



Original Research

DOI: 10.36959/547/645

Antibiotic Resistance Pattern of Bacteria Causing Hospital Acquired Infections in the New Mansoura General Hospital, Egypt

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Abstract

Background: This study aims to describe the antibiotic resistance pattern among patients with hospital acquired infections in Mansoura New General Hospital (MNGH), Egypt and to identify the multidrug resistant organisms.

Methods: A descriptive study was carried out in different departments of MNGH. All the 272 microbiological samples (blood, urine, swabs and others) from 259 patients with hospital acquired infections during the study period were processed in the bacteriology laboratory on different culture media. Bacterial isolates were identified by Gram-stain, cultures on routine media (e.g Blood agar, MacConkey agar) and specific biochemical tests following standard procedures. Antibiotic susceptibility testing was performed using disk diffusion methods. Multidrug-resistant (MDR) was defined as isolate non-susceptible to at least one agent in more than three antimicrobial categories.

Results: The prevalence of methicillin-resistant *Staphylococcus aureus* spp. (*S. aureus*) (MRSA) was 55.8%, methicillin-resistant Coagulase-negative (CoNS) was 100%, and vancomycin-resistant *Enterococcus* spp. (VRE) was 20%. Carbapenem resistant *E. coli* was 8.2%. Cephalosporin resistant (CephRy-*Klebsiella* spp.) was 85%, and carbapenem resistant *K. pneumoniae* spp. was 21.6. MDR-*P. aeruginosa* was 43.6% and MDR *A. baumannii* spp. was 100%.

Conclusion: There is a need to integrate testing bacteria for antibiotics sensitivity in all nosocomial infections surveillance system. Policies on the control of antibiotic usage have to be implemented to avoid the emergence of newer generations of resistant pathogens.

Keywords

Hospital acquired infections, Antibiotic resistant, Multidrug resistant organism

Introduction

The emergence of antimicrobial resistance (AMR) is a global public health problem, particularly for pathogens causing nosocomial infections. Rates of AMR are increasing rapidly and resistance patterns show large variations between countries [1]. Infections caused by resistant pathogens result in significant morbidity and mortality, and contribute to increase healthcare costs worldwide. Despite the availability of newer antibiotics, emerging antimicrobial resistance has become an increasing problem in many pathogens throughout the world [2].

The hospital is an epicenter for colonization and infection by drug resistant pathogens due to the frequent usage of

potent antimicrobial agents in severely ill or immune compromised patients and suitable circumstances for patients to acquire resistant organisms, from reservoirs such as oth-

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Accepted: February 13, 2021

Published online: February 15, 2021

Citation: Hassan R, Gilany AHE, Elaal AMA, et al. (2021) Antibiotic Resistance Pattern of Bacteria Causing Hospital Acquired Infections in the New Mansoura General Hospital, Egypt. Arch Community Med 3(1):16-21

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er patients, the environment, shared equipment, or hospital personnel [3].

Despite the presence of few studies in Egypt on antibiotic resistance none was done in Mansoura New General Hospital (MNGH). The objectives of this study are to describe the antibiotic resistance pattern among patients with nosocomial infections in MNGH, Egypt and to identify multidrug resistant organisms.

Materials and Methods

This descriptive study was done in MNGH, Egypt from 1/1/2017 to 31/12/2017. MNGH is a tertiary care hospital with 400 beds; it serves the Delta region of Egypt. It has 5 intensive care units (ICU) with 57 beds [general ICU (16 beds), Neonatal intensive care unit (NICU) (20 incubator), Pediatric intensive care unit (PICU) (6 beds), Cardiology care unit (CCU) (8 beds) and a neurosurgery ICU (7 beds)]. It has different internal medicine departments as General Internal Medicine, Nephrology, Neuromedicine, Pediatrics, and different surgical departments as General Surgery, Orthopedics, Neurosurgery, Ear, Nose and Throat, Obstetrics & Gynecology, Urology, Vascular, Cardiothoracic, and Maxillofacial.

Every patient admitted to the hospital during the study period was monitored daily for developing nosocomial infections using standard definitions described by CDC [4]. A total of 272 microbiological specimens (87 blood, 83 urine, 61 surgical site swabs, 30 bronchial lavage/aspirate and 11 others) from 259 patients were processed in the bacteriology laboratory where they were isolated on different cultures. Bacterial isolates were identified by Gram-stain, cultures on routine media (e.g Blood agar, MacConkey agar) and specific biochemical tests following standard procedures. Antibiotic susceptibility testing was performed using disk diffusion methods and the result was interpreted according to the Clinical and Laboratory Standards Institute (CLSI) [5].

Multidrug-resistance (MDR) was defined according to CDC [6] as isolates which are non-susceptible to at least one agent in more than three antimicrobial categories. Specifically, an

isolate of *A. baymannii* spp. was defined as having multidrug resistance (MDR) if it tested non-susceptible (i.e., resistant or intermediate) to at least one drug in three of the following six antimicrobial agents/groups: piperacillin or piperacillin/tazobactam, extended-spectrum cephalosporins (cefepime or ceftazidime), aminoglycosides, ampicillin/sulbactam, carbapenems, and fluoroquinolones. For *Pseudomonas aeruginosa* spp. (*P. aeruginosa*) isolates, MDR was defined as testing non-susceptible (i.e., either resistant or intermediate) to at least one drug in three of the five following antimicrobial groups: piperacillin or piperacillin/tazobactam, extended-spectrum cephalosporins (cefepime or ceftazidime), fluoroquinolones, aminoglycosides, and carbapenems.

Data was analyzed using SPSS program version 16. Variables were presented as number and percent.

Results

The total number of isolated bacteria was 272 with 29.4% Gram positive bacteria (GPB) and 70.6% Gram negative bacteria (GNB). The most frequent GPB were *S. aureus* and *Enterococcus* spp. while the most frequent GNB were *Klebsiella pneumoniae* spp. (*K. pneumoniae*), *E. coli* spp. and *P. aeruginosa* spp. (Table 1).

The majority (74.4%) of *S. aureus* spp. isolates were resistant to penicillin followed by resistance to ceftazidime (55.8%). CoNS exhibits 100% resistance to ceftazidime and 75% resistance to penicillin. *Enterococci* spp. isolates were mostly resistant to ampicillin (88%) and penicillin (80%) (Table 2).

Third generation cephalosporin resistance was detected for different GNB. Resistance to ceftazidime was exhibited by 85% of *K. pneumoniae* spp., 71.8% of *P. aeruginosa* spp., 71.4% of *A. baumannii* spp., 69.7% *E. coli* spp. and 60.9% *Proteus* spp. Resistance to cefotaxime was exhibited by 85% of *K. pneumoniae* spp. 79.6% of *E. coli* spp. and 73.9% of *Proteus* spp., Resistance of *E. coli* spp., *Proteus* spp. and *K. pneumoniae* spp. to cefoperazone were 77.6%, 69.6%, and 66.2%; respectively. Resistance to the fourth generation cephalosporin (cefepime) was exhibited by 84.6% of *P. aeruginosa* spp.,

Table 1: Types of isolated pathogens.

	Total isolates	% of total isolates (272)	% of subtotal*
Gram positive bacteria	80	29.4	100
<i>S. aureus</i>	43	15.8	53.75
<i>Enterococci</i>	25	9.2	31.25
CoNS	8	2.9	10.0
<i>B hemolytic Streptococci</i>	4	1.5	5.0
Gram negative bacteria	192	70.6	100
<i>K. pneumoniae</i>	74	27.2	38.54
<i>E. coli</i>	49	18.0	25.52
<i>P. aeruginosa</i>	39	14.3	20.31
<i>Proteus</i>	23	8.5	11.95
<i>Acinetobacter</i>	7	2.6	3.65

*Subtotal from either GPB or GNB

Table 2: Antibiotic resistance pattern of isolated Gram positive organisms.

	<i>S. aureus</i> (43)	<i>CoNS</i> (8)	<i>Enterococci</i> (25)	<i>B hemolytic Streptococci</i> (4)
	N (%)	N (%)	N (%)	N (%)
Penicillin	32 (74.4)	6 (75)	20 (80)	1 (25)
Ampicillin	NT	NT	22 (88)	1 (25)
Cefoxitin	24 (55.8)	8 (100)	NT	NT
Clindamycin	16 (39)*	3 (50)*	NT	2 (50)
Erythromycin	15 (36.6)*	3 (37.5)*	15 (60)	1 (25)
Vancomycin	6 (13.9)	1 (12.5)	5 (20)	0
Linezolid	10 (23.3)	1 (12.5)	4 (16)	0
Levofloxacin	8 (18.6)	2 (25)	17 (68)	0
Gentamicin	9 (20.9)	2 (25)	17 (68)	NT
Amikacin	18 (41.9)	3 (37.5)	NT	NT
Chloramphenicol	NT	NT	6 (24)	0

NT: Not tested; *Not tested with urine (2 samples); Nitrofurantoin tested only with urine samples with % resistant to both *Staphylococcus aureus* and *CoNS* (50%), and with *Enterococcus* resistant (83.3%), Norfloxacin tested only with urine with % resistant to *Enterococcus* (66.7%)

Table 3: Antibiotic resistance pattern of isolated Gram negative organisms.

	<i>K. pneumoniae</i> (74)	<i>E. coli</i> (49)	<i>Proteus</i> (23)	<i>P. aeruginosa</i> (39)	<i>Acinetobacter</i> (7)
	N (%)	N (%)	N (%)	N (%)	N (%)
Ampicillin	64 (86.5)	42 (85.7)	NT	NT	NT
Ampicillin/sulbactam	61 (82.4)	29 (59.2)	20 (87)	NT	5 (71.4)
Piperacillin/Tazobactam	62 (83.8)	30 (61.2)	9 (39)	22 (56.4)	7 (100)
Cefazolin	65 (87.5)	46 (93.9)	21 (91.3)	NT	NT
Ceftazidime	63 (85)	34 (69.7)	14 (60.9)	28 (71.8)	5 (71.4)
Cefotaxime	63 (85)	39 (79.6)	17 (73.9)	NT	NT
Cefoperazone	49 (66.2)	38 (77.6)	16 (69.6)	NT	NT
Cefepime	58 (78.4)	32 (65.3)	18 (78.3)	33 (84.6)	5 (71.4)
Imipenem	16 (21.6)	4 (8.2)	5 (21.7)	10 (25.6)	5 (71.4)
Aztreonam	54 (73)	29 (59.2)	8 (34.8)	27 (69.3)	NT
Gentamicin	42 (56.8)	22 (44.9)	15 (65.2)	17 (43.6)	5 (71.4)
Tobramycin	37 (50)	20 (40.8)	NT	13 (33.3)	5 (71.4)
Amikacin	23 (31)	7 (14.3)	9 (39)	12 (30.8)	6 (85.7)
Ciprofloxacin	54 (73)	40 (81.6)	NT	NT	5 (71.4)
Levofloxacin	26 (3)	16 (32.7)	7 (30.4)	9 (23)	4 (57.1)
Chloramphenicol	36 (48.7)	5 (10.2)	8 (34.8)	NT	NT
Tetracycline	44 (59.5)	18 (36.7)	16 (69.6)	NT	3 (42.9)

NT: Not tested; "Nitrofurantoin tested only with urine samples with % resistant to *Klebsiella* spp. (33.3%), *E. coli* (17.2%), and Norfloxacin tested only with urine samples with % resistant to *Klebsiella* spp. (50%), and to *Pseudomonas* spp. (28.6%) and to *E. coli* (72.5%)

78.4% of *K. pneumoniae* spp., 78.3% of *Proteus* spp., 71.4% of *A. baumannii* spp., and 65.3% of *E. coli* spp. (Table 3).

Carbapenems (imipenem) resistance was observed in 71.4% of *A. baumannii* spp., 25.6%, 21.7% of *P. aeruginosa* spp. and 21.6% of *Proteus* spp., Resistance to Ciprofloxacin

was found in *E. coli* spp. (81.6%), *P. aeruginosa* spp. (73%) and *A. baumannii* spp. (71.4%). Levofloxacin resistance was found in 57.1% of *P. aeruginosa* spp. and 35% of *K. pneumoniae* spp. (Table 3).

MRSA was 55.8%, *MR CoNS* was 100%, and *VRE* was 20%.

Table 4: Resistance patterns for isolated organisms.

	Total isolates	Resistant isolate*	
		Type of resistant	N (%)
<i>S. aureus</i>	43	MRSA	24 (55.8)
<i>CoNS</i>	8	Methicillin resistant	8 (100)
<i>Enterococci</i>	25	VRE	5 (20)
<i>E. coli</i>	49	Carbapenem resistant	4 (8.2)
<i>K. pneumoniae</i>	74	CephR-Klebsiella	63 (85)
		Carbapenem resistant	16 (21.6)
<i>Acinetobacter</i>	7	MDR	7 (100)
<i>P. aeruginosa</i>	39	MDR	17 (43.6)

*From total isolates.

E. coli spp. resistance to carbapenem was 8.2%. Ceph R-*Klebsiella* spp. was 85%, and Carbapenem resistant *K. pneumoniae* spp. was 21.6%. MDR-*Pseudomonas* spp. was 43.6% and MDR *Acinetobacter* spp. was 100% (Table 4).

Discussion

In this study 74.4% *S. aureus* spp. isolates was resistant to penicillin. *CoNS* exhibit 100% and 75% resistant to cefoxitin and penicillin; respectively. *Enterococci* spp. isolates were mostly resistant to ampicillin (88%) and penicillin (80%). A study in three teaching hospitals in North of Iran, reported that 100% *S. aureus* spp. was resistant to penicillin, cefoxitin and quinolones. *CoNS* were resistant to penicillin, cefoxitin and quinolones (100%, 66% and 100%; respectively) [7]. In another study in Iranian hospital found that resistance to cefoxitin was 39.1%, quinolones resistant *S. aureus* spp. was 39.1%, and *CoNS* resistant to quinolones was 100%. *Enterococci* spp. resistance to ampicillin was 57.1% and vancomycin resistance was 42.9% [8].

Although linezolid antibiotic considered from second line treatment, it exhibits resistance by 23% 12.5% and 16% of *S. aureus* spp., *CoNS* by 12.5%, and *Enterococci* spp.; respectively. These results agreed with study in tertiary care University Hospital in India which revealed 77.5 % of organisms are resistant to linezolid [9]. Although in another study in China, revealed no resistant to linezolid [10]. Linezolid should be used if there is resistant to vancomycin and not prescribed routinely, however some clinicians use it as first line of treatment without indication this could explain the arising resistance for it.

In this study there is increase in resistant of GNB to both third (ceftazidime, cefotaxime, and cefoperazone), and fourth generation cephalosporin (cefepime). The rate of resistance to these generations of cephalosporins varies worldwide. An Iranian study found that 39% of *P. aeruginosa* spp. were resistant to cefepime, and 68% are resistant to ceftazidime [11]. A study in Morocco, showed that *P. aeruginosa* spp. resistance to ceftazidime was 35.6%, *K. pneumoniae* spp. resistance to ceftriaxone was 75.0% and to ceftazidime was 69.5%, and *E. Coli* spp. resistance to ceftriaxone was 31.9% and to ceftazidime was 21.7% [12].

This study revealed that 71.4%, 25.6%, 21.7% and 21.6%

of *Acinetobacter* spp., *P. aeruginosa* spp., *Proteus* spp., *K. pneumoniae* spp.; respectively were resistant to imipenem. A previous Egyptian study reported that resistance to imipenem was totally absent or very low [13]. Another study in three large tertiary care university hospitals in Egypt, Imipenem resistance was detected in 23.5% of *P. aeruginosa* spp. isolates and in 27.6% of *A. baumannii* spp. isolates [1]. Studies in Turkey, Italy, and France reported the presence of low levels of resistance to imipenem [14].

Quinolones antibiotics (ciprofloxacin and levofloxacin) exhibit resistance by different GNB as 81.6%, 73%, and 71.4% of *E. coli* spp., *K. pneumoniae* spp., and *Acinetobacter* spp. were found to be Ciprofloxacin-resistant; respectively. Furthermore, 57.1%, 35%, 32.7%, 30.4%, and 23% *Acinetobacter* spp., *K. pneumoniae* spp., *E. coli* spp., *Proteus* spp., and *P. aeruginosa* spp. were Levofloxacin resistant; respectively. A study in the National Cancer Institute, Egypt, *E. coli* spp. resistance to levofloxacin was 62.9% and ciprofloxacin resistance was 55.9%. *K. pneumoniae* spp. resistance to levofloxacin was 30.7% and ciprofloxacin resistance was 36% [15]. *Acinetobacter* spp. and *E. coli* spp. showed the highest resistance to ciprofloxacin in an Iranian study [16].

There has been a dramatic increase in nosocomial infections due to antibiotic resistance and MDR pathogens throughout the world. MDR bacteria of concern include *MRSA*, *VRE*, *MDR P. aeruginosa* spp., and *MDR A. baumannii* spp. Most of the high-profile nosocomial organisms are MDR e.g. methicillin-resistant *S. aureus* spp. (*MRSA*). Multidrug-resistant-gram negative organisms (MDR-GNRs) have become increasingly prevalent in many hospitals [17]. In this study *MRSA* was 55.8%, Methicillin resistant *CoNS* was 100%. In a study at Assiut University Hospitals, Egypt stated that *MRSA* was 18.9% and *CoNS* methicillin resistance was 16% [18]. Worldwide, *MRSA* rates vary widely, from 1% in Denmark, Sweden, and The Netherlands to 40% in the United Kingdom, Greece, and Italy [19]. The US rate of *r43* was 52.9%, and *CoNS* methicillin resistance was 76.6% [20]. *VRE* in this study was 20%. This is similar to a study in Korea [21]. However much higher rate was reported in Iran (42.9%) [8].

The high rate of GNP isolated from patients with nosocomial infections has a two clinical significance: A high prev-

absence of MDR strains combined with limited therapeutic options; and a higher associated mortality, particularly for Gram-negative bacteraemia [22]. *P. aeruginosa* spp. had emerged in Egypt in recent years and seen mainly in nosocomial infections [23]. In this study MDR *P. aeruginosa* spp. was 43.6%. This high rate of MDR has been reported in previous studies. In Menofia University Hospital MDR *P. aeruginosa* spp. was 52% [24]. In another study in Egypt observed that MDR *P. aeruginosa* spp. was 36% [25]. On the other hand, in study in Iran detected that 30% of isolates were MDR with 100% MDR *A. baumannii* spp. [26]. A multicenter study exhibited in 46 ICUs in 11 Egyptian hospitals, *Acinetobacter*-MDR strains were 100% [27]. In the US National Healthcare Safety Network approximately 70% of *Acinetobacter* spp. was MDR [28]. In an Indian study multidrug resistance was seen in 63.3% of the *A. baumannii* spp. infections [29].

The high percentage of antimicrobial resistance in this study could be explained on the basis of prescription behaviors in the hospital as there is no established antibiotic policy; prescription has no standard regulation, overusing of empiric treatment without laboratory confirmation of susceptibility patterns and incomplete treatment courses with antibiotics.

Study Limitations

This is a single hospital study during a single year. Its results cannot be generalized to other hospital or during different periods. There is no breakdown of the resistance patterns by specific ward or department. Information from the specific departments may show specific strains dominating in those areas.

Conclusions

These results underline the need to integrate bacteria antibiotics sensitivity in all nosocomial infections surveillance system. Policies on the control of antibiotic usage have to be enforced and implemented to avoid the evolution of newer generations of pathogens with higher resistance, not only to the older generation drugs, but also to the relatively new ones. A nation-wide study is warranted to give the full picture of antibiotic resistance. Ongoing surveillance and test for antibiotic resistance will show the changing trends over time. These will help policy makers to develop a policy for antibiotic use in health care facilities.

Funding

None.

Conflict of Interest

None.

Ethical considerations

The study protocol was approved by IRB, Faculty of Medicine, Mansoura University as well as the Director of MNGH.

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DOI: 10.36959/547/645