4% to 90.5% resistance to cephalosporin antibiotics. Imipenem displayed 100-90% antimicrobial activity(11). Whole genomic sequences approaches could reduce the time required to identify significant antimicrobial resistance genes, aiding sepsis diagnosis and antibiotic susceptibility testing. For the typing of pathogenic bacteria, including MDR and XDR *Pseudomonas aeruginosa*, there is typically no programmed infection control and monitoring system in place (Zhou et al 2022). Very little data on the molecular epidemiology of MDR are available in poor nations such as Pakistan.

MATERIAL AND METHOD

Samples were gathered from patients at the Khyber Teaching Hospital in Peshawar, Khyber Pakhtunkhwa, between April 2025 and August 2025, after clearance from the research board committee at Islamia College. The individuals showed positive urine culture growth of bacteriuria. During the regular medical examination, individuals were recommended by their physicians to undergo diagnostic testing. Sterile, wide-mouth, leak-proof urine containers were used to collect midstream urine specimens with a volume ranging from 20 to 30 ml. The specimens were suitably labeled in accordance with the requirements of the microbiological investigation.

Culture and Biochemical Testing:

The specimens were subjected to inversion (2 to 3 times) and subsequently distributed onto Petri dish of Macconkey and Blood agar plates (Oxoid; used for Gram-negative bacteria) using a wire loop and incubated for 24 hours at 37 ^{0}C in incubators containing 5% CO2 (12). After 24 hours, we examined the plate and determined the bacterial count in colony-forming units per millilitre (CFU/mL). The CFU/mL was obtained by serial dilution at a dilution factor of 10^5. For biochemical analysis catalase, coagulase and indole test were applied.

Antibiotics Susceptibility

The testing of antibiotic susceptibility was performed using the Kirby Bauer disc diffusion technique(13). In which test bacteria, with a turbidity of 0.5 McFarland and a concentration of 1.5 × 10^8 CFU/mL, was streaked on the Muller Hinton Agar (MHA) plate (14). The drugs applied for sensitivity testing involve Ampicillin, Imipenem, Tigecycline, Nitrofurantoin, Meropenem, Amikacin, Gentamicin, Ampicillin, Aztreonam, Cefepime, Ceftazidime, Amoxicillin-clavulanate, Cefixime, Ceftriaxone, Fosfomycin, Amoxicillin, Trimethoprim/sulfamethoxazole, Piperacillin-tazobactam (Bioanalyse, *Turkey*).

DNA Extraction

DNA was extracted according to protocol fellow of (15). The bacterial colony was picked using a sterilized wire loop and mixed with 500 µL of pre-warmed lysis solution at a temperature between 60-65°C. 10 µL of Reagent D, 20 µL of Reagent K, and 1.6 µL of MerC Solution were combined. The sample underwent incubation at temperatures ranging from 60-65°C for 1-2 hours for bacterial samples, and overnight incubation for tissue samples. Next, 700 µL of ChI Buffer was added to the sample. The centrifugation was conducted at 13,000 revolutions per minute (rpm) for 10 minutes. The liquid layer was moved to a new tube, then 950 µl of Wash buffer A was added. Centrifugation was conducted at 13,000 revolutions per minute (rpm) for 15 minutes. The liquid on top was removed, and then 500 µL of Wash Buffer B was added to the solid residue. The material was centrifuged at 8000 revolution per minute (rpm) for 5 to 10 minutes. The liquid component was extracted and discarded. The wooden pallet was air dried. 40-45 µL of Elusion Buffer was added. The incubation lasted 10 to 15 minutes at 60 ℃ to aid in dissolving the pellet.

Note: Purified extracted material is kept at -20℃.

Gel Electrophoresis of *Pseudomonas aeruginosa*

Purified PCR products were run on 1% Agarose gel. 30mL of 1% gel was prepared by adding 0.3g of Agarose in 30mL 1x TBE buffer. Solution was boiled for 1 minute in microwave and cooled down a bit before adding 5 µL Ethidium Bromide.

2µL PCR purified Samples are then loaded on the gel. The gel electrophoresis condition was 110V with 100A current show in the figure (1).

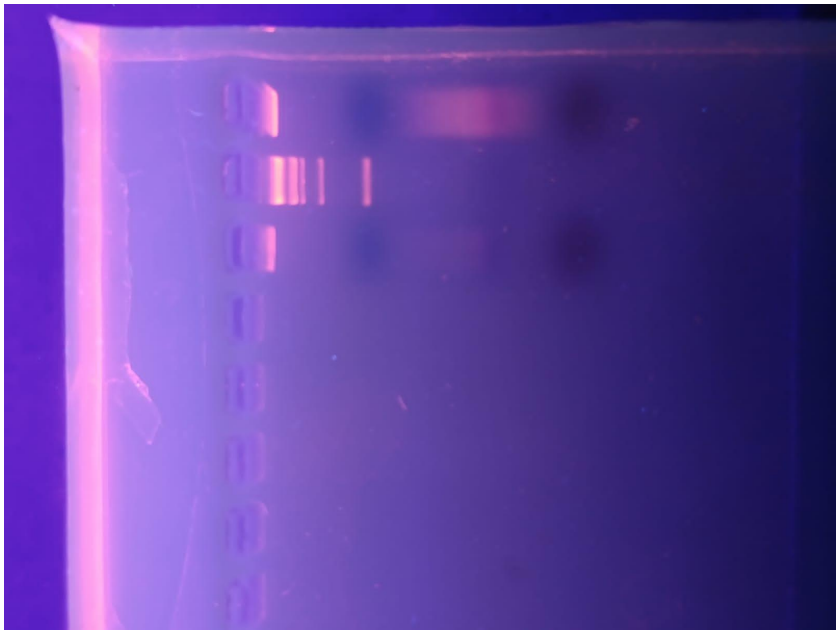

Figure 1: Agarose Gel Electrophoresis Picture of Pseudomonas aeruginosa

Bioinformatics Analysis

DNA from the sample is extracted (100 ng) and sequenced using Illumina technology at china BGI (https://www.bgi.com/global). The *P. aeruginosa* isolate was adapter- and quality-filtered on the Illumina MiSeq low-passage reads using Trimmomatic. Raw paired-end Illumina MiSeq reads generated from the *Pseudomonas aeruginosa* UTI isolate were subjected to adapter and quality trimming using Trimmomatic to remove low-quality bases and sequencing artifacts. The cleaned reads were then aligned to the *P. aeruginosa* PAO1 reference genome (NC_002516) using BWA-MEM v0.7.5a, employing default parameters. Variants were called with SAMtools mpileup and VarScan v2.3.6, using an allele frequency threshold of 80% single nucleotide polymorphisms (SNPs), and short insertion-deletion (indel) variants. Distinctive variants found in SNP where there was either too much SNP density (>3 SNPs per 1000 bp) which could suggest recombination, misalignment, or selective pressure were discarded in subsequent analysis. Devnovo reads were also assembled in silico using MLST typing with Velvet, through BLAST querying of the pubMLST *P. aeruginosa* data base (16). Illumina reads were optionally aligned to a PacBio-based draft genome and polished with Pilon, to enable accurate genome correction. Phylogenies was done using whole-genome variants to be clade specific (17).

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Based on the de novo assembly with k-mer size of 81 in Velvet we assembled trimmed reads to find out the sequence type of the isolate. The assembled contigs were compared against P. aeruginosa multilocus sequence typing (MLST) database downloaded in PubMLST repository (http://pubmlst.org/paeruginosa/) using BLASTn to predict in silico sequence type assignment. To ensure more accuracy and error correction, optional alignments of Illumina reads were done on a draft genome that had been produced by whole genomic sequence. The draft assembly was generated with RS_HGAP_Assembly.3 pipeline in SMRT Portal v2.2.0 with the corrected indel errors polished using Pilon. All script and pipelines including variant calling and phylogenetic inference were downloaded from a publicly available repository at: https://github.com/joshquick/snp_calling_scripts.

RESULT:

Phenotypic Antibiotics Resistance:

Pseudomonas aeruginosa strain isolated had multidrug-resistant (MDR) manifestation, which was tested against various antimicrobials with the Kirby-Bauer disk diffusion method, according to the CLSI guidelines. Though sensitive to meropenem and colistin, the isolate was also resistant to various other agents, such as 1) 3-lactams, 2) fluoroquinolones, 3) aminoglycosides and 4) carbapenems (imipenem), which justified its description as multidrug-resistant P. aeruginosa. The antimicrobials screened were piperacillin-tazobactam, ceftazidime, cefepime, imipenem, meropenem, ciprofloxacin, levofloxacin, gentamicin, amikacin and colistin. The isolation was found to be non-sensitive to at least three antimicrobial categories thus being MDR. Interpretation of zone diameters was as follows shown in figure no 1:

Antibiotic	Disk Content	Zone Diameter (mm)	Interpretation
Piperacillin-Tazobactam	100/10 µg	12	Resistant
Ceftazidime	30 µg	14	Resistant
Cefepime	30 µg	13	Resistant
Imipenem	10 µg	16	Resistant
Meropenem	10 µg	22	Sensitive
Ciprofloxacin	5 µg	13	Resistant
Levofloxacin	5 µg	12	Resistant
Gentamicin	10 µg	14	Resistant
Amikacin	30 µg	17	Resistant
Colistin	10 µg	18	Sensitive

Figure no 1 Shows the AST report of Pseudomonas strain by disk diffusion method

QC Report on Sequenced Bacterial Strain:

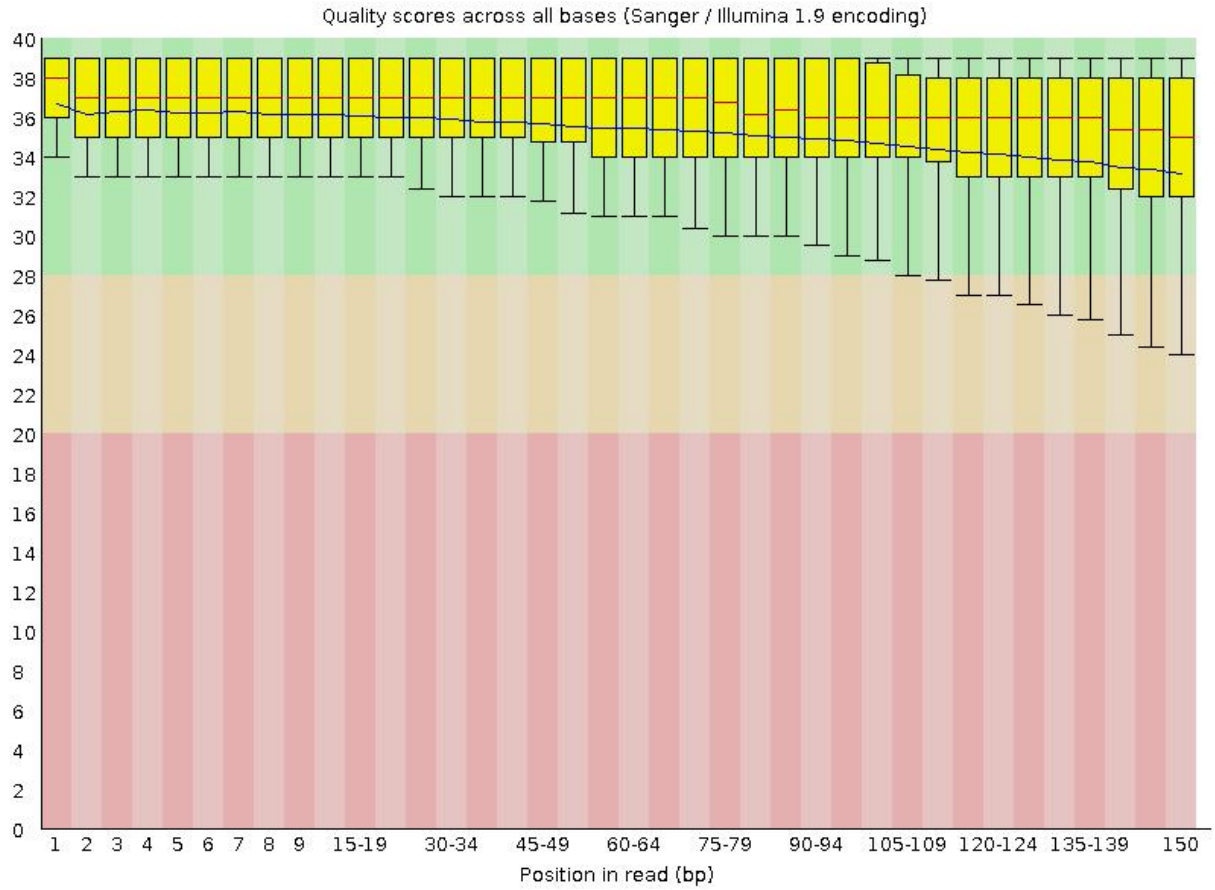


Figure no 2 shows that Based on the plot it can be assumed that the data of the sequencing is of good quality, but the quality scores are high at the head of the read. The quality scores, however, dropped at the end of the read which could suggest that there was degradation of the data. It is information that can be utilized to inform downstream analysis and processing of the sequencing data.

Genotypic Characterization of Antimicrobial Resistance:

Pseudomonas aeruginosa isolate sequencing of the entire genome and subsequent resistance gene identification through STARAMR tool showed a wide variety of antimicrobial resistance (AMR) genes, which proved the high level of multidrug resistance (MDR). A number of aminoglycoside-modifying enzyme genes were observed which include aac(3)-Id, aac(6')-Il, aadA11, aph(3'')-Ib, aph(3')-IIb and aph(6)-Id. These genes confer gentamicin, streptomycin and kanamycin resistance by means of acetylation, phosphorylation and adenylation resulting in enzyme inactivation of the

antibiotics. The description of the association of resistance to 2-lactam antibiotics with the blaOXA-488 and blaPAO genes enabled overcoming the production of 2-lactam. The blaOXA-488 gene codes the resistance to ampicillin due to a class D beta-lactamase whereas blaPAO codes the broad phenotype resistance of ampicillin, amoxicillin/clavulanic acid, cefoxitin and ceftriaxone, thus making the strain resistant to penicillin and extended-spectrum cephalosporin. Moreover, the strain encoded the catB7 floR genes that conferred chloramphenicol resistance by the action of an enzyme and efflux pump, respectively. Two fluoroquinolone resistance related genes were identified which are plasmid mediated crpP and qnrVC1 that are related to decreased susceptibility or resistance to ciprofloxacin. The mechanism of action of such genes is the decreased accumulation of antibiotics or protection of the gyrase DNA target. It also featured dfrB5 and sul2, which encodes dihydrofolate reductase and dihydropteroate synthase resistant variants, giving the isolate resistance to the trimethoprim and sulfisoxazole drugs. Moreover, resistance to Fosfomycin may also be attributed to the availability of the fosA gene that produces a glutathione S- transferase to modify the pharmaceutical.

Table no.2 AMR Genes of Sequenced Pseudomonas Strain

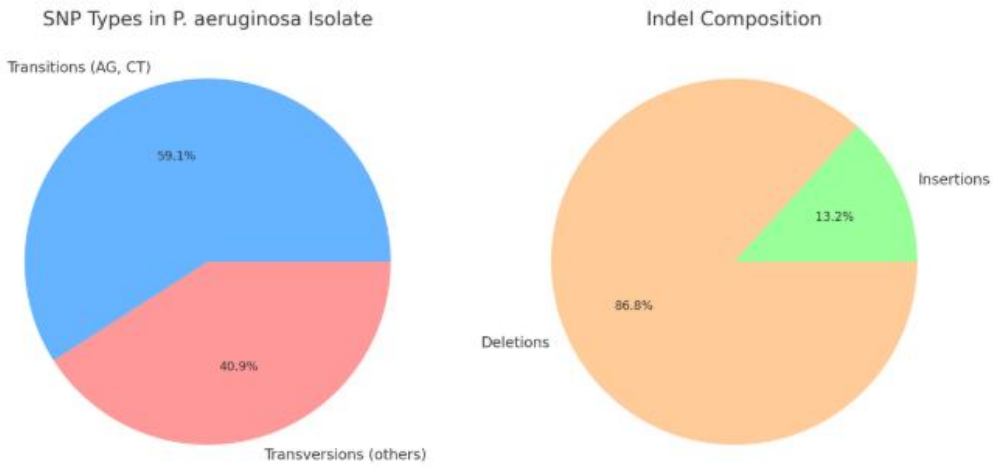
AMR Genes	Antibiotics Susceptibility	Predicted Phenotype
aac(3)-Id	Resistance	gentamicin
aac(6')-Il	Resistance	gentamicin
aadA11	Resistance	streptomycin
aph (3'')-Ib	Resistance	streptomycin
aph(3')-IIb	Resistance	kanamycin
aph(6)-Id	Resistance	kanamycin
blaOXA-488	Resistance	ampicillin
blaPAO	Resistance	ampicillin, amoxicillin/clavulanic acid, cefoxitin, ceftriaxone
catB7	Resistance	chloramphenicol
crpP	Resistance	ciprofloxacin I/R
dfrB5	Resistance	trimethoprim
floR	Resistance	chloramphenicol
fosA	Resistance	Fosfomycin
qnrVC1	Resistance	ciprofloxacin I/R
sul2	Resistance	sulfisoxazole

Indel, insertion and SNPS Analysis:

Table no 3 is detailed output from a genome alignment and variant analysis, likely generated by a tool like NUCmer. It indicates a complete decomposition of the genomic variation found in two comparative studies of Pseudomonas aeruginosa, namely SNPs (Single Nucleotide Polymorphisms), GSNPs (Gene-associated SNPs) Indels (insertions and deletions) and GIndels (gene-associated indels). The two samples/two views (i.e. reference vs query) of the same genome alignment analyzed in the columns each contain 59,227 total SNPs. The SNPs are then grouped by their nucleotide change, that is TC, TA, TG, and others and the row gives the number and the percentage used to the total SNPs. The most common of them are AG and GA transitions (purine-to-purine or pyrimidine-to-pyrimidine substitutions) making up ~1821% of the mutations as expected of natural mutational biases. less frequent are the transversions (e.g. TA, GT). The section, TotalSNPs, further refines these SNPs to gene-associated SNPs, which are of interest due to their potential impact on protein or regulatory sequences, and thus help determine antibiotic resistance or pathogenicity. The second half of the table refers to Indels (insertions and deletions) that may be found in both directions and give a total of 3,330 events. They are categorized by the base added or removed and whether it was done prior to the position or after the position (e.g., "T", T.") The frequencies imply that deletions and insertions of C, G and A bases are somewhat normal and have symmetrical frequencies per sample. The GIndels subset (gene-associated indels) has 219 events and displays the indels that reach genes only. These are very important since insertions or deletions as minute as a single base can lead to shifts in the frame or coding sequences and this may change the resistance genes or efflux pumps functions or any other virulence factor. The presented difference indicates a significant genomic plasticity of the MDR P. aeruginosa strain, likely to represent the evidence of evolutionary changes under the impact of antibiotics or other stress factors.

TotalSNPs	Reference Genome	Query Genome
TC	11297(19.0741%)	10046(16.9619%)
TA	774(1.3068%)	696(1.1751%)
TG	1969(3.3245%)	1513(2.5546%)
CA	1621(2.7369%)	2095(3.5372%)
CG	3144(5.3084%)	3029(5.1142%)
CT	10046(16.9619%)	11297(19.0741%)
GA	10822(18.2721%)	12221(20.6342%)
GT	1513(2.5546%)	1969(3.3245%)
GC	3029(5.1142%)	3144(5.3084%)

AG	12221(20.6342%)	10822(18.2721%)
AT	696(1.1751%)	774(1.3068%)
AC	2095(3.5372%)	1621(2.7369%)
TotalSNPs	30724	30724
CA	735(2.3923%)	979(3.1864%)
CG	1356(4.4135%)	1355(4.4102%)
CT	5506(17.9208%)	6173(20.0918%)
TC	6173(20.0918%)	5506(17.9208%)
TA	322(1.0480%)	298(0.9699%)
TG	938(3.0530%)	683(2.2230%)
GT	683(2.2230%)	938(3.0530%)
GC	1355(4.4102%)	1356(4.4135%)
GA	5833(18.9852%)	6546(21.3058%)
AG	6546(21.3058%)	5833(18.9852%)
AT	298(0.9699%)	322(1.0480%)
AC	979(3.1864%)	735(2.3923%)
TotalIndels	3330	3330
T.	268(8.0480%)	288(8.6486%)
C.	529(15.8859%)	599(17.9880%)
G.	508(15.2553%)	580(17.4174%)
A.	310(9.3093%)	248(7.4474%)
.G	580(17.4174%)	508(15.2553%)
.A	248(7.4474%)	310(9.3093%)
.C	599(17.9880%)	529(15.8859%)
.T	288(8.6486%)	268(8.0480%)
TotalGIndels	219	219
C.	31(14.1553%)	48(21.9178%)
T.	14(6.3927%)	20(9.1324%)
G.	25(11.4155%)	36(16.4384%)
A.	24(10.9589%)	21(9.5890%)
.A	21(9.5890%)	24(10.9589%)
.G	36(16.4384%)	25(11.4155%)
.T	20(9.1324%)	14(6.3927%)
.C	48(21.9178%)	31(14.1553%)



Here is a visual summary of your genomic variation analysis:

- The left pie chart shows that the majority of SNPs are **transitions** (AG and CT), which are typical and often less disruptive.
- The right pie chart indicates that most small indels are **deletions**, with insertions representing a smaller proportion.

DISCUSSION:

The present study confirmed that the *Pseudomonas aeruginosa* isolate recovered from a urinary tract infection exhibited a multidrug-resistant (MDR) phenotype, demonstrating resistance to β-lactams, fluoroquinolones, aminoglycosides, and imipenem, while remaining susceptible to meropenem and colistin. This resistance profile agrees with previous reports showing that MDR *P. aeruginosa* has become a major cause of healthcare-associated infections due to its ability to acquire resistance against multiple antimicrobial classes. Whole-genome sequencing showed strong agreement with the phenotypic antimicrobial susceptibility results by identifying several clinically important resistance genes. Aminoglycoside resistance was associated with the presence of aac(3)-Id, aac(6')-II, aadA11, aph(3'')-Ib, aph(3')-IIb, and aph(6)-Id, which encode aminoglycoside-modifying enzymes. Similar resistance determinants have been widely reported in clinical MDR *P. aeruginosa* isolates and are recognized as major contributors to aminoglycoside resistance. The close correlation between phenotypic and genotypic findings highlights the value of whole-genome sequencing for accurate prediction of antimicrobial resistance. The identification of blaOXA-488 and blaPAO explains the observed resistance to β-lactam antibiotics, including ceftazidime, cefepime, and

piperacillin-tazobactam. Previous studies have similarly reported that OXA-type β-lactamases contribute significantly to β-lactam resistance in *P. aeruginosa*, particularly when combined with intrinsic chromosomal resistance mechanisms. Likewise, the detection of crpP and qnrVC1 supports the phenotypic resistance to ciprofloxacin and levofloxacin. These genes have increasingly been identified in MDR clinical isolates and are associated with reduced susceptibility to fluoroquinolones through target protection and antibiotic modification. Additional resistance genes, including fosA, catB7, floR, dfrB5, and sul2, indicate that the isolate possesses a broad resistome capable of conferring resistance to multiple antibiotic classes. Similar combinations of resistance determinants have been described in recent genomic studies, suggesting that accumulation of diverse resistance genes is an important factor in the successful persistence and dissemination of MDR *P. aeruginosa* in hospital environments. Although the isolate was resistant to imipenem, it remained susceptible to meropenem and colistin. Comparable findings have been reported in previous studies, where differences in carbapenem susceptibility were attributed to variations in porin expression, efflux pump activity, and β-lactamase production. The retained susceptibility to colistin indicates that this antibiotic may still represent a valuable therapeutic option for severe MDR *P. aeruginosa* infections, although its use should be carefully monitored to limit the emergence of resistance. Genome-wide SNP and indel analyses demonstrated considerable genetic variation within the isolate, with transition mutations occurring more frequently than transversions. Such mutational patterns have also been reported in previous genomic investigations and reflect the adaptive evolution of *P. aeruginosa* under antimicrobial pressure. Gene-associated SNPs and indels may alter the function or regulation of resistance-associated genes, thereby contributing to antimicrobial resistance and bacterial persistence. Overall, the findings demonstrate a strong correlation between phenotypic antimicrobial resistance and genomic resistance determinants. The coexistence of multiple AMR genes together with extensive genomic variation highlights the remarkable adaptability of *P. aeruginosa* and emphasizes the importance of integrating conventional susceptibility testing with whole-genome sequencing for surveillance, resistance monitoring, and selection of appropriate antimicrobial therapy. Future studies involving larger numbers of clinical isolates will provide a better understanding of the molecular epidemiology and evolution of MDR *P. aeruginosa* in clinical settings.

CONCLUSION:

The studied *Pseudomonas aeruginosa* isolate exhibited multidrug resistance supported by both phenotypic and genomic analyses. Multiple antimicrobial resistance genes and

genomic variations were identified, explaining their resistant phenotype. These findings highlight the importance of whole-genome sequencing for antimicrobial resistance surveillance and infection control.

REFERENCES

1. Liu D, Zhou H, Xu T, Yang Q, Mo X, Shi D, et al. Multicenter assessment of shotgun metagenomics for pathogen detection. 2021;74:103649.
2. Langille MG, Zaneveld J, Caporaso JG, McDonald D, Knights D, Reyes JA, et al. Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. 2013;31(9):814-21.
3. Tian Z, Liang MJNC. Renal metabolism and hypertension. 2021;12(1):963.
4. Basavaraju M, Gunashree B. Escherichia coli: an overview of main characteristics. Escherichia coli-Old and New Insights. 2022.
5. Fatima T, Rafiq S, Iqbal A, Husnain SJSCCM. Prevalence and antibiogram of MDR E. coli strains isolated from UTI patients—1-Year retrospective study at Nishtar medical hospital, Multan. 2020;2(4):423-31.
6. Upadhyay P, Surar F, Kim G, Reddy J, Shakir S, Alexander BD, et al., editors. 2223. A comparative analysis of the detection of UTI pathogens via culture method and the Open Array-nanofluidic real time PCR method. Open Forum Infectious Diseases; 2022: Oxford University Press US.
7. Edirisinghe L, Vidanagama DJGMJ. A retrospective analysis of urine culture results issued by the microbiology department, Teaching Hospital, Karapitiya. 2008;13:40-4.
8. Jia K, Huang S, Shen C, Li H, Zhang Z, Wang L, et al. Enhancing urinary tract infection diagnosis for negative culture patients with metagenomic next-generation sequencing (mNGS). 2023;13:218.
9. Shaik S, Singh A, Suresh A, Ahmed NJM. Genome informatics and machine learning-based identification of antimicrobial resistance-encoding features and virulence attributes in escherichia coli genomes representing globally prevalent lineages, including high-risk clonal complexes. 2022;13(1):e03796-21.
10. Barraud O, Ravry C, François B, Daix T, Ploy M-C, Vignon PJIjoaa. Shotgun metagenomics for microbiome and resistome detection in septic patients with urinary tract infection. 2019;54(6):803-8.
11. Al-Khfaji ZA, Sagban SH, Al-Musawi AF. Prevalence of Drug-Resistant Strains of Escherichia coli and Klebsiella pneumoniae Isolated from Women with Urinary Tract Infections in Karbala City, Iraq %J Egyptian Journal of Botany. 2023;63(1):295-303.

12. Wilson ML, Gaido L. Laboratory diagnosis of urinary tract infections in adult patients. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America. 2004;38(8):1150-8.
13. Biemer JJ. Antimicrobial susceptibility testing by the Kirby-Bauer disc diffusion method. Annals of Clinical & Laboratory Science. 1973;3(2):135-40.
14. Bauer A, Kirby W, Sherris JC, Turck MJAjocp. Antibiotic susceptibility testing by a standardized single disk method. 1966;45(4_ts):493-6.
15. Alves MS, Dias RCdS, de Castro ACD, Riley LW, Moreira BM. Identification of clinical isolates of indole-positive and indole-negative Klebsiella spp. Journal of clinical microbiology. 2006;44(10):3640-6.
16. Hasman H, Saputra D, Sicheritz-Ponten T, Lund O, Svendsen CA, Frimodt-Møller N, et al. Rapid whole-genome sequencing for detection and characterization of microorganisms directly from clinical samples. Journal of clinical microbiology. 2014;52(1):139-46.
17. Leekitcharoenphon P, Kaas RS, Thomsen MCF, Friis C, Rasmussen S, Aarestrup FM, editors. snpTree-a web-server to identify and construct SNP trees from whole genome sequence data. BMC genomics; 2012: BioMed Central.
18. Prakash D, Saxena RS. Distribution and antimicrobial susceptibility pattern of bacterial pathogens causing urinary tract infection in urban community of meerut city, India. International scholarly research notices. 2013;2013.
19. Yang X, Chen H, Zheng Y, Qu S, Wang H, Yi F. Disease burden and long-term trends of urinary tract infections: A worldwide report. Frontiers in Public Health. 2022;10:888205.
20. Johnson CY, Rocheleau CM, Howley MM, Chiu SK, Arnold KE, Ailes EC, et al. Characteristics of women with urinary tract infection in pregnancy. Journal of women's health. 2021;30(11):1556-64.
21. Muhammad A, Khan S, Ali N, Rehman M, Ali I. Prevalence and antibiotic susceptibility pattern of uropathogens in outpatients at a tertiary care hospital. New Microbes and new infections. 2020;36:100716.
22. Villar HE, Jugo MB, Macan A, Visser M, Hidalgo M, Maccallini GC. Frequency and antibiotic susceptibility patterns of urinary pathogens in male outpatients in Argentina. The Journal of Infection in Developing Countries. 2014;8(06):699-704.