High Burden of Antibiotic Resistant Bacteria Isolated from Tracheal Culture in a Tertiary Care Institute

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ABSTRACT

Introduction: Multidrug resistant bacteria is causing a very serious problem in the proper treatment and management of sick patients in ICU's. Study aimed to find out antimicrobial susceptibility pattern of bacterial isolates from tracheal culture.

Material and methods: This study was carried over a period of 6 months from July to December 2017 in the department of microbiology. Total of 470 tracheal aspirates were studied. Each specimen was streaked on 5% sheep blood agar and MacConkey agar. After isolation and identification, sensitivity of selected organisms against different antibiotics was studied

Results: Out of 470 tracheal aspirates, 328 samples showed single bacterial growth, 76 were sterile; contaminants were grown in 58 samples and in remaining 8 samples yeast were grown. The incidence of positivity in our study was 83.8%, with gram negative bacteria outnumbering the gram positive ones. Of the 328 samples which showed bacterial growth, *Acinetobacter spp* 159(40.3) was the most common organism followed by *Klebsiella pneumoniae* 72(18.2), *Pseudomonas spp* 46(11.6), *Escherichia coli* 27(6.8), *Staphylococcus aureus* 13(3.2), *Klebsiella oxytoca* 5(1.26), *Enterococcus spp* 3(0.76), *Proteus spp*, *Citrobacter spp*, *Providencia stuartii* 1(0.25) each. Also XDR (extensively drug resistant) bacteria were isolated at a high frequency (67%) with Acinetobacter spp. being the most common 128(56.6)) followed by *Klebsiella spp.* 39(17.2) *Pseudomonas spp.* 38(16.8), and *E.coli* 12(5.3).

Conclusion: Gram negative were main organisms responsible for lower respiratory tract infections in hospitalized patients and the majority of the isolates belong to XDR and MDR category.

Keywords: Tracheal Aspirates, XDR, MDR.

INTRODUCTION

Hospital acquired infection (HAI) is most serious and burning problem and responsible for high rate of morbidities and mortalities worldwide.[1] HAI are more common in developing countries and underdeveloped countries. However, there are no systematic surveillance programs in these countries. The risk of nosocomial infection in ICU is 5-10 times greater than those acquired in general medical and surgical wards.[2]

Since ICU is mainly responsible for caring of the patients suffering from life threatening infections, constant vigilance and monitoring, support with modern surgical apparatus and lifesaving medications has to be provided with ultimate aim to give proper relief to the patients. Most ICU patients that acquire infections are associated with the use of invasive devices such as catheters and mechanical ventilators.[3] While mechanical ventilation helps to prevent deaths due to respiratory failure, it poses great threat, by leading to life threatening lung infections like VAP.4 Mechanical ventilation is responsible for 6 to 10 fold increase in the risk of respiratory tract infections.[5,6] Moreover, the ICU mortality of infected patients is more than twice that of non-infected patients.[1] To initiate empiric antimicrobial therapy knowledge of local antimicrobial resistance patterns are essential, so our aim of the study was to detect spectrum of bacterial isolates from tracheal culture and their antimicrobial sensitivity.

MATERIAL AND METHODS

This study was carried during a period of 6 months from July to December 2017 in the department of microbiology. Total of 470 tracheal aspirates were studied. Culture was performed, and each specimen was streaked on MacConkey agar and 5% sheep blood agar. Plates were incubated at 37°C for 16-24 hours. These ETA (endotracheal aspirate) cultures were read and various biochemical tests were performed for the identification of these isolates. After isolation and identification, sensitivity of selected organisms against different antibiotics was studied according to CLSI guidelines. Antibiotic discs used were amikacin (30mcg), amoxyclavulanate (20/10mcg), ampicillin (30mcg), cefoperazone/sulbactam (75mcg/10mcg), cefoxitin (30mcg), ciprofloxacin (5mcg), levofloxacin (mcg), clindamycin (2mcg), polymixin b (10mcg), cotrimoxazole (25mcg), erythromycin (15mcg), gentamicin (10mcg), imipenem (10mcg), linezolid (30mcg), piperacillin/tazobactam (100/10mcg), Cefoperazone/sulbactam (100/10mcg) and vancomycin (30mcg), ceftazidime (30mcg), tobramycin (30mcg), ticarcillin/ clavulanate (100/10mcg), carbenicillin

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Sr. No	Organism	No. (%)
1	Acinetobacer spp.	159(40.3)
2	Klebsiella pneumoniae	72(18.2)
3	Pseudomonas spp.	46(11.6)
4	Escherichia coli	27(6.8)
5	Staphylococcus aureus	13(3.2)
6	Klebsiella oxytoca	5(1.26)
7	Enterococcus spp.	3(0.76)
8	Proteus spp.	1(0.25)
9	Citrobacter spp.	1(0.25)
10	Providencia stuartii	1(0.25)
Total		328

Table-1: Distribution of organisms isolated

Ab'S	E. coli (158)	K.pneumoniae	P.mirabilis	Citrobacter	Acinetobacter spp	Pseudomonas spp
	R	R	R	R	R	R
AK	9(33.7)	44(80)	0(0)	1(100)	144(90.6)	38(82.7)
GEN	15(55.5)	43(78.2)	1(100)	1(100)	145(91.2)	41(89.2)
TE	13(48.1)	26(47.2)	1(100)	1(100)	130(81.8)	42(91.4)
PB	0(0)	0(0)	0(0)	0(0)	0(0)	0(0)
CIP	23(85.2)	54(98.1)	1(100)	1(100)	155(97.5)	42(91.4)
LE	20(74.1)	55(100)	1(100)	1(100)	150(94.4)	45(97.9)
PIT	22(81.5)	52(94.5)	0(0)	1(100)	152(95.6)	43(93.5)
CFS	25(92.6)	52(94.5)	0(0)	1(100)	152(95.6)	41(89.2)
IMP	10(37.1)	34(61.8)	1(100)	1(100)	127(79.9)	23(50)
MRP	21(77.8)	55(100)	1(100)	1(100)	150(94.4)	44(95.7)
CAZ	-	-	-	-	-	27(58.7)
TOB	-	-	-	-	-	38(82.6)
TCC	-	-	-	-	-	36(78.3)
AZT	-	-	-	-	-	34(74)

Table-2: Antibiogram of Gram negative Bacteria.

Antibiotics	Staphylococcus aureus	Enterococcus spp.
	R	R
AMP	13(100)	7(87.5)
AMC	12(92.3)	7(87.5)
CX	12(92.3)	-
E	9(69.3)	-
CD	7(53.9)	-
LE	12(92.3)	2(66.7)
COT	6(46.2)	-
LZ	0(0)	0(0)
VA	0(0)	0(0)

Table-3: Antibiogram of Gram Positive Bacteria.

Sr. No.	Organism	XDR No.(%)
1	Acinetobacer spp	128(56.6)
2	Klebsiella pneumoniae	39(17.2)
3	Pseudomonas spp	38(16.8)
4	Escherichia coli	12(5.3)
5	Staphylococcus aureus	6(2.6)
6	Enterococcus spp	2(0.88)
7	Citrobacter spp.	1(0.44)
	Total	226(67.2)

Table-4: XDR organisms isolated from tracheal aspirates.

(10mcg), aztreonam (30mcg), tetracycline (30mcg) (Clinical and Laboratory Standards Institute (CLSI) 2017).[7]

RESULTS

A total number of 470 tracheal aspirate samples were received in the microbiology lab in a course of 6 months period. Out of 470 tracheal aspirates, 328 samples showed single bacterial growth, 76 were sterile; contaminants were grown in 58 samples and in remaining 8 samples yeast were grown.

Of the 328 samples which showed bacterial growth, *Acinetobacter spp* 159(40.3) was the most common organism followed by *Klebsiella pneumoniae* 72(18.2), *Pseudomonas spp* 46(11.6), *Escherichia coli* 27(6.8), *Staphylococcus aureus* 13(3.2), *Klebsiella oxytoca* 5(1.26), *Enterococcus spp* 3(0.76), *Proteus spp*, *Citrobacter spp, Providencia stuartii* 1(0.25) each [Table 1].

Out of total number of 470 tracheal aspirate samples received; 458 samples were received from SICU and 12 samples from NICU.

DISCUSSION

Since 1940s when antibiotics were introduced into medicine, the health and well-being of people worldwide has significantly improved. However, after many decades of success, the world is facing a serious threat of antibiotic resistance in microorganisms which is present in all countries in the world, contributing to "post-antimicrobial era".

Among healthcare settings of high-risk infection, intensive care unit (ICU) is considered an "epicenter of infections".[8] The emergence of antimicrobial resistance in ICUs is of great concern as it increases the likelihood of drug interactions/side effects and cost of therapy due to use of newer antibiotics. Resistance may also be responsible for prolonged hospital stays and can affect prognosis.[3] This study was conducted to find out antimicrobial susceptibility pattern of bacterial isolates from tracheal culture in a tertiary care hospital.

The incidence of positivity in our study was 83.8%, with gram negative bacteria outnumbering the gram positive ones. Also according to Priyanka et al gram negative bacteria were most common cause of respiratory infection in ICU patients.[3] Among gram negative bacteria most prevalent was Acinetobacter spp. followed by Klebsiella, Pseudomonas, E.coli, Citrobacter and Proteus (table-2).

Acinetobacter baumannii is an important nosocomial pathogen in hospitalized patients. It is a persistent colonizer due to its ability of forming biofilm which is an important virulence factor for device associated infections.[9] It has been found to be more resistant to antibiotics and causes outbreaks difficult to treat in ICUs.[10] Similarly in a study in Bangladesh, incidence of Acinetobacter was highest (25%) followed by Pseudomonas (15%) and Klebsiella (10%).[11] On the other hand, in the study of D K Azar et al[12] and Adair et al.[13] Enterobacter was the most common isolate followed by Pseudomonas aeruginosa.

In gram positive bacteria most common isolate was Staphylococcus aureus followed by Enterococcus spp. (table-3) which is in accordance with a study conducted by Ghosh B et al.[14] Also XDR (extensively drug resistant) bacteria were isolated at a high frequency (67%) with Acinetobacter spp. being the most common 128(56.6) followed by Klebsiella spp. 39(17.2) Pseudomonas spp. 38(16.8), and E.coli 12(5.3)

In our study, 67.2% isolates were XDR (table-4) which is in accordance with studies from Maroc[15] and Mangalore[16] where 76% and 76.84% XDR isolates were found respectively. Where as in studies from Dehradun[17] XDR, (89%) and Hyderabad[18] (XDR, 88.1%) prevalence of XDR pathogens was very high. Due to misuse of the antibiotics different pathogens are becoming increasingly resistant. Lack of regulatory policies regarding antibiotic prescription leads to their easy accessibility and promotes antibiotic overuse.

CONCLUSION

Lower respiratory tract infections in hospitalized patients, are on the increase and the majority of the isolates belong to XDR and MDR category. So, institutional guidelines for the empirical therapy need to be laid down to provide adequate antibiotic cover for these patients along with enhanced infection preventive measures thus preventing emergence of antibiotic resistance and spread of these resistant organisms. Prevention of the emergence and dissemination of resistant microorganisms will reduce adverse events and their attendant costs. Appropriate antimicrobial stewardship will prevent or slow the emergence of resistance among microorganisms.

Abbreviations

MDR: Nonsusceptible to atleast one agent in three antimicrobial categories, XDR: Nonsusceptible to atleast one agent in all but two or fewer antimicrobial categories, AMP: Ampicillin, AMC: Amoxycilin/clavulanic acid, AK: Amikacin, CX: Cefoxitin, CIP: Ciprofloxacin, CFS: Cefoperazone/sulbactam, CD: Clindamycin, CAZ: Ceftazidime, COT: Cotrimoxazole, E: Erthromycin, GEN: Gentamicin, IMP: Imipenem, LE: Levofloxacin, LZ: Linezolid, MDR: Multidrug resistant, MRP: Meropenem, PB: Polymyxin B, PIT: Piperacillin/tazobactam, TOB: Tobramycin, TCC: Ticarcillin/clavulanic acid, TE: Tetracycline, VA: Vancomycin, XDR: Extensively drug resistant

REFERENCES

1. Peleg AV, Hooper DC. Hospital acquired infections due to gram negative bacteria. N Engl J Med. 2010; 362:1804-43.
2. Vincent J.L Bihari David J, Suter M Peter. Prevalence of nosomial infection in ICU in Europe. JAMA,1995;274:639-644.
3. Soni Priyanka, Parihar R. S, Khatri P. K, Soni laxman Kumar, Agarwal Ramesh, Duggal Swati et al. Antibiogram of bacterial isolates from tracheal aspirate of ICU patients at tertiary care hospital In western, Rajasthan. International Journal of Current Research July, 2015;7:18125-18129.
4. Geetanjali Panda, Bishnu Prasad Mohapatra, Sidharth Sraban Routray, Rajat Kumar Das, Basant Kumar Pradhan. Organisms isolated from endotracheal aspirate and their sensitivity pattern in patients suspected of ventilator associated pneumonia in a tertiary care hospital Int J Res Med Sci. 2018;6:284-288
5. Chastre J, Fagon JY. Ventilator-associated pneumonia. Am J Respir Crit Care Med. 2002;165:867-903.
6. Niderman M, Craven D, Bonten M, Chastre J, Craig W, Fagon J, et al. Guidelines for the management of adults with hospital acquired, ventilator-associated, and healthcare-associated pneumonia. Am J Respir Crit Care Med. 2005;171:388-416.
7. Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 22nd informational supplement (M 100-S27), Wayne, PA: CLSI;2017.
8. Rosales – Reyes R, Alcantar – Curiel MD, Jarillo – Quijada MD, Gayosso – Vazquez C, Morfin – Otero Mdel R, Rodriguez – Noriega E et al. Biofilm Formation and Susceptibility to Polymyxin B by a Highly Prevalent Clone of Multidrug – Resistant Acinetobacter baumannii from a Mexican Tertiary Care Hospital. Chemotherapy, 2015; 61: 8-14.
9. Gebhardt MJ, Gallagher LA, Jacobson RK, Usacheva EA, Peterson LR, Zurawski DV et al. Joint Transcriptional Control of Virulence and Resistance to Antibiotic and Environmental Stress in Acinetobacter baumannii. mBio. 2015;31; 6: e01660-15.
10. Tarar M.R., Naeem T., Iqbal S., Hadjirul H., Ghouri M., Ishaq M et al. Temporal pattern and control of an

outbreak of Extensively drug resistant Acinetobacter baumannii in ICU. Biomedica, 2015; 31: 36-41.
11. Lamya Hoque, S M Mostofa Kamal & Zakaria Ahmed. Isolation, Identification and Antimicrobial Sensitivity Pattern Of Bacterial Isolates From Tracheal Aspirate Of ICU Patients Of Central Dhaka, Bangladesh. International Journal Of Research In Applied, Natural and Social Sciences 2013;1:11-16.
12. Khosravi AD, Parhizgari N, Montazeri EA, Mozaffari A, Abbasi F. The prevalence of bacteria isolated from endotracheal tube of patients in Golestan Hospital, Ahvaz, Iran, and determination of their antibiotic susceptibility patterns. Jundishapur Microbiol. 2013;5:67-71.
13. Adair CG, Gorman SP, Byers LM, Jones DS, Feron B, Crowe M, et al. Eradication of endotracheal biofilm by nebulised gentamicin. Intensive Care Med. 2012; 28:426- 431.
14. Ghosh B, Ghosh K, Roy A, Pal D, Ghosh A, Mondal K. Correlation between colonized bacteria of ET tube among suspected pneumonia patients of ICU. International Journal of Recent Trends in Science And Technology 2014;11:245-248.
15. Uwingabiye J, Frikh M, Lemnouer A, Bssaibis F, Belefquih B, Maleb A et al. Acinetobacter infections prevalence and frequency of the antibiotics resistance: comparative study of intensive care units versus other hospital units. Pan Afr Med J 2016;23:191-19618.
16. Shridhar S, Bhat S. Clinicomicrobiological Study of infections caused by Acinetobacter species. Asian J Pharm Clin Res 2017; 10:223-224.
17. Chaudary A, Pandya N. Emergence of multi drug resistant Acinetobacter baumannii as nosocomial pathogen. J Dent Med Sci 2015; 14:40-44.
18. Swathi Akula, Guru Prasad Manderwad, Ravi Shankar Reddy Anukolu, HRV Rajkumar. Emergence of Extensively drug-resistant Acinetobacter spp in a tertiary care centre of Hyderabad, Telangana state Indian J Microbiol Res 2017;4:448-452.

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