Citation: Dalia H. Mansour and Musa A. Ali. Detection of Drug Resistant Strains of *Pseudomonas aeruginosa* isolated from Patients attending Kosti Hospitals (White Nile State). African Journal of Medical Sciences, 2018, 3 (4) ajmsc.info

Detection of Drug Resistant Strains of *Pseudomonas aeruginosa* isolated from Patients attending Kosti Hospitals (White Nile State)

Dalia H. Mansour and Musa A. Ali
Al Neelain University, Khartoum, Sudan.

Abstract

Background: *Pseudomonas aeruginosa* (*P. aeruginosa*) is an opportunistic pathogen in human. The most worrisome characteristic of this bacterium is its low antibiotic susceptibility. Unfortunately, rates of antibiotic resistance in *P. aeruginosa* are increasing worldwide. Besides, some of the strains have shown resistance to multiple antibiotics, which could be mediated by several mechanisms including production of hydrolyzing enzyme, loss of outer membrane protein, efflux systems and target mutations. These isolates were named multi-drug resistant (MDR), extremely drug-resistant (XDR) and pan-drug resistant (PDR).

Objective: To detect the drug resistant strains of *Pseudomonas aeruginosa* isolated from patients attending Kosti Hospitals (White Nile State)

Materials and methods: Disk diffusion method was used for detection of antimicrobial susceptibility in clinical isolates of *P. aeruginosa* according to the Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: In this study, the antimicrobial susceptibility of hundred *P. aeruginosa* isolates against 14 agents from 7 antimicrobial categories was determined. Altogether, the highest susceptibility was shown for polymyxin antimicrobials (93% and 95%, respectively, for colistin, and polymyxin B). In this study, 58 isolates (58%) was recognized as MDR, 33 isolates (33%) as XDR and there was not PDR among 100 clinical isolates of *P. aeruginosa* isolated from patients in Kosti Hospitals. However, high prevalence rate of MDR was reported in the studies defined MDR as resistance to ≥ 3 classes of antibiotics.

Conclusion: The multidrug and extremely drug resistant frequency rate of *P. aeruginosa* in Kosti Hospitals was high and worrisome.

Key words: *Pseudomonas Aeruginosa,* MDR, XDR, PDR, Kosti Hospitals

Introduction

Pseudomonas aeruginosa is an opportunistic pathogen and a common Gram-negative rod-

shaped bacterium that leads to significant morbidity and mortality in humans. *P. aeruginosa* has the ability to survive on minimal nutrition and tolerate a variety of physical insults leading to its persistence in the community and hospital settings. Despite the wide distribution of *P. aeruginosa* in nature and the potential for community-acquired infections, serious infections with this bacterium are predominantly hospital-acquired infections. The most worrisome characteristic of this bacterium is its low antibiotic susceptibility, which is attributable to low permeability of the bacterial cellular envelopes and action of multidrug efflux pumps. In addition to this intrinsic resistance, *P. aeruginosa* can gets resistance by mutation either in chromosomally encoded genes or by the horizontal gene transfers of antibiotic resistance determinants[1].

Unfortunately, rates of antibiotic resistance in *P. aeruginosa* are increasing worldwide. Besides, some strains have shown resistance to multiple antibiotics, which could be mediated by several mechanisms including production of hydrolyzing enzyme, loss of outer membrane protein, efflux systems and target mutations. These isolates were named multidrug resistant (MDR), extremely drug resistant (XDR) and pan-drug resistant (PDR), according to the extreme of their resistance. Infections with these resistant isolates may be associated with increased morbidity and mortality, which can be attributed to limited effective antimicrobial options[2].

Known for many years to be a cause of serious wound and surgical infections, *P. aeruginosa* can often regarded as a secondary or opportunistic invader rather than a cause of primary infection in healthy tissues. Review of literature on MDR of *P. aeruginosa* has revealed considerably different definitions. The absence of specific definitions for MDR in clinical study protocols makes the comparison of data difficult. In addition, the true prevalence rate of MDR isolates cannot be well established. However, in the majority of the published studies, multidrug resistance was defined as a resistance to at least three drugs from a variety of antibiotic classes, mainly aminoglycosides, antipseudomonal penicillins, cephalosporins, carbapenems and fluoroquinolones[3].

Materials and methods

100 isolates of *P. aeruginosa* were isolated from wound, urine, and external ear swabs specimens collected from medical laboratories of two hospitals in Kosti (White Nile State). Clinical isolates of *P. aeruginosa* were fully identified based on general phenotypic methods (morphology, colonial pigmentation, oxidase test, oxidative carbohydrate utilization).

Disk diffusion susceptibility method was used for detection of antimicrobial susceptibility of clinical isolates of *P. aeruginosa* according to the Clinical and Laboratory Standards Institute (CLSI) guidelines[4].

The following antibiotics disks were used: gentamicin (GEN, 10µg), tobramycin (TM, 10µg), amikacin (AN, 30µg), imipenem (IPM, 10µg), meropenem (MEM, 10µg), ceftriaxone (CRO, 30µg), cefuroxime (CXM, 30µg), ciprofloxacin (CIP, 5µg) , levofloxacin (LVX, 5µg), ticarcillin-clavulanic acid (TCC, 85 µg), piperacillin tazobactam (TZP, 110µg), aztreonam (ATM, 30µg), colistin (CS, 10µg), and polymyxin B (PB, 300U). Control strains used for all antibiotics disks was *P. aeruginosa* ATCC27853, except for ß-lactamase inhibitors, which was *E. coli* ATCC35218.

Detection of MDR and XDR isolates: Defining of MDR and XDR in *P. aeruginosa* isolates were performed according to the new standardized international document[5], by the results of antimicrobial susceptibility of *P. aeruginosa* to all antimicrobial agents listed in Table (1). Therefore, isolates of *P. aeruginosa*, which have shown non-susceptibility to at least one agent in ≥ 3 antimicrobial categories are considered MDR, and isolates exhibit non-susceptibility to at least one agent in ≥ 6 antimicrobial categories are considered XDR.

Table (1): Antimicrobial categories and agents proposed for characterization of MDR, XDR, and PDR of *P. aeruginosa*

Antimicrobial categories	**Antimicrobial agents**
Aminoglycoside	Gentamycin -Tobramycin - Amikacin
Cephalosporins	Cefuroxime - Ceftriaxone
Carbapenems	Imipenem - Meropenem
Fluoroquinolones	Ciprofloxacin - Levofloxacin
Penicillins/β-lactamase inhibiters	Ticarcillin-Clavulanic acid-Piperacillin- Tazobactam
Monobactams	Aztreonam
Polymyxacin	Polymyxacinb-Colistin

Results

Antimicrobial susceptibility of 100 *P. aeruginosa* isolates is shown in Table (2). Three isolates (3%) were not susceptible to any of the tested antimicrobial categories. Non-susceptibility to one and two categories were seen in 30 (30%) and 25 (25%) isolates respectively. In addition, non-susceptibility to three, four, five, six and seven categories were seen in 12 (12%), 8 (8%), 10 (10%), 26 (26%) and 3 (3%) isolates respectively. Therefore, non-susceptibility to ≥ 3 antimicrobial categories was seen in 58 isolates (58%), which are considered MDR-*P. aeruginosa.* Also non-susceptibility to ≥ 6 antimicrobial categories were seen in 33 isolates (33%), which are considered XDR-*P. aeruginosa*. Furthermore, PDR of *P. aeruginosa* was not detected in this study because non-susceptibility to all antimicrobial agents was not observed in any isolate.

Discussion

In this study, the antimicrobial susceptibility of 100 *P. aeruginosa* isolates against 14 antimicrobial agents from 7 antimicrobial categories was determined. Altogether, the highest susceptibility was shown for polymyxin antimicrobials (colistin 93% and polymyxin B 95%). Resistance of *P. aeruginosa* clinical isolates to all antibiotics except the polymyxin was reported by many medical centers[5].
These agents may not be as effective as the first-line agents; and may be associated with more significant adverse reactions[6].

Table (2): Antibiotic susceptibility of *P. aeruginosa* isolates

Categories	Antibiotic	Resistant	Intermediate	Sensitive
Aminoglycosides	GEN	95(95%)	3(3%)	2(2%)
	TM	20(20%)	20(20%)	70(70%)
	AN	88(88%)	2(2%)	10(10%)
Carbapenems	IPM	13(13%)	10(10%)	77(77%)
	MEM	10(10%)	7(7%)	83(83%)
Cephalosporins	CXM	87(87%)	2(2%)	11(11%)
	CRO	88(88%)	2(2%)	10(10%)
Fluoroquinolones	CIP	20(20%)	15(15%)	65(65%)
	LVX	66(66%)	14(14%)	20(20%)
Penicillin/β-lactamase Inhibiters	TCC	67(67%)	6(6%)	27(27%)
	TZP	27(27%)	7(7%)	58(58%)
Monobactams	ATM	47(47%)	10(10%)	43(43%)
Polymyxacin	PB	3(3%)	2(2%)	95(95%)
	CS	2(2%)	5(5%)	93(93%)

Legend

Gentamicin (GEN) Tobramycin (TM) Amikacin (AN) Imipenem (IPM)
Meropenem (MEM) Ceftriaxone (CRO) Cefuroxime (CXM) Ciprofloxacin (CIP)
Levofloxacin (LVX) Colistin (CS) Aztreonam (ATM) Polymyxin B (PB).
Ticarcillin-clavulanic acid (TCC) Piperacillin tazobactam (TZP)

Susceptibility to gentamicin and amikacin was lower (2% and 10%, respectively) as compared tobramycin (70%) susceptibility. In addition, susceptibility to ticarcillin-clavulanic acid was

much less than piperacillin-tazobactam (27% and 58%, respectively). This is probably due to antagonism of the bactericidal activity of clavulanate with ticarcillin which has been shown by other researchers[7].

On the other hand, 58 isolates (58%) were detected as MDR, 33 isolates (33%) as XDR, and none PDR isolates were detected among the 100 clinical isolates of *P. aeruginosa.* This study revealed a high frequency rate of MDR and XDR in Kosti hospitals; and it is recommended to apply proper measures to prevent the spread of these strains.

Conclusion: The multidrug and extremely drug resistant frequency rate of *P. aeruginosa* in Kosti Hospitals was high and worrisome.

References

1.Strateva T, Yordanov D. *Pseudomonas aeruginosa* a phenomenon of bacteria resistance. *J Med Microb.*2009;58:1133–48. [PubMed]

2. Hirsch EB, Tam VH. Impact of multidrug-resistant *Pseudomonas aeruginosa* infection on patient outcomes. *Expert Rev Pharmacoecon Outcomes Res.* 2010;10(4):441–51. [PMC free article] [PubMed]

3. Morales E, Cots F, Sala M, Comas M, Belvis F, Riu M, et al. Hospital costs of nosocomial multi-drug resistant *Pseudomonas aeruginosa* acquisition. BMC Health Serv Res. 2012;12:122. [PMC free article][PubMed]

4. CLSI . Performance Standards for Antimicrobial Susceptibility Testing; Twenty-Third Informational Supplement. CLSI document M100–S23. Wayne, PA: *Clinical and Laboratory Standards Institute*; 2013]

5. Bonomo RA, Szabo D. Mechanisms of multidrug resistance in *Acinetobacter* species and *Pseudomonas aeruginosa*. *Clin Infect Dis*. 2006;43(Suppl 2):S49–56. [PubMed]

6. Kim J, Lee KH, Yoo S, Pai H. Clinical characteristics and risk factors of colistin-induced nephrotoxicity.*Int J Antimicrob Agents*. 2009;34(5):434–8. [PubMed]

7. Lister PD, Gardner VM, Sanders CC. Clavulanate induces expression of the *Pseudomonas aeruginosa* AmpC cephalosporinase at physiologically relevant concentrations and antagonizes the antibacterial activity of ticarcillin. *Antimicrob Agents Chemother*. 1999;43:882–9. [PMC free article] [PubMed]