Global High-Risk Clones of *Pseudomonas aeruginosa* and Their Antimicrobial Resistance Profiles in Clinical Isolates from Hospitals in Greater Accra, Ghana

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Article

Global High-Risk Clones of *Pseudomonas aeruginosa* and Their Antimicrobial Resistance Profiles in Clinical Isolates from Hospitals in Greater Accra, Ghana

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Abstract

Background: *Pseudomonas aeruginosa* is an opportunistic pathogen with both intrinsic and acquired antimicrobial resistance. High-risk clones are associated with carbapenem resistance because they frequently harbour and disseminate carbapenemase genes and other resistance determinants, enabling their persistence and spread in healthcare settings. Carbapenem-resistant strains have limited treatment options. However, genomic data on high-risk clones circulating in Ghana remain limited**. Methods:** This cross-sectional study was conducted between December 2023 and January 2024 in eight government hospitals in Accra, Ghana. Clinical isolates were collected from multiple specimen types and identified using standard antimicrobial susceptibility testing in accordance with CLSI guidelines to determine resistance profiles, and subsequently confirmed by MALDI-TOF-MS, Whole-genome sequencing was carried out using the Illumina NextSeq 2000 platform. Bioinformatic analyses were then conducted to determine sequence types, identify antimicrobial resistance genes and virulence factors, and assess phylogenetic relationships among the isolates. **Results**: High-risk international clones (ST235, ST244, ST308, and ST773) predominated. Low SNP differences (≤10 SNPs) indicated recent clonal transmission within and between hospitals. Serotype O11 was dominant and strongly associated with high-risk clones. Isolates carried multiple resistance determinants, including aminoglycoside-modifying enzymes and ESBL genes (*bla*CTX-M-15, *bla*TEM-1B) — carbapenemase genes, particularly blaNDM-1, coexisted with *bla*OXA-50 variants. Findings demonstrate local clonal expansion, global relatedness, and the emergence of a novel sequence type (ST5336) in Ghana. **Conclusion:** High-risk clones, especially ST773, are widely circulating in hospitals across Accra, indicating ongoing transmission and clonal expansion. The emergence of the novel ST5336, emphasize the urgent need for enhanced genomic surveillance and antimicrobial stewardship in Ghana. **Significance of this research article:** This work strengthens the evidence base needed to inform infection prevention strategies, antimicrobial stewardship programs, and the implementation of routine genomic surveillance to curb the spread of high-risk, carbapenem-resistant clones in Ghana and similar resource-limited settings.

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1. Introduction

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Pseudomonas aeruginosa remains one of the most clinically important opportunistic pathogens worldwide, renowned for its intrinsic resistance, remarkable genomic plasticity, and ability to acquire diverse antimicrobial resistance (AMR) and virulence determinants [1]. Multiple factors, including horizontal gene transfer, chromosomal mutations, and clonal expansion of high-risk lineages, drive its adaptability. These characteristics have positioned *P. aeruginosa* as a leading cause of multidrug-resistant (MDR) and carbapenem-resistant infections in hospital settings, particularly among critically ill or immunocompromised patients. In recognition of these threats, the World Health Organization (WHO) lists carbapenem-resistant *P. aeruginosa* (CRPA) as a "critical priority" pathogen for global surveillance and research[2].

Globally, several high-risk clones—such as ST235, ST244, ST308, and the recently emerging ST773—have been associated with widespread dissemination of β-lactamase and metallo-β-lactamase determinants, enhanced virulence traits, and sustained nosocomial outbreaks across Europe, Asia, and the Americas[3]. These clones are often characterized by the presence of potent virulence effectors such as ExoU, a type III secretion system (T3SS) cytotoxin strongly linked to severe disease outcomes.[3] The co-occurrence of extensive drug resistance and hypervirulence in these lineages emphasizes the urgent need for routine genomic surveillance, particularly in low- and middle-income countries where data remain limited.

In Ghana, the molecular epidemiology of *P. aeruginosa* is poorly characterized despite clinical concerns regarding MDR and CRPA infections[4]. While sporadic reports have described Carbapenemase-producing isolates in parts of West Africa, comprehensive genomic data across multiple hospitals are lacking[5]. Such information is essential to uncover the diversity of circulating clones, detect potential outbreaks, examine transmission pathways, and inform antimicrobial stewardship and infection-prevention interventions.

This study aimed to address this gap by conducting whole-genome sequencing of *P. aeruginosa* isolates collected from major hospitals in Accra, Ghana. We investigated the distribution of sequence types, the presence of high-risk clones, their resistance and virulence gene repertoires, and their phylogenetic relationships in a global context. The findings provide crucial insights into the evolving population structure of *P. aeruginosa* in Accra, Ghana and highlight the importance of integrating genomic surveillance with clinical risk profiling to strengthen infection control and public health responses.

2. Materials and Methods

2.1. Study Settings

A cross-sectional study was conducted from December 2023 to January 2024 in eight government-supported acute care hospitals in Accra, the business centre of the Greater Accra Region and the national capital of Ghana. Among the 31 government-supported acute care hospitals in the region, nine offer microbiological services, including culture and antimicrobial susceptibility testing. Eight of these nine hospitals consented to participate. The study sites included three teaching hospitals [University of Ghana Medical Centre (1,000 beds), Korle-Bu Teaching Hospital (2,000 beds), Greater Accra Regional Hospital (420 beds)], two secondary hospitals [Ledzokuku-Krowor Municipal Assembly Hospital (100 beds), Tema General Hospital (400 beds)], and 3 primary hospitals [Maamobi Government Hospital (70 beds), Ga North Municipal Hospital (100 beds), Dodowa Government Hospital (244 beds)] [6].

2.2. Sampling and Data Extraction

The study isolates were prospectively collected from December 2023 to January 2024 from eight government-supported Hospitals in the Greater Accra Region of Ghana, through routine laboratory testing on different sample types, including urine, catheter tip, wound, blood, ear swab, and eye swab. Sputum. A data extraction form was used to extract information from the Lightwave Health Information Management System (LHIMS) on each patient sample for which *P. aeruginosa* was the cause of infection. The duration of admission, type of samples, previous antibiotic use, comorbidity, biographic data, hospitalisation status, and invasive procedures were documented.

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2.3. Bacterial Isolates Recovery, and Antimicrobial Susceptibility Testing

Presumptive *Pseudomonas aeruginosa* isolates from various sites were transported in SSI medium to the University of Ghana Medical Microbiology Department. The isolates were purified on MacConkey agar, re-stocked, and stored at 5 °C[7]. Standard microbiological methods and MALDI-TOF-MS (Bruker Daltonics) with BioTyper 2.0 software were used for identification. Only isolates confirmed as *P. aeruginosa* (log score ≥2.0) were included in the study[8]. Antibiotic susceptibility testing was carried out on Muller-Hinton agar according to the Clinical Laboratory Standard Institute (CLSI) guideline (M100-2025). A loopful of the standardised inoculum was swabbed onto the Muller-Hinton agar plate to ensure confluent growth. Susceptibility testing involved a bacterial inoculum of 0.5 McFarland standard. The selected antibiotics included Piperacillin/tazobactam (100/10 ug), Ceftazidime (30 ug), Cefepime (30 ug), Amikacin (30 ug), Ciprofloxacin (5 ug), Meropenem (10 ug), and Aztreonam (30 ug). The antibiotic discs were firmly applied to the agar plate and incubated aerobically at 35°C-37°C for 18 to 24 hours. After incubation, the zone of inhibition for the various antibiotics was measured and interpreted as per the CLSI M100,2025[7]. Isolates with these zone diameter breakpoints less or equal to the lower limit of each antibiotics were both considered to be resistant and zones of inhibition for the various antibiotics were interpreted according to CLSI M100™breakpoints piperacillin/tazobactam [100/10 µg](14≥21), ceftazidime [30 µg](14≥18), cefepime [30 µg],(14≥18), amikacin [30 µg](14≥17, ciprofloxacin [5] µg](18≥25, and meropenem [10 µg](15≥19), Aztreonam [30 µg](12≥18) Oxoid Basingstoke,(CLSI M02,2025)[9].

2.4. Genomic DNA Extraction and Sequencing

Confirmed isolates were Whole Genome Sequenced (WGS). DNA from overnight cultures on nutrient agar was incubated aerobically at 35°C - 37°C for 18 to 24 hours and extracted using QIA amp Mini Spin Kit (Qiagen), following the manufacturer's protocol[10]. DNA concentration was measured with a Qubit 4.0 Fluorometer and Qubit HS dsDNA Kit (Invitrogen, MA, USA), and extracts were stored at −20 °C. DNA was diluted to 100–500 ng/µl (30 µl volume) for library preparation using the Illumina DNA Prep (M) Tagmentation Kit (Illumina Inc., San Diego, CA). Library quality and concentration were checked with the Agilent 2100 Bioanalyzer and Qubit 4.0. Libraries were normalized to 2 ng/µl, pooled, and sequenced on the Illumina NextSeq 2000 (2 × 150 cycles). Raw FastQ reads were retrieved from the platform after three days[11].

2.5. Bioinformatic Analysis

Raw reads from the Illumina NextSeq 2000 platform were assessed using FASTQC v0.12.1 and cleaned with Trimmomatic v0.39 to remove adapters and bases with Phred scores <20. Cleaned reads were assembled de novo using Unicycler v0.5.0, excluding contigs <200 bp. Assembly quality was evaluated with QUAST v5.2.0. Genomes with <20× coverage or >300 contigs were flagged for re-sequencing. Species identification, resistance genes, virulence factors, sequence types, and plasmid replicons were identified using KmerFinder v4.1, ResFinder v4.5.0, VFDB, MLST v2.0, and Plasmid Finder v2.1, respectively. Bactinspector v0.1.3 was used to select the best reference genome. Phylogenetic relationships were inferred using CSI Phylogeny with reference genome NC_002516.2, and visualised using iTOL. All tools were run with default settings unless specified. Cluster analysis was conducted. Genomes were submitted to GenBank.

2.6. Data Analysis

Data generated from laboratory investigations were recorded in Microsoft Excel version 2024 for editing and analysis. The WGS results were discussed using descriptive analysis with proportions and percentages.

3. Results

3.1. Circulating Clones of Pseudomonas aeruginosa in the Hospital Environment in Accra, Ghana

The study identified two major clades, both of which included high-risk clones (Fig.4.2 below). Clade 1 (C1) comprised ST244, detected across four hospitals, and both ST235 and ST308 were

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restricted to a single site, together with some rare clones that were distributed across multiple hospitals. In contrast, Clade 2 (C2) was a single sequence type ST773. A total of twelve (n=12) genetically distinct sequence types were identified, including isolates belonging to ST235(2), ST244(4), ST308(2), ST569(1), ST773(20), ST782(1), ST941(1), ST988(1), ST1062(1), ST1116(1), ST195(1), and novel ST5336(1). Phylogenetic analysis showed that all sequence types (STs) carried at least one aminoglycoside-modifying enzyme, potentially conferring reduced aminoglycoside susceptibility, and at least one β-lactamase gene. Clade 1 showed pairwise SNP differences of 1 and 6 SNPs among the isolates sampled at study site 6 (four genomes: P2371074, 123092628, P23081023, P23011820), indicating a high degree of genetic relatedness typical of recent divergence, clonal transmission, and local outbreak [12] [13].

Similarly, a close genetic relatedness between twelve genomes in C2 was identified. Only one to ten SNPs separated the genomes of ten from site 6 (12300154, 123095583; P216005, 123692656; P27063, P23060374; 12309461, 1230917679; and 12309042, 12309461) and two from site 8 (C2487 and 1349)[14]. A common clinical source, endemic sequence type, intra-hospital transmission, and anticipated transmission clusters are all suggested by this low SNP variation [14].SNP difference across isolates from the various study sites showed that, at a threshold of ≤10 SNPs, there were cases of close genetic relatedness. This raises the possibility of shared infection origins or clone migration between facilities. ST244 of subclade C1a, was identified in four different hospitals with resistance genes to fluoroquinolones, macrolides, chloramphenicol, and Fosfomycin. The ST244 lineage also carried β-lactamase and metallo-β-lactamase (MBL) genes. In subclade C1b, ST235 was shown to accumulate β-lactamase genes with extended-spectrum activity. The ST235 isolates from a single hospital had *bla*OXA-396 + *bla*TEM-1B together with other resistance genes for aminoglycosides, chloramphenicol, and Fosfomycin were present. The ST773 from Clade 2 carried either multiple Carbapenemase genes or a single Carbapenemase gene. For example, *bla*OXA-395 + *bla*NDM-1, blaOXA-395, *bla*OXA-396, and blaOXA-50 were only detected in ST 773. In contrast, globally reported ST773 clones carried different combinations, such as *blaVIM* + *blaOXA-10*(India), *bla*OXA-181 (UK), and *blsaVIM* + *blaIMP-2* (Iran) [15]; [16]; [17]. The ST773 emerged as the most predominant sequence type, with widespread detection likely driven by either importation or local adaptation, consistent with previous findings [18]; [19]. This contrasts with work from Vietnam, where ST235 predominated [19]. A novel ST5336(1) was identified in blood, and this carried aminoglycoside-modifying enzymes and at least one β-lactamase gene, together with resistance determinants for chloramphenicol and Fosfomycin.

3.2. Clonal Diversity and Carbapenemase Genes

Analysis of the isolates revealed a predominance of serotype O11, with other serotypes—including O12, O5, O6, O7, O4, O3, and O1 occurring at comparatively lower frequencies. The O11 serotype was strongly associated with high-risk international clones, notably ST773, ST235, ST244, and ST308, which have been widely implicated in nosocomial outbreaks globally. High prevalence of Carbapenemase-encoding genes, particularly *bla*NDM-1, was frequently identified among O11 serotype isolates. The coexistence of *bla*TEM-1B and *bla*CTX-M-15 with *bla*OXA-95 was found in isolates carrying the O11 serotype. *bla*OXA-50 variant was detected among all isolates. The *bla*OXA-50 variants are intrinsic chromosomally encoded β-lactamases in *P. aeruginosa* but are often overexpressed in resistant strains, contributing to elevated resistance against carbapenems. Their coexistence with acquired MBL genes, including *blaNDM-1* and *blaVIM-5*, suggests synergistic resistance mechanisms that critically limit therapeutic options (fig 4.3)

3.3. Pathotype Distribution Among Sequence Types

A total of twelve sequence types were identified, with O11 serotypes being the most common, followed closely by O12, O7, O6, O5, O4, and O1 serotypes. The sequence types also commonly express T3SS exoU+/exoS- pathotypes. T3SS pathotypes were distributed as follows: of the 36 isolates, 25 isolates expressed exoU+/exoS-, 10 isolates expressed ExoT+/exoS+, and exoU+/exoS+/ExoT+ was expressed by only one isolate. Among the high clones (28 isolates), the exoU+/exoS+ pathotypes were recovered from (8isolates), while exoU+/exoS- was expressed by (20 isolates) (fig 4.4)

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3.4. Horizontally acquired Beta-Lactamase Genes In the Study Isolates

Horizontally acquired β-lactamase genes were identified among the study isolates, particularly within the high-risk global clones ST308, ST244, ST773, and ST235. These sequence types harboured a diverse array of acquired β-lactamase determinants. These included class A enzymes, such as *bla*CTX-M-15 and *bla*TEM-1B. Two sequence type ST 308 coexpressed two ESBL genes (blaCTX-M-15 and blaTEM-1*B).* Among the class B metallo-β-lactamases, *bla*NDM-1 was extensively expressed in ST773 (13 isolates), and *bla*IMP-15 was identified in ST244 (3 isolates). All sequence types carried at least one blaOXA-50 variant, including blaOXA-396**,** blaOXA-395**,** and *bla*OXA-488**.** Notably, among the sequence types, blaOXA-395 was identified in 20 isolates, Table 4.7.

3.5. Genetic Relatedness and Global Distribution of P. Aeruginosa Sequence Types

The *P. aeruginosa* PubMLST database (accessed in July 2025) revealed a total of 45 genomes represented 15 unique sequence types. Thirty-six (36) genomes from Ghana and nine (9) global genomes from eight (8) global countries. The MST reveals clustering of closely related sequence types and instances of global spread of certain.

This study revealed 12 sequence types (11 previously reported and the novel ST5336), of which four (4) STs were high-risk clones (ST235, ST244, ST308 and ST773), an indication of the diversity of clones across Accra, Ghana. Nevertheless, a previous report also identified these international clones in Ghana, which contrasts our findings: ST233, ST235, ST244, ST277, ST357, ST308, ST446, ST654, and ST773 [20]. The minimum spanning Tree (MST) (Fig. 5) presents the phylogenetic relationship among Ghanaian *P. aeruginosa* STs compared to global STs

4. Discussion

The *blaNDM-1* was the most frequent Carbapenemase gene in our isolates, consistent with Ghanaian reports identifying NDM-type enzymes, particularly blaNDM-1, as the dominant carbapenemases among non-fermenters [21]. Nearly all *P. aeruginosa* in our study carried chromosomally encoded *blaOXA-50* family variants (OXA-395, OXA-396, OXA-488), which exhibit weak carbapenem-hydrolysing activity and are not clinically significant carbapenemases on their own. In our collection, *blaOXA-50* variants consistently co-occurred with acquired carbapenemases, including MBLs (NDM-1, VIM-5, IMP-15) and Class A enzymes (GES-2, GES-5), suggesting that the carbapenemases phenotype in our isolates is primarily driven by these acquired enzymes [22]. It is noteworthy that, because *blaOXA-50* variants are ubiquitous in our Ghanaian isolates, studies of Carbapenemase production should interpret phenotypic results cautiously to avoid false positives from blaOXA-50 derivatives and structural cell modifications.

The study identified high-risk clones and novel sequence types in blood specimens, which emphasized the possible difficulty in adhering to infection prevention and control and treatment protocols. This stresses the need for ongoing monitoring and infection control measures to reduce the transmission of these drug-resistant pathogens in this low-resource environment. The newly discovered sequence type raises concerns on distinct transmission dynamics or evolutionary pressures in Ghana, necessitating additional research and highlighting the need for ongoing genomic surveillance.

In the phylogenetic tree of this research, ST244 (C1a) were identified in four hospitals. Its SNP difference was less than 10, indicating close genetic relatedness among the genomes from other hospitals and potentially inter-hospital transmission and endemicity [23]. The ST244 carried the *bla*OXA-50variant with a metallo-beta-lactamase(*bla*OXA-396 +*bla*VIM-5),aminoglycoside-modifying enzymes(aph(3)1b,ant(2)1a,ciprofloxacillin-modifying enzyme, sulphonamide-resistant gene, Fos genes and some virulence genes such as *exoS, exoU, LasB* and plcH [23]. This finding is consistent with previous reports from Europe and Asia, where ST244 has been described as a widely disseminated lineage associated with β-lactamase and metallo-β-lactamase (MBL) determinants, as well as key virulence genes that contribute to carbapenem resistance [24; 25]. In contrast, the ST235 (C1b) was confined to a single hospital in Accra, carried a *bla*OXA-50 variant with ESBLs or metallo-beta-lactamase gene (*bla*OXA-396 + *bla*TEM-1B) or (*bla*OXA-395 + *bla*VIM-5), aminoglycoside-modifying enzymes (*aph(3)1b, aac(3)11*), chloramphenicol acetyltransferase gene (cat B), Fos gene along with

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virulence determinants such as *exoS*, *exoU, lasB and plcH*. Globally, ST235 has been recognized as one of the most successful pandemic clones, frequently reported as the predominant lineage in outbreaks across Asia, Europe, and America [24; 25]. For example, studies from Vietnam and Japan highlighted ST235 as the leading high-risk clone driving carbapenem resistance (Tada *et al*., 2016; Shibata *et al*., 2020). The localised distribution of sequence type ST235 in a single study centre in Ghana contrasts with these global reports, suggesting that ST235 may be less successful at inter-hospital spread in this setting, potentially due to competition with hypervirulent ST773 and ST244 (Shibata *et al*., 2020).

ST773 (C2) emerged as the predominant clone in this study and carried the *bla*OXA-50 variant with a metallo-beta-lactamase (*bla*OXA-396 + *bla*NDM-1), aminoglycoside-modifying enzyme (*aac (3-11), aph(3)1b*), chloramphenicol (catB, crpP), quinolone(qnrVC1), tetracycline (Tet), and fosmycin (FosA) detected in isolates from multiple hospitals. Global studies documented alternative Carbapenemase genes carried by ST773, such as *bla*VIM + *bla*OXA-10 in India, *bla*OXA-181 in the UK, and *bla*VIM + *bla*IMP-2 in Iran [15,16 17]. These differences in regional reports highlight the diversification and adaptation of ST773. Importantly, its dominance in Ghana parallels recent reports from Norway and parts of Africa, where ST773 has emerged as a new high-risk [26].

The enormous virulence potential of *P. aeruginosa* is evident in this study, with over 200 genes associated with toxin production, biofilm formation, immune evasion, and stress adaptation. Like earlier reports, *exoT* and *exoY* were abundantly dispersed compared with the single exclusive T3SS effectors *exoU*+ expressed by the study isolates [27]. Similarly, *exoU+/exoS-* were the dominant genotypes. These virulence factors influence pathogenicity and have severe implications for patient outcomes. According to this study, exoU was found in 28(100%) of the Global high-risk sequence types, and these sequence types express exoU+/exoS- T3SS pathotypes 19(67.86%). The prevalence of exoU+ indicates a more virulent strain, which could be linked to serious consequences and acute infections [28,29].

This study revealed that while ST308, ST235 and ST244 mirror global patterns of MDR dissemination, the predominance of ST773 in Ghana suggests shifting epidemiological dynamics. Unlike Vietnam, where ST235 dominates, or Europe, where ST244 remains prevalent, Ghana appears to be experiencing expansion of ST773, possibly due to local adaptation or importation [29]. These findings emphasize the importance of continuous genomic surveillance to track the emergence and diversification of high-risk *P. aeruginosa* lineages in Accra, Ghana, and beyond [30].

The study revealed that ST773 accounted for over half of all genomes, indicating local expansion or ongoing clonal spread within hospitals in Accra. Ghanaian ST235 clustered with ST235 genomes from Brazil, France, and Italy, suggesting shared ancestry or possible importation through recent global dissemination of the resistant strain [31, 32]. One Ghanaian genome (ST244) showed close genetic relatedness to a Russian ST244, while another appeared more divergent, demonstrating heterogeneity within the lineage. In contrast, rare STs, ST1116, ST654, and ST549 appeared phylogenetically distinct, suggesting limited global spread [32]. Of particular note, the novel sequence type ST5336, identified exclusively in Ghana, showed no genetic relatedness to any global clone. This suggests the emergence of a locally evolving lineage with no evidence of global dissemination. This highlights the ongoing evolution of *P. aeruginosa* populations and emphasize the value of local genomic surveillance in detecting novel or underreported clones [32]. These findings emphasise the need for continuous molecular surveillance to detect the emergence, evolution, and dissemination of high-risk *P. aeruginosa* lineages, particularly in settings with limited resources but increasing antibiotic resistance challenges.

The study revealed that inpatient status and invasive procedures within the preceding three months were independently associated with increased odds of both CRPA and MDRPA infection. Hospitalization increases exposure to antibiotic pressure and contaminated clinical environments, while procedures and device use create portals for colonisation and biofilm formation—conditions repeatedly linked to CRPA acquisition in meta-analyses and cohort studies [33;34].Notably, prior carbapenem exposure and the presence of indwelling devices are among the strongest risk factors reported internationally, alongside ICU stay and recent broad-spectrum antibiotics[35;36]. From a clinical and public health perspective, the shared risk factors CRPA and MDRPA point to common preventive priorities. These include stricter carbapenem stewardship, rigorous implementation of

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infection-prevention (IPC) bundles, and, where feasible, unit-level surveillance (e.g., in intensive care units) to identify transmission points and assess intervention impact over time.

Study Limitations

The study has a few limitations. The sample size of 267 isolates from a few hospital sites may not represent the full diversity of *P. aeruginosa* strains and infection types, a common limitation noted in similar multi-centre studies with a regional focus. The focus on hospital-based isolates means that the results may not apply to community settings. The findings of this study may have limited generalizability to other geographical areas. Due to resource constraints, the use of a limited panel of tests may have missed uncommon resistance mechanisms. While we adjusted for several key clinical factors, detailed data on prior antibiotic exposure and specific comorbidities were not collected. This lack of granular data means that residual confounding cannot be entirely ruled out. Despite inherent limitations, the study offers multicentre evidence on the occurrence of *P. aeruginosa* infections across varied clinical specimens and hospital settings. Our findings highlight the urgent need for judicious antibiotic stewardship to minimize carbapenem use and underscore the importance of rigorous device care and IPC practices to limit the spread of carbapenem resistance in *P. aeruginosa* and global high risk

5. Conclusions

Among clinical isolates examined from the eight participating hospitals, the prevalence of *P. aeruginosa* infections was comparatively low (0.319%). The pathogen was recovered from a variety of sample types, especially surgical site infections and urinary tract infections. Despite the low prevalence of *P. aeruginosa,* several global hypervirulent clones were identified, highlighting the need for continuous genomic surveillance.

Multidrug-resistant *P. aeruginosa* and Carbapenemase-resistant *P. aeruginosa*, mainly $bla_{\text{NDM-1}}$ producers are major causes of *P. aeruginosa* infection in the Greater Accra Hospital settings. Restricting carbapenem use through stewardship and strengthening infection control are essential to limit carbapenem-resistant *P. aeruginosa* (CRPA) spread.

This study found that *P. aeruginosa* was widespread throughout study hospitals, both within and between facilities. Recent local distribution was indicated by closely related genomes (≤10 SNPs), whereas inter-facility transmission was suggested by genomes with ≤10 SNP variations across hospitals. Novel sequence type, ST5336, and global high-risk clones were detected. These trends show a combination of clonal diversification, local adaptability, and global importation.

Clinical and epidemiological risk factors for the acquisition of both multidrug-resistant *P. aeruginosa* (MDRPA) and carbapenem-resistant *P. aeruginosa* (CRPA) were found to be independently associated with inpatient status, wound specimen, invasive procedures, and admission to a tertiary care hospital.

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