Research Square

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Molecular Characteristics and Antimicrobial Susceptibility Profile of Pseudomonas aeruginosa isolated from patients attending Healthcare Facilities in Mthatha, South Africa

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Abstract

Background *Pseudomonas aeruginosa* is a common pathogen causing healthcare-associated infections most especially in critically ill and immunocompromised patients. This pathogen poses a public health threat due to its innate resistance to many antimicrobial agents and its ability to acquire new resistance mechanisms under pressure. Infections with Extended spectrum β-lactamases (ESBL)-producing isolates result into outbreaks that lead to serious antibiotic management concerns with higher mortality and morbidity and significant economic causatives. In this study, we evaluated the antimicrobial resistance patterns and characterized genetically the ESBLs and Metallo- β-lactamases (MBL) produced by this pathogen.

Methods Isolates of *P. aeruginosa* cultured from patients who attended Nelson Mandela Academic Hospital and other clinics in the four district municipalities of the Eastern Cape between August 2017 and May 2019 were identified; and their antibiotic resistance patterns were tested against amikacin, aztreonam, cefepime, ceftazidime, ciprofloxacin, doripenem, gentamicin, imipenem, levofloxacin, meropenem, piperacillin, piperacillin/tazobactam and tobramycin using the bioMérieux VITEK® 2 and confirmed by Beckman autoSCAN-4 System. Real-time PCR was done using Roche Light Cycler 2.0 to detect the presence of ESBLs; blaSHV, blaTEM and blaCTX-M genes; and MBLs; blaIMP, blaVIM.

Results High antibiotic resistance in decreasing order was observed in piperacillin (64.2%), aztreonam (57.8%), cefepime (51.5%), ceftazidime (51.0%), piperacillin/tazobactam (50.5%), and imipenem (46.6%). A total of 75 (36.8%) multidrug resistant (MDR) isolates were observed of the total pool of isolates. The blaTEM, blaSHV and blaCTX-M was detected in 79.3%, 69.5% and 31.7% isolates (n=82), respectively. The blaIMP was detected in 1.25% while no blaVIM was detected in any of the isolates tested.

Conclusions The study showed a high rate of MDR *P. aeruginosa* in our setting. The vast majority of these resistant isolates carried blaTEM and blaSHV genes. Continuous monitoring of antimicrobial resistance and strict compliance towards infection prevention and control practices are the best defence against spread of MDR *P. aeruginosa*.

Background

P. aeruginosa is an opportunistic pathogen causing infections especially in immunocompromised patients. It is the leading cause of nosocomial infections such as urinary tract infections, surgical site infections, pneumonia, bacteremia and septicaemia [1–3] It is one of the ESKAPE pathogens that is most medically and epidemiologically significant and has been implicated as a principal cause of chronic lung infections in cystic fibrosis (CF) patients and severe infections in burn victims [4–7]. The World Health Organization (WHO) has categorized P. aeruginosa as a critical priority pathogen which needs urgent novel antibiotics intervention and has been given a serious threat level due to multidrug resistance displayed to many antibiotics [8, 9]. The growing resistance of P. aeruginosa to several antibiotics, as a result of excessive antibiotic administration, has resulted to the accumulation of antibiotic resistance and

cross-resistance between antibiotics and the advent of multidrug-resistant (MDR) forms of P. aeruginosa. P. aeruginosa infections are generally linked with high mortality; this is due to its innate resistance to several antimicrobial agents and acquired resistance via mutation and horizontal transfer [10, 11] Various mechanisms involved in the resistance of P. aeruginosa include over expression of efflux pump, acquisition of Extended-Spectrum β-Lactamases (ESBLs) and Metallo-β-Lactamases (MBLs) [12]. ESBLs are a cluster of β-lactamases that inactivates β-lactams especially oxymino-β-lactams and monobactams, and are repressed by β-lactamase inhibitors, such as clavulanic acid. They are encoded on plasmids and can easily be conveyed from one organism to another [13, 14]. ESBLs were first discovered in 1983 and ever since over 500 diverse β-lactamases have been described to date [15, 16]. ESBL enzymes according to Ambler classification are categorized into two, A and D. The most prevalent enzymes in class A include bla_{TEM}, bla_{CTX-M} and bla_{SHV}, and has been described in P. aeruginosa strains [13, 17, 18]. The emergence of beta-lactamase enzymes is majorly due to chromosomal mutation and procurement of resistance genes which are moved about on various mobile genetic elements (MGEs) such as bacteriophages, genomic islands, integrons, plasmids and insertion sequences [19]. The production of these enzymes is a going concern for infection control supervision because it restricts therapeutic choices. Continuous monitoring and timely detection of ESBL and MBL producing organisms is critical to establish suitable antimicrobial therapy and to thwart their spread [16]. Polymerase chain reaction (PCR)-based methods are critical to establish the prevalence and characterization of beta lactamases due to the presence of multiple resistance genes in some microorganisms [20]. Real-time PCR detection of ESBL enhances faster diagnosis and timely management of epidemiological information for monitoring outbreak situations [21]. Several studies have documented the antimicrobial resistance in P. aeruginosa including genotypic detection of ESBLs and MBLs [21–25]. Studies on ESBL-producing P. aeruginosa in South Africa have also been documented [26–29] but scarce data exist in the Eastern Cape particularly in the former Transkei region on the molecular characteristics of ESBLs and MBLs in P. aeruginosa. Antibiotic surveillance studies are important for the design of control strategies for preventing bacterial resistance and establishing therapeutic guidelines as well as for a better understanding of bacterial epidemiology. The aim of this study was to examine the antimicrobial susceptibility profiles of clinical isolates of P. aeruginosa from Mthatha and surrounding districts and to investigate their ESBL resistance mechanisms.

Materials And Methods

Study Design

A prospective, descriptive study based on laboratory analysis. Samples from patients were collected from August 2016 to May 2019.

Study Setting

This was a laboratory analysis at the Microbiology Laboratory of the National Health Laboratory Services (NHLS) at Nelson Mandela Academic Hospital (NMAH) and the Department of Laboratory Medicine and

Pathology, Faculty of Health Sciences, WSU. In this study, 204 non-duplicate isolates from patients were arbitrarily obtained from August 2016 to May 2019. The samples were drawn from four district municipalities of the Eastern Cape Province which include Alfred Nzo, Amathole, Joe Gqabi and Oliver Reginald (OR) Tambo district Municipalities. Health facilities include primary health centres/clinics, secondary district hospitals and a tertiary academic hospital located in Mthatha. Clinical samples were sent from various primary and secondary clinics in the afore- mentioned municipalities to Mthatha at the NHLS for analysis.

Specimen collection and analysis

Non-duplicate *P. aeruginosa* isolates were collected from Mthatha, other clinics and hospitals from the four district municipalities. Specimens included throat swabs, wound swabs, swabs from abscesses, sputum, urine, blood culture and catheter tips. Demographic characteristics of patients and medical histories were collected from medical records including date of specimen collection, gender, age, test ordered and hospital/clinic. All samples were routinely cultured on MacConkey and Blood agar plates. Blood and sputum were also cultured on chocolate agar. Suspected colonies were plated on Cetrimide agar and identified by gram staining, colony characteristics, motility, pyocyanin production and characteristics grape-like odour (30, 31). Strains were identified to the species level with Vitek 2 GN (bioMérieux, Inc. USA) ID cards and confirmed by Microscan NID 2 panels (Beckman Coulter, Inc. USA).

Antimicrobial susceptibility

Antimicrobial susceptibility was obtained by determining MIC using Microscan dehydrated broth microdilution negative MIC Panel Type 44 (NM44) (Beckman Coulter, Inc. USA) following the manufacturer's guidelines [32, 33] and Clinical Laboratory Standards Institute. MICs were interpreted following CLSI guidelines (M100-S27 breakpoints) [34]. The following antibiotics were tested in the panels: amikacin, aztreonam, cefepime, ceftazidime, ciprofloxacin, doripenem, gentamicin, imipenem, levofloxacin, meropenem, piperacillin/tazobactam, piperacillin and tobramycin.

Criterion for Multidrug resistance

The classification of MDR was performed according to Magiorakos *et al.,* [35]. (MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial categories).

Molecular confirmation of strains and Real-Time PCR for identification

DNA extraction was done using Roche MagNA Pure Bacteria lysis buffer, MagNA Pure Compact Nucleic Acid Isolation kit and PCR grade water (Roche Applied Science, Indianapolis), following manufacturer's instructions.

Real time PCR was carried out in the Light Cycler 2.0 instrument (Roche Applied Science, Germany) using Fast start Light Cycler 480 Hybprobes Master kit (Roche Diagnostics, USA). Specific primers targeting the genes *gyrB* were amplified by singleplex *rPCR* using primers and probes shown in Table 1 and were used

to confirm identity of the isolates. Primers were designed by TIB-Molbiol (Berlin, Germany). rPCR assay was performed according to previously published protocol [18]. Absolute quantification was carried out using the Light Cycler software 4.05. *P. aeruginosa* ATCC 27853 was used as a positive control.

Molecular ESBL and MBL Detection by Singleplex rPCR

Real-time PCR for $bla_{CTX\text{-}M}$, bla_{SHV}, bla_{TEM}, bla_{IMP} and bla_{VIM}. Real time PCR was carried out in the Light Cycler 2.0 instrument (Roche Applied Science, Germany) using Fast start Light Cycler 480 Hybridization probes Master kit (Roche Diagnostics, USA). Specific primers and probes (Table 1) targeting the genes $bla_{CTX\text{-}M}$, bla_{SHV}, bla_{TEM}, bla_{IMP} and bla_{VIM} were amplified by singleplex rPCR. Primers were designed by TIB-Molbiol (Berlin, Germany). rPCR assay was performed in a 32 carousels using 20 μL capillaries with each capillary containing a total volume of 20 μL including 2μL of Light Cycler FastStart DNA Master Hybridization Probe, 2 μL of primers (0.5mM for each forward and reverse), 2.4 μL of MgCl2, 2 μL of extracted DNA, and water to make up the volume of 20 μL. DNA amplification was carried out with the following run conditions: Pre-incubation for 5 minutes at 95^0C, followed by 45 cycles of amplification with denaturation at 95^0C for 30 seconds, annealing and extension for 1 minute at 60^0C without the third step, and then a single cycle of cooling for 30 seconds at 40^0C [18]. Absolute quantification was carried out using the Light Cycler software 4.05. Positive control strains used include *Escherichia coli* NCTC 13461 (CTX-M). *Klebsiella pneumoniae* ATCC 700603 (SHV), *Escherichia coli* NCTC 13351 (TEM). *P. aeruginosa* NCTC 13437 (VIM), *Escherichia coli* NCTC 13476 (IMP). These were obtained from the National Institute of Communicable Diseases (NICD), Johannesburg, South Africa.

Statistical analysis

The data was coded and entered into a database on an Excel spreadsheet and analyzed using Statistical Package for the Social Sciences (SPSS) version 23.0. The descriptive analysis was performed to calculate the frequency and categorical variables were expressed as proportions (%). All statistical analysis was done with statistical significance set at $\leq$0.05.

Table 1

Primer sequences for detection of bla_{CTX-M}, bla_{SHV}, bla_{TEM}, $bla_{IMP,}$ bla_{VIM} genes and gyrB

Target gene	Primers	Primers sequences (5'-3')	Tm in 0^0C	References
bla_{CTX-M}	CTX-M forward primer	ATGAGYACCAGTAARGTKATGGC	58.7	36
	CTX-M reverse primer	ATCACKCGGRTCGCCIGGRAT	59.3	
	CTX-M Probe	FAM-CCCGACAGCTGGGAGACGAAACGT-BBQ	70.2	
bla_{SHV}	SHV forward primer	TCCCATGATGAGCACCTTTAAA	56.8	37
	SHV reverse primer	TCCTGCTGGCGATAGTGGAT	58.6	
	SHV Probe	FAM-TGCCGGTGACGAACAGCTGGAG-BBQ	68.3	
bla_{TEM}	TEM forward primer	GCATCTTACGGATGGCATGA	56.6	37
	TEM reverse primer	GTCCTCCGATCGTTGTCAGAA	57.7	
	TEM Probe	FAM-CAGTGCTGCCATAACCATGAGTGA-BHQ1	62.2	
bla_{IMP}	IMP forward primer	GGGCGGAATAGAGTGGCTTA	57.6	38
	IMP reverse primer	GGCTTGAACCTTACCGTCTTTTT	59.3	
	IMP Probe	FAM-CGATCTATCCCCACGTATGCATCTGAATTAACA-BHQ1	67.4	
bla_{VIM}	VIM forward primer	TGCGCTTCGGTCCAGTAGA	59.0	38
	VIM reverse primer	TGACGGGACGTATACAACCAGAT	58.5	
	VIM Probe	FAM-CTTCTATCCTGGTGCTGCGCATTCG-BHQ1	67.6	
gyrB	gyrB forward primer	CCT GAC CAT CCG TCG CCA CAA		39
	gyrB reverse primer	CGC AGC AGG ATG CCG ACG CC		

Target gene	Primers	Primers sequences (5'-3')	Tm in 0^0C	References
	gyrB probe	6-FAM-CCG TGG TGG TAG ACC TGT TCC CAG ACC-BHQ 6-FAM-CCG TGG TGG TAG ACC TGT TCC CAG ACC-BBQ		This study

Results

Identification of P. aeruginosa and demographics

During the study period, a total of 204 P. aeruginosa isolates were recovered from a range of clinical specimens of patients hospitalized in various wards of NMAH, Mthatha Regional hospital, Secondary district hospitals and primary health care clinics in Mthatha and other towns in four District municipalities of the Eastern Cape Province. The isolates were confirmed by Vitek 2 system (bioMérieux, Inc., USA), Microscan autoscan-4 system (Beckman Coulter, Inc. USA) and rPCR using specific primer and probes targeting gyrB [39]. The majority of the isolates were recovered from male patients (60%) while 40% belonged to female patients. The isolates were predominantly from pus and wound swabs (80.4%) while the samples originated from Surgical (33.3%), General (18.1%) and Paediatrics (11.3%) wards.

Table 2
General characteristics of patients and specimen from whose isolates were recovered

Variable	Number, n (%)
Gender	
Male	122 (59.8)
Female	82 (40.2)
Age (Years) (mean ± SEM)	
≤ 15 (7.4 ± 0.6)	44 (21.6)
16–30 (23.9 ± 0.7)	48 (23.5)
31–45 (37.2 ± 0.6)	44 (21.6)
46–60 (54.1 ± 0.8)	30 (14.7)
> 60 (71.7 ± 1.3)	21 (10.3)
Specimen source	
Pus and wound swab	164 (80.4)
Sputum	22 (10.8)
Fluid aspirate	7 (3.4)
Catheter tip	6 (2.9)
Urine	3 (1.5)
Tissue	2 (1.0)
MDR status	
MDR	75 (36.8)
Non-MDR	129 (63.2)
District Municipality	
Alfred Nzo	27 (13.2)
Amathole	12 (5.9)
Joe Gqabi	1 (0.5)
OR Tambo	164 (80.4)

The mean age of patients was 32.8 years ranging from 6 days to 84 years. The male population have a mean age of 30.5 years ranging from 6 days to 83 years while the female mean age was 36.2 years with age ranging from 22 days to 84 years. These patients were drawn from four district municipalities with OR Tambo having the most at 80.4% with the least patient drawn from Joe Gqabi at 0.5% (Table 2)

Antimicrobial Susceptibility

Out of 204 isolates tested to various antibiotics, high antibiotic resistance in decreasing order was observed in piperacillin (64,2%), aztreonam (57.8%), cefepime (51.5%), ceftazidime (51.0%), piperacillin/tazobactam (50.5%), and imipenem (46.6%). Percentages of low resistance in reducing order were observed in gentamicin (35.3%), meropenem (24.0%), amikacin (20.1%), levofloxacin (19.1%), ciprofloxacin (11.3%), doripenem (11.3%), and tobramycin (8.3%) (Fig. 1) The study also revealed a total of seventy-five isolates (36.8%) were multidrug resistant out of the tested isolates while non-MDR constituted 63.2% of the total.

Molecular Detection Of Esbl- And Mbl-encoding Genes

Of 204 P. aeruginosa isolates, 82 were tested by singleplex rPCR for molecular detection of ESBL and MBL. These data revealed that ESBL- genotypic resistance is driven in Mthatha by bla_{TEM} (79.3%) followed by bla_{SHV} (69.5%) and lastly bla_{CTX-M} (31.7%). MBL-genotypic resistance, bla_{VIM}, was not detected in all isolated tested while only one bla_{IMP} (1.25%) was detected in all the tested isolates (Table 3) The most common ESBL-genotype combination among the P. aeruginosa was a combination of bla_{TEM} + bla_{SHV} at 49 (40.5%).

Table 3
ESBL genotypes in P. aeruginosa isolates

Positive by PCR for ESBL genes	Number amplified (N = 82)	Total (%)
A. Single ESBL gene		
bla_{TEM} only	65	79.3
bla_{SHV} only	57	69.5
bla_{CTX-M} only	26	31.7
bla_{IMP} only	1	1.25
bla_{VIM} only	0	0
B. Two or more ESBL genes	121	
bla_{TEM} + bla_{SHV}	49	40.5
bla_{TEM} + bla_{CTX-M}	22	18.2
bla_{SHV} + bla_{CTX-M}	26	21.5
bla_{TEM} +bla_{IMP}	1	0.8
bla_{TEM} +bla_{SHV} +bla_{CTX-M}	22	18.2
bla_{TEM} +bla_{SHV} +bla_{IMP}	1	0.8
bla_{TEM} +bla_{SHV} +bla_{CTX-M} +bla_{IMP}	0	0

In ESBL-producing P. aeruginosa the highest level of resistance was observed against piperacillin (52.7%), followed by aztreonam (47.3%), ceftazidime (44.6%), cefepime (41.9%) and imipenem and piperacillin/tazobactam (both at 40.5%); while in non-ESBL-producing isolates, highest level of resistance was observed to gentamicin and ceftazidime (62.5%) and low resistance level to levofloxacin (12.5%) (Table 4).

Table 4
Resistance pattern of ESBL and non-ESBL Pseudomonas aeruginosa isolates

Antibiotics	Total (N = 82) No (%)	ESBL (N = 74) No (%)	Non-ESBL (N = 8) No (%)
Amikacin	26 (31.7)	23 (31.1)	3 (37.5)
Aztreonam	38 (46,3)	35 (47.3)	3 (37,5)
Cefepime	37 (45.1)	31 (41.9)	6 (75.0)
Ceftazidime	38 (46.3)	33 (44.6)	5 (62.5)
Ciprofloxacin	15 (18.3)	13 (17.6)	2 (25.0)
Doripenem	17 (20.7)	17 (23,0)	0 (0.0)
Gentamicin	33 (40.2)	28 (37.8)	5 (62.5)
Imipenem	33 (40.2)	30 (40.5)	3 (37.5)
Levofloxacin	16 (19.5)	15 (20.3)	1 (12.5)
Meropenem	27 (32,9)	25 (33.8)	2 (25.0)
Piperacillin	43 (52.4)	39 (52.7)	4 (50.0)
Piperacillin/tazobactam	34 (41,5)	30 (40.5)	4 (50.0)
Tobramycin	16 (19.5)	13 (17.6)	3 (37.5)

Different parameters were tested in relationship to the production of ESBL by rPCR in our tested isolates. The samples were drawn from both secondary district hospitals and tertiary level of hospital setting. No sample was recovered from the primary health care center. Our data revealed that the hospital type had no significant effect on the acquisition of ESBL and that the effect of tertiary hospital on ESBL is 43% lesser than the secondary hospital (OR: 0.57; CI: 0.132–2.49; P:0.458). (Table 5).

The relationship between specimen type and ESBL production revealed that sputum was found to be associated with ESBL-producing P. aeruginosa at 95% confidence interval range of 0.03–0.92 and OR of 0.16 (Table 6).

Table 5
Multivariate analysis of factors associated with ESBL-positive and ESBL-negative isolates

Variable	ESBL No (%)	Non-ESBL No (%)	OR (95% CI)	p-value
Gender				
Male	49 (91)	5 (9)		
Female	25 (89)	3 (11)	0.85 (0.187-3.90)	0.833
Hospital type				
Secondary	47 (92.2)	4 (7.8)	0.57 (0.132–2.49)	0.458
Tertiary	27 (87.1)	4 (12.9)		

Table 6
Relationship between ESBL and selected parameters (Adjusted OR)

Variables		OR (95% CI)	CI	P
Hospital	Secondary	1		
	Tertiary	0.574	0.132–2.48	0.458
Age	Less 15 years	1		
	16–30	0.68	0.08–5.49	0.721
	31–45	1.10	0.14–8.63	0.924
	46 and more	1		
Gender	Male	1		
	Female	0.85	0.18–3.85	
Specimen	Pus and wound	1		
	Sputum	0.16	0.03–0.92	0.040
	Fluid	0.11	0.07–1.54	0.101
	Urine	0.11	0.07–1.54	0.101

Discussion

The current study revealed a moderate to high antibiotic resistance in decreasing order was observed in piperacillin (64.2%), aztreonam (57.8%), Cephalosporins (cefepime 51.5% and ceftazidime 51.0%),

antipseudomonal penicillins + β-lactamase inhibitor (piperacillin/tazobactam 50.5%) and imipenem (46.6%). (Fig. 1). Low resistance in reducing order were observed in gentamicin (35.3%), meropenem (24.0%), amikacin (20.1%), fluoroquinolones (levofloxacin 19.1% and ciprofloxacin 11.3%), doripenem (11.3%), and tobramycin (8.3%). Data from surveillance on isolates of P. aeruginosa in the South African private laboratories is not in agreement with our study [40]. They reported a much lower resistance rates of 28.2%, 26.3%, 31.9%, 37.8%, 35.5% and 35.5% in cefepime, ceftazidime, doripenem, imipenem, meropenem and piperacillin respectively. The isolates were recovered from blood culture only, possibly this might account for the difference in resistance rate, alternatively this might be due to regional variations in the empirical use of these antimicrobials [40]. In our study, the percentage of resistance of 11.3% to ciprofloxacin was within the same range of 13.4% described by Ramsamy et al., [28]. The data obtained were from nine public sector hospitals in Kwazulu-Natal Province. Additionally, gentamicin resistance of 17% and imipenem resistance of 13% as reported in the study was lower in comparison with resistance reported in our study at 35.3% and 46.6% respectively. The susceptibility ranges of 75%-92% of P. aeruginosa isolates in this study to routine antibiotics considered for therapy is encouraging but the increase in resistance exhibited to cephalosporins and imipenem is concerning. This might be due to selective pressure to those antibiotics and it will be important to monitor the prescription of these antibiotics. Owing to endless alteration, resistance exhibited to range of β-lactam antibiotics is challenging, thus making β-lactamase production the commonest cause of drug resistance and antimicrobial treatment tragedy [10, 41]. Our study detected an average resistance of 45.7% to cephalosporins (ceftazidime and cefepime) in ESBL P. aeruginosa. Piperacillin and gentamicin resistance in ESBL isolates was 52.4% and 40.2% respectively (Table 4) which is similar to the findings of Farhan et al., [10]. The emerging level of resistance displayed to the cephalosporins highlight the development of cephalosporinases among resistant strains of these organisms. The cephalosporins due to their wide spectrum of activity are a significant class of antimicrobials used in controlling several infections however, the emergence of cephalosporinases can in effect hamper their clinical usefulness [42]. The reported increasing penicillinase-producing β-lactamases strains among these organisms validates the noticeably observable high rate resistance of our isolates to piperacillin [42]. Antibiotic resistance is a public health menace with an alarming proportion that is getting collective attention more so that several studies have found a correlation between level of antibiotic prescription with the prevalence of antibiotic resistance [43–44]. Patients with resistant P. aeruginosa infections have a poor prognosis hence it is imperative that P. aeruginosa strains presenting severe drug resistance is monitored [23]. The swift spread and the emergence of MBL- and ESBL-producing P. aeruginosa of clinical origin is distressing and of great threat. Furthermore, level of antibiotic usage, horizontal gene transfer (HGT) event and environmental factors may account for variations in resistance patterns among strains isolated from diverse countries and regions. Antimicrobial susceptibility testing and proper screening for ESBL and MBL production has to be embarked upon before antimicrobial therapy [10]. In the present study, 36.8% of our isolates were MDR (defined as non-susceptibility to at least one agent in three or more antimicrobial categories). Similarly, MDR rate of 45% was reported by Fazeli et al., [45] however Sahoo et al., [46] reported a higher rate of resistance at 72.69%.

The emergence of ESBL-producing P. aeruginosa is increasingly reported as a major cause of health-care associated infections. In the hospital locale, infections resulting from these resistant organisms are increasingly challenging to treat due to the intensity of resistance exhibited to the most commonly recommended antibiotics. Antimicrobial treatment is further hampered by the production of extended spectrum beta-lactamases and metallo beta-lactamases [20, 47]. As at now, ESBLs in P. aeruginosa are described globally with MBLs also being reported on a growing basis in recent years [15, 22]. Various studies have reported the existence of ESBLs in clinical isolates of P. aeruginosa [16, 19, 48]. Class A ESBLs are typically recognized in P. aeruginosa isolates presenting resistance to extended-spectrum cephalosporin. Traditional ESBLs have developed from restricted-spectrum class A TEM and SHV β-lactamases although a variety of non-TEM and non-SHV class A ESBLs have been described including CTX-M, PER, VEB, GES, and BEL [49]. The ESBL genotype differs in various parts of the world. This study found out that the most prevalent genotype for ESBL production was bla_{TEM} which was detected in 65 (79.3%) isolates followed by bla_{SHV} at 57 (69.5%) and bla_{CTX-M} at 26 (31.7%) (Table 3) Since it has been reported that ESBL genes show variation depending on the geographical location, the findings of Erhlers et al., [50], Chen et al., [15], Miranda et al., [51], Bokaeian et al., [52] and Khurana et al., [20] in South Africa, China, Brazil, Iran and India respectively corroborated the prevalent genotype to be bla_{TEM} while contrarily Jamali et al., [53] and Rezai et al., [54] reported the prevalent gene to be bla_{SHV} at 75% and 86.66% respectively. The predominant ESBL and MBL genes detected in a study conducted in Durban on MDR P. aeruginosa isolates were GES-2, OXA-21, and VIM-2 [55]. The least detected ESBL genotype was CTX-M in 26 (31.7%) isolates similar to Miranda et al., [51]. The MBL genotype, bla_{IMP} was only detected in 1 sample (1.25%) while bla_{VIM} was not detected in any of the sample. Similar findings were reported in Egypt by Abbas et al., [56], where no VIM genes was detected by PCR analysis. In contrast, Zafer et al., and Adjei et al., [49, 55] reported a prevalence of 58.2% and 29% respectively in VIM-2. MDR P. aeruginosa encoding bla_{VIM-2} gene have been reported in a tertiary hospital in Cape Town, which was responsible for an outbreak, and in a public hospital in Port Elizabeth [57, 58]. The study of Arunagiri et al., [59] reported low rate of bla_{IMP} in 2(3%) isolates which is similar to our study. The phenotypic resistance displayed to the carbapenems particularly imipenem which is not validated by the genotypic MBL result may be due to other resistance mechanism such as efflux over expression or forfeiture of exterior membrane protein [60, 61].

Several researchers have reported on the concurrence of different β-lactamase genes found in the same isolates [46, 49, 62]. The most common ESBL combination among our isolates by genotype was a combination of bla_{TEM} + bla_{SHV} at 49 (40.5%) but contrary to Chen et al., [15] and Sahoo et al., [46], who reported the commonest to be bla_{SHV} + bla_{CTX-M}. The second most common genotype combination was a combination of bla_{SHV} + bla_{CTX-M} which is similar to the study from Syria and Philippines [63, 64]. Our study showed the most predominant ESBL gene to be TEM which was corroborated by other studies. Prior to now, TEM used to be the most prevalent but recent reports suggest that the CTX-M-type group of ESBLs may now be the most predominant type globally [46, 65].

Conclusion

Our study is the first surveillance report on molecular characteristics and antimicrobial susceptibility testing of P. aeruginosa isolates from clinical samples of patients in Mthatha, Eastern Cape Province South Africa. The study showed a high rate of MDR P. aeruginosa in our setting. The vast majority of these resistant isolates carried bla_{TEM} and bla_{SHV} genes. Fortunately, we did not detect any bla_{VIM} in all the tested isolates with bla_{IMP} reported as just one. ESBLs are becoming progressively multifaceted and diverse. Early detection and characterization is critical to contain their dissemination, prevent outbreak and enhance intervention strategies and optimise therapy. Continuous monitoring of antimicrobial resistance and strict compliance towards infection control practices are the best defence against continuous spread of MDR P. aeruginosa.

Abbreviations

ESBL: extended-spectrum beta-lactamase; MBL: metallo-β-lactamases; AST: antimicrobial susceptibility testing; rPCR: Real-time polymerase chain reaction; MDR: multidrug-resistant; HGT: horizontal gene transfer; NMAH: Nelson Mandela Academic Hospital; NHLS: National Health Laboratory Services; NICD: National Institute of Communicable Diseases; CLSI: Clinical Laboratory Standards Institute; WHO: World Health Organization; CDC: Centre for Disease Prevention and Control.

Declarations

Authors' contributions

M.C.H., T.A., S.V Conceived and designed the experiment. M.C.H., S.D. performed the experiments: M. C. H., T. A. analysed the data: M.C.H. wrote the manuscript: M.C.H., T.A., S.V., G.E.O analysis and interpretation of data; proof reading of manuscript. All authors read and approved the final manuscript

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Competing interests

The authors declare that they have no competing interests.

Availability of data and materials

All data generated or analysed during this study are included in this published article.

Ethics approval and consent to participate

Ethical approval for the study was granted by the Health Research Ethics and Biosafety Committee of the Faculty of Health Sciences, Walter Sisulu University (WSU) Reference number 024/2016 while permission to conduct the study was obtained from the National Health Laboratory Services (NHLS).

Consent for publication

Not applicable

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Figures

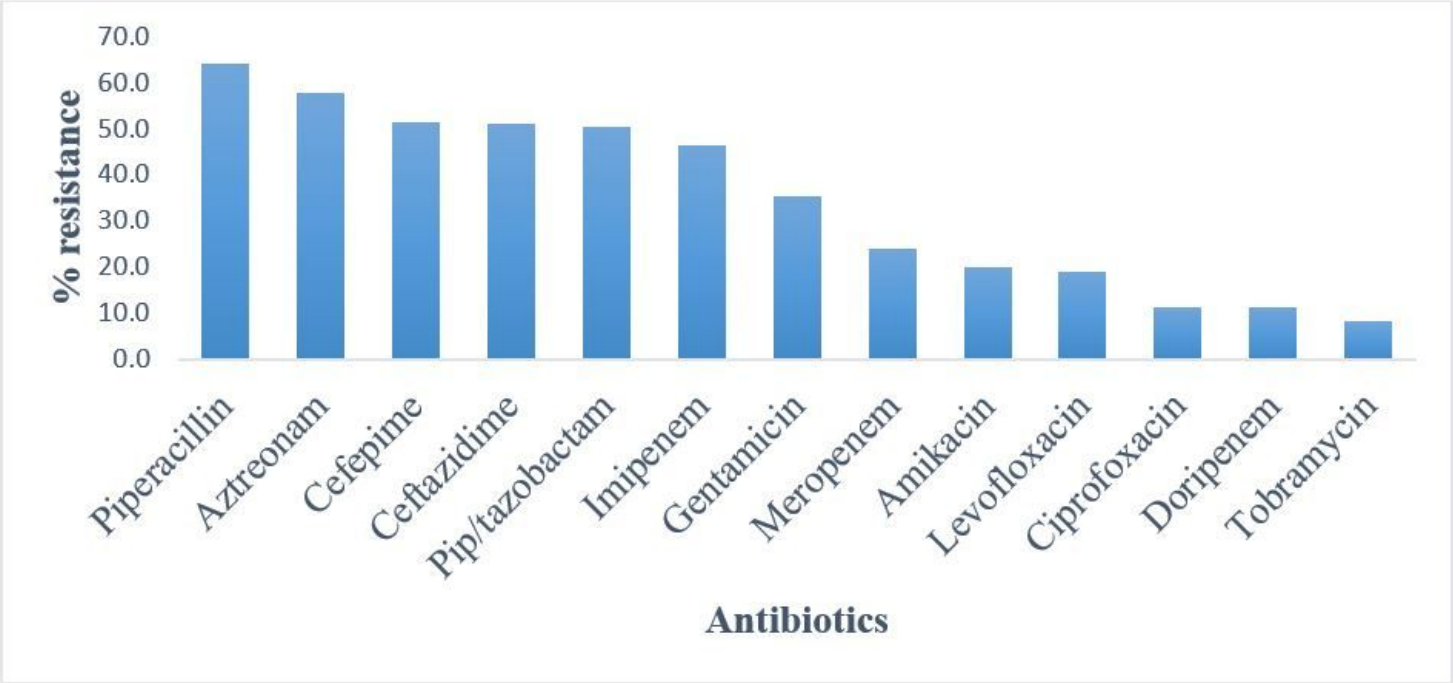

Figure 1

Antibiotic resistant pattern of the isolates (N=204) Molecular Detection of ESBL- and MBL-encoding genes