

Imipenem Resistance Gram-Negative Bacilli Isolated from Patients of a Tertiary Care Hospital in Dhaka, Bangladesh

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Abstract

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Introduction: The emergence of antibiotics resistance bacteria is a persistent global problem affecting public health. The occurrence and widespread resistance to Imipenem among hospital bacterial isolates can constitute a significant threat to chemotherapy.

Objectives: This cross-sectional study aimed to investigate the imipenem resistant pattern among gram-negative bacilli isolated from different samples in Dhaka medical college hospital.

Methods: A total of 300 samples (wound swab, urine, endotracheal aspirate, blood, and sputum) were collected from July 2015 to June 2016. Two hundred four gram-negative bacilli were isolated and tested for resistance to imipenem by the disc diffusion method.

Results: Among 204-gram negative bacilli, 39.21% imipenem resistance was detected by the Disc Diffusion method. 14.7% imipenem resistance gram-negative bacilli were from wound swab. 83.33% of *Acinetobacter baumannii* were Imipenem resistant.

Conclusions: Imipenem resistance is widespread among gram-negative bacilli isolated from human infections. Imipenem resistance (39.21%) found in the study is quite worrisome.

Key Words:

Antibiotic resistance, Imipenem, Gram-negative bacilli.

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Introduction

Resistance patterns among bacterial pathogens are one of the most critical problems in hospitals that may vary widely from country to country, and its-related mortality and morbidity remain extremely high.¹ The rate of bacterial resistance is markedly higher in many developing countries, probably because of a lack of supervision, poor

infection prevention practices, inappropriate use of limited resources, and overcrowding of hospitals.^{2,3} It seems that the overuse of effective antibiotics is also a potent cause of bacterial resistance, especially in these countries. Imipenem has retained in vitro activities that are superior to those of other antimicrobials. In many centers, it has been selected as the first choice for patients with infections caused by gram-positive and gram-negative bacteria.⁴⁻⁹ Imipenem remains the most active drug; recently, Imipenem retained activity against 100% of strains, and in some previous reports, the only active drug was Imipenem.¹⁰ However, recent analyses of hospital outbreaks have documented the spread of resistance to this antibiotic, and it is currently a significant problem among gram-negative bacteria.

In the present study, we tried to describe the rate of gram-negative isolates resistance to Imipenem is an antibiotic that is widely used in our country.

Materials and methods

A total of 300 samples (wound swab, urine, endotracheal aspirate, blood, and sputum) were collected from July 2015 to June 2016 in Dhaka Medical College Hospital in a cross-sectional study. All the wound swab, urine, pus, and

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endotracheal aspirate samples were inoculated in blood agar and MacConkey agar media and incubated at 37p C aerobically for 24 hours.

Incubated plates were then examined for the presence of colonies of bacteria. Primary blood culture was done in Trypticase soya broth; then, the subculture was done on blood agar and MacConkey agar media. 204-gram negative bacilli were isolated.

Susceptibility to Imipenem of all isolates was done by Kirby Bauer modified disk diffusion technique using Muller Hinton agar plates, and zones of inhibition were interpreted according to CLSI guidelines (CLSI, 2015).

Antibiotic discs imipenem (10 µg) was used. The examined clear zone of inhibition around the disc on the test organisms were interpreted as resistant and sensitive.

All strains were tested for antibiotic susceptibility by Disk Diffusion and were designated for Imipenem as susceptible if the inhibition zone diameter was ≥ 22 mm, intermediate if the inhibition zone diameter was 19–21 mm, and resistant if the inhibition zone diameter was ≤ 18 mm, as recommended by Clinical and Laboratory Standard Institute (CLSI) (2015).¹¹

Result

Of the total 300 samples, 150 were wound swabs, 65 were urine, 40 were endotracheal aspirates, 30 were blood, and 15 were sputum. From these 300 samples, 204 (68%)

gram-negative bacteria were isolated (Table 1). In Table 2, Out of 204 isolated gram-negative bacteria, 80 (39.21%) imipenem resistant strains were detected. Of which, 30 (14.7%) from wound swab, 6 (2.94%) from urine, 37 (18.13%) from ETA, 5 (2.45%) from blood and 2 (0.98%) from sputum samples were detected. Twelve (27.9%) of the 43 *Esch.coli*, 9 (34.61%) of the 26 *K. pneumoniae*, 4 (30.76%) of the 13 *K. oxytoca*, 6 (37.5%) of the 16 *Citrobacter freundii*, 2 (28.57%) of the 7 *Proteus vulgaris*, one (16.67%) of the 6 *Proteus mirabilis*, 2 (20%) of the 10 *Enterobacter aerogenes*, 20 (83.33%) of the 24 *Acinetobacter baumannii*, 24 (46.15%) of the 52 *Pseudomonas aeruginosa* were Imipenem resistant. None of the *Citrobacter koseri* and *Salmonella spp.* were Imipenem resistant.

Table I

Isolated gram negative bacteria from different samples (N=300).

Type of samples	Number of samples	Isolated gram negative bacteria n(%)
Wound swab	150	121(80.66)
Urine	65	33(50.80)
Endotracheal aspirate	40	35(87.50)
Blood	30	9(30.00)
Sputum	15	6(40.00)
Total	300	204(68.00)

N= Total number of bacteria.n = Total number of positive cases.

Table-II

Imipenem resistant organisms among different species of isolated gram negative bacteria from different samples.(N=204)

Organism	Wound swab n (%)	Urine n (%)	ETA n (%)	Blood n (%)	Sputum n (%)	Total n (%)
<i>Esch. coli</i> (N=43)	5(11.62)	2(4.26)	3(6.97)	2(4.65)	0(0.00)	12(27.90)
<i>K.pneumoniae</i> (N=26)	2(7.60)	1(3.84)	3(11.53)	2(7.69)	1(3.80)	9(34.61)
<i>K. oxytoca</i> (N=13)	2(15.30)	0(0.00)	1(7.69)	0(0.00)	1(7.70)	4(30.76)
<i>C. freundii</i> (N=16)	2(12.50)	1(6.25)	3(18.75)	0(0.00)	0(0.00)	6(37.50)
<i>C. koseri</i> (N=5)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
<i>P. vulgaris</i> (N=7)	2(28.57)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	2(28.57)
<i>P. mirabilis</i> (N=6)	1(16.66)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(16.67)
<i>E.aerogenes</i> (N=10)	1(10.00)	0(0.00)	1(10.00)	0(0.00)	0(0.00)	2(20.00)
<i>Salmonella spp.</i> (N=2)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
<i>A.baumannii</i> (N=24)	3(12.50)	0(0.00)	16(66.67)	1(4.16)	0(0.00)	20(83.33)
<i>P.aeruginosa</i> (N=52)	12(23.07)	2(3.85)	10(19.23)	0(0.00)	0(0.00)	24(46.15)
Total	30(14.70)	6(2.94)	37(18.13)	5(2.45)	2(0.98)	80(39.21)

N=Total number of bacteria n= Total number of positive case

Discussion

Infection due to gram-negative bacteria is a leading cause of morbidity and mortality worldwide (Giske *et al.*, 2008).¹² In the present study, 204 (68%) gram-negative bacteria were isolated from 300 wound swabs, urine, ETA, blood samples, and sputum (Table 1).

In the present study, 80 (39.21%) imipenem resistant organisms were identified among 204-gram negative bacteria. Of which, 37 (18.13%) from ETA, 30 (14.7%) from wound swab, 6 (2.94%) from urine, 5 (2.45%) from blood and 2 (0.98%) from sputum samples (Table 2). A previous study by Farzana (2013) (13) in DMCH found that 28.77% of gram-negative organisms isolated from wounds were resistant to Imipenem. In another study, Afrin (2013) (14) in DMCH found that 47.42% of gram-negative bacteria isolated from ETA were resistant to Imipenem. The reasons behind the higher isolation rate of Imipenem resistant organisms in Afrin (2013) study might be because all the samples of Afrin (2013) were collected from ICU. All were ETA, but in the present study, samples were collected from both general wards and ICU, which were wound swab, urine, ETA, blood, and sputum. In another study in DMCH by Khatun (2014) (15), 18.07% from ETA, 10.5% from wound swab, 3.36% from urine, and 3.36% from blood samples were resistant to Imipenem. In the present study, the most common 66.67% Imipenem resistant organism isolated from ETA was *Acinetobacter baumannii*; the findings were close to Khatun (2014) data 70.96% *Acinetobacter baumannii* were resistant to Imipenem.

Conclusion:

Imipenem is currently associated with nosocomial isolates; one of the most worrisome concerns is the spread of these Imipenem resistant strains in the community. This study represents a significant threat to public health, warranting increased efforts towards detection and infection control strategies.

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