International Journal of Science and Research (IJSR)
ISSN: 2319-7064
SJIF (2022): 7.942

Antibiotic Sensitivity Pattern of Bacterial Isolates from Respiratory Samples of Patients with Respiratory Tract Infection in a Tertiary Care Teaching Hospital of Pune: A Hospital Record-Based Study

Lt Col (Dr) Manas Dixit[1], Maj (Dr.) Neha Singh[2], Surg Cdr (Dr) Muzafar Ahmad Bhat[3], Dr Richa Jaiswal[4], Lt Col (Dr) Prashant Patil[5]

[1, 2, 3] Microbiology Resident, Department of Microbiology, Armed Forces Medical College, Pune – 411040

[4]Faculty of pathology, Jehangir Hospital, Pune-411040

[5]Faculty of Microbiology, Army Institute of Cardio Thoracic Sciences, Pune – 411040

Abstract: ***Background: Antibiotics are frequently used for various infectious diseases like acute lower respiratory tract infection (LRTI). Injudicious use of antibiotics often leads to antibiotic resistance which is an emerging problem worldwide. The objective of this study was taken up to analyse the antimicrobial sensitivity pattern of pathogens isolated from the respiratory samples of patients admitted with symptoms of acute LRTI in a tertiary care teaching hospital. Objective: To study the Antibiotic sensitivity pattern of bacterial isolates from respiratory samples of patients with respiratory tract infection. Method: This study was a hospital record based retrospective study of 243 patients. Result: Klebsiella pneumoniae was the most common organism isolated followed by Pseudomonas aeruginosa and Acinetobacter baumannii. Klebsiella pneumoniaewas most sensitive to Colistin and Doripenem. Pseudomonas aeruginosa and Acinetobacter baumannii were most sensitive to Colistin, Amikacin, Aztreonam, Trimethoprim / Sulfamethoxazole. Conclusion: The study highlights the extent of antibiotic resistance in common respiratory pathogens isolated from the respiratory samples.***

Keywords: Antibiotic resistance, *Klebsiella*, *Acinetobacter*, Lower respiratory tract infection

1. Introduction

Globally, antimicrobial-resistant infection skills at least 700 000 people each year; within 30 years, resistant infections are predicted to kill 10 000 000 per year, greatly exceeding deaths from cancer [1]. Most antibiotic resistant infections are nosocomial [2]. Over 25% of healthcare-associated infections are caused by antibiotic-resistant bacteria [1]. Antibiotics can also eliminate susceptible microbial populations, reducing competition and expanding the resources available to resistant bacteria [3]. Antimicrobial resistance is spreading rapidly because once a resistance gene evolves in one bacterium, it can spread to other cells and other bacterial species [4].

Antibiotic resistance in respiratory pathogens is of particular concern. For instance, Many *K. pneumoniae* strains have acquired a variety of β-lactamases against penicillin, cephalosporins and carbapenems. Carbapenems are frequently used to treat infections with gram-negative bacteria, but the increase of *K. pneumoniae* carbapenemases (KPC) -producing strains, renders such infections more and more difficult to treat [5]. Additionally, some *K. pneumoniae* strains express the metallo-β-lactamase NDM-1 [6]. The presence of New-Delhi Metallobetalactamase (NDM-1) has increased the prevalence of carbapenem-resistant *K. pneumoniae* strains, which has made the use of other antibiotics such as Aminoglycosides and Fluoroquinolones increasingly necessary.

Because of the increasing incidence of multidrug-resistant *A. baumannii* strains globally, the WHO classified *A. baumannii* as critical (in the priority group 1) for the development of new antimicrobial agents [7].

The Gram-negative bacterium *P. aeruginosa* is also listed in the WHO priority group 1 of pathogens that urgently require new treatment options. It intrinsically shows low susceptibility to many antimicrobial drugs and a high propensity to develop resistance. Reduced porin permeability together with AmpC overproduction leads to increased carbapenem resistance in *P. aeruginosa* [8]. Inaddition, *P. aeruginosa* can express KPCs, Extended Spectrum Beta lactamases (ESBLs) and Imipenemase metallo-β-lactamases, resulting in high-level carbapenem resistance.
In this study, we aimed to study the pattern of antibiotic susceptibility in respiratory samples.

2. Methods

Study design

This study was a hospital record based retrospective study.

Study setting
The study was conducted in the Microbiology department of Army Institute of Cardio Thoracic Sciences (AICTS), one of affiliated hospitals of Armed Forces Medical College, Pune.

Study duration:
The study duration was 6 months from Oct 2021 to Mar 2022.

Sample size:
A total of243 respiratory samples (Bronchoalveolar lavage, Sputum, Tracheal aspirate, Pleural fluid) were included in this study.

Inclusion criteria:
All patients admitted with respiratory infections in In-patient wards of Army Institute of Cardio Thoracic Sciences were included in the study.
Samples with Bartlett grading of+1 and above on direct gram stain of the samples were included in the study.

Exclusion criteria:
Samples not meeting the Bartlett criteria were excluded.
Antimicrobial agents that were used infrequently or rarely for sensitivity testing were excluded from the study.
Samples received in unsterile conditions, leaking sample container were excluded

3. Study Techniques

The respiratory samples were collected from clinically diagnosed acute LRTI patients who were admitted in various departments of the hospital during the study period. The samples were collected in sterile wide mouth container and transported immediately to the microbiology lab of AICTS. The sputum samples were divided into two parts-one part was processed for bacteriological culture and other part was used for making slides for gram stain. The Sputum, BAL, Tracheal aspirate samples were inoculated on Blood agar, MacConkey agar, Chocolate agar and were incubated in CO_2 chamber by using candle jar method for 18-24 hrs. The culture plates were examined after 18-24 hours and the preliminary identification by colony characteristics and biochemical reactions were done. The colonies were further processed for identification and antimicrobial susceptibility by automated method (Vitek 2 MS). Also, the antibiotic susceptibility of the isolates was performed by modified Kirby-Bauer disc diffusion method, according to CLSI 31 and 32 edition (M100) recommendations. Control strains were used for checking the quality of discs and reagents.

4. Results

A total of 350 respiratory samples were collected during the study period among which 243 samples were given as culture positive reports according to policy and guidelines of hospital.

Amongst the total organisms isolated, *Klebsiella pneumoniae* n = 108 (44.44%) was the most isolated organism followed by *Pseudomonas aeruginosa* in 28.4% of samples (n=69) and *Acinetobacter baumannii* in 8.64% of samples (n=21).
The list of organisms isolated in our study is as shown in Table 1.

Table 1: Organisms isolated (n = 243)

Organism	N (%)
Klebsiella*oxytoca*	6 (2.47%)
Acinetobacter baumannii	21 (8.64%)
Enterobacter cloacae	9 (3.70%)
Enterococcus sp.	3 (1.23%)
E. Coli	15 (6.17%)
Klebsiella pneumoniae	108 (44.44%)
Pseudomonas aeruginosa	69 (28.40%)
Serratia marcescens	3 (1.23%)
S. aureus	6 (2.47%)
Staphylococcus, coagulase negative	3 (1.23%)

/

Klebsiella pneumonia was mostly susceptible to Colistin followed by Doripenem.

The Antibiogram of *Klebsiella pneumoniae* is shown in Table 2. All 108 samples were found to be sensitive to Colistin and Doripenem. *K. pneumoniae* strains were completely resistant to Ampicillin and Aztreonam. They were highly sensitive to Ertapenem, Ticarcillin / Clavulanic acid, Tigecycline – 84.6, 66.7 and 80% respectively and that was statistically significant.

Table 2: Antibiotic Sensitivity pattern of *Klebsiella pneumoniae*
/

Antibiotic sensitivity pattern of *Pseudomonas aeruginosa*is shown in table 3: All 69 samples were found to be sensitive to Colistin and Amikacin. *P. aeruginosa* strains were completely resistant to Ceftriaxone. Resistance was also noted with a majority of samples with Piperacillin / Tazobactam (80%), Imipenem (71.4%), Meropenem (71.4%), Gentamycin (71.4%), ciprofloxacin (71.4%), Trimethoprim / Sulfamethoxazole (71.4%), Minocycline (80%) and this was statistically significant.

Table 3: Antibiotic Sensitivity pattern of *Pseudomonas aeruginosa*
/

Antibiotic sensitivity pattern of *Acinetobacter baumannii* is shown in Table 3.

All 21 samples were found to be sensitive to aztreonam and Trimethoprim / Sulfamethoxazole. All samples were resistant to Ampicillin. They were highly sensitive to Piperacillin / Tazobactam (81.8%), Gentamycin (73.9%), Colistin (86.4%) and this was statistically significant.

Table 3: Antibiotic sensitivity pattern of *Acinetobacter baumanii*
/

S. No	Antibiotic	Resistant (%)			Intermediate (%)			Sensitive (%)		
		Kpn	Pae	Aba	Kpn	Pae	Aba	Kpn	Pae	Aba
1	Piperacillin / Tazobactam	52	80	9.1	8	0	9.1	40	20	81.8
2	Cefoperazone / Sulbactam	54.5	0	30	0	50	0	45.5	50	70
3	Cefepime	70	57.1	33.3	0	14.3	0	30	28.6	66.7
4	Imipenem	61.1	71.4	39.1	2.8	0	0	36.1	28.6	60.9
5	Meropenem	55.6	71.4	30.4	0	0	0	44.4	28.6	69.6
6	Gentamicin	44.4	71.4	21.7	0	0	4.3	55.6	28.6	73.9
7	Amikacin	44.4	0	34.8	2.8	0	0	52.8	100	65.2
8	Ciprofloxacin	65.7	71.4	30.4	8.6	0	0	25.7	28.6	69.6
9	Tigecycline	20	***	90	0	***	0	80	***	10
10	Colistin	0	0	4.5	0	0	0	100	100	86.4
11	Trimethoprim / Sulfamethoxazole	63	***	0	0	***	0	37	***	100
12	Levofloxacin	57.1	50	40	14.3	0	5	28.6	50	55
13	Tetracycline	50	***	0	0	***	50	50	***	50
14	Ticarcillin / Clavulanic acid	33.3	50	31.2	0	0	37.5	66.7	50	31.2
15	Ceftazidime	75	60	30	0	0	15	25	40	55
16	Doripenem	0	50	33.3	0	0	0	100	50	66.7
17	Minocycline	50	75	50	16.7	0	50	33.3	25	0
18	Ceftriaxone	80.6	***	76.47	0	***	0	19.4	***	23.53
19	Amoxicillin / Clavulanic acid	60.9	***	**	13	***	**	26.1	***	**
20	Cefuroxime	78.9	85.71	5	0	0	0	21.1	14.29	95
21	Ertapenem	15.4	***	**	0	***	**	84.6	***	**

**Klebsiella pneumoniae* is Intrinsically resistant to Ampicillin and Ticarcillin.
***Acinetobacter baumanii* is Intrinsically resistant to Ampicillin, Amoxicillin, Amoxicillin Clavulanate, Aztreonam, Ertapenem, Trimethoprim, Chloramphenicol, Fosfomycin.
****Pseudomonas aeruginosa* is Intrinsically resistant to Ampicillin, Amoxicillin, Piperacillin, Ticarcillin, Ampicillin Sulbactam, Amoxicillin Clavulanate, Piperacillin Tazobactam, Cefotaxime, Aztreonam, Imipenem, Meropenem, Ertapenem, Tetracycline. Tigecycline, Trimethoprim, Trimethoprim Sulfamethoxazole, Chloramphenicol

/

5. Discussion

In our study *Klebsiella pneumonia* was the most predominant organism isolated which was in concordance to study done by Debnath S et al [10], Ahmed et al [11], Promite et al [12] and Manikandan et al [13] showing 52.16%, 59.7%, 42.5% and 28.4% frequency respectively.

In this study, *Klebsiella pneumoniae* was sensitive to Colistin, Ticarcillin / Clavulanic acid, Doripenem and Ertapenem. In other studies, it was sensitive to Amikacin and Gentamycin [12] whereas Debnath S et al [10] found *Klebsiella* to be sensitive to Amikacin, Imipenem, Gentamycin, Gatifloxacin, Levofloxacin, Ciprofloxacin, Piperacillin / Tazobactam and Cefuroxime.

In this study, the other common pathogens isolated from respiratory samples were *Acinetobacter baumannii* (8.64%) and *Pseudomonas aeruginosa* (28.40%). Debnath S et al [10] and Ali et al [14] found similar proportion of *Acinetobacter (*13.49% and 13.69%). Agarwal et al also found *Acinetobacter* and *Pseudomonas* as commonly encountered pathogens and the prevalence was 34.8% and 23.9% respectively. [15]

In the study by Debnath S et al [10], *Pseudomonas* was highly sensitive to Imipenem, Piperacillin / Tazobactam, and was sensitive to Gentamycin, Ceftazidime / Clavulanic acid. However, in our study, *Pseudomonas* was resistant to all these antibiotics. Instead, all the samples where *Pseudomonas aeruginosa* was isolated were sensitive to Colistin and Amikacin.

In various contemporary studies like Nepal et al [16], Thomas et al [17], *Acinetobacter* was found to be resistant to a host of antibiotics like Ceftriaxone, Amoxicillin, Cefixime, Ciprofloxacin, Azithromycin, Ceftazidime, Cefepime, Gentamicin. However, in our study, it was found to be sensitive to Aztreonam, Trimethoprim / Sulfamethoxazole, Piperacillin / Tazobactam, Gentamycin, Colistin and this was statistically significant.

6. Conclusion

The study highlights the extent of antibiotic resistance in common respiratory pathogens isolated from the respiratory samples. More such studies are needed from different geographic locations to know the local sensitivity pattern of the microbes. It is of hope that these studies will help in guiding clinical decisions and the impact of resistant should discourage reckless empirical antibiotic therapy, especially for viral infections like common cold and even COVID-19.

7. Limitations

The atypical organisms were not isolated from samples.

Funding: No funding sources

Conflict of interest: None declared

Acknowledgements: None.

Ethical approval: The study was approved by the Institutional Ethics Committee

References

[1] O'Neill J. Review on antimicrobial resistance. Antimicrobial resistance: tackling a crisis for the health and wealth of nations.2014 Dec 11; 2014 (4).
[2] Cheong E, Gottlieb T, Crook D, Kizny Gordon A, Kotay S, Mathers A, Peto T, Stoesser N, Walker A. The Hospital Water Environment as a Reservoir for Carbapenem-Resistant Organisms Causing Hospital-Acquired Infections-A Systematic Review of the Literature.
[3] Conlan S, Thomas PJ, Deming C, Park M, Lau AF, Dekker JP, Snitkin ES, Clark TA, Luong K, Song Y, Tsai YC. Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae. Science translational medicine.2014 Sep 17; 6 (254): 254ra126-.
[4] Juhas M. Horizontal gene transfer in human pathogens. Critical reviews in microbiology.2015 Jan 2; 41 (1): 101-8.
[5] Reyes J, Aguilar AC, Caicedo A. Carbapenem-resistant Klebsiella pneumoniae: microbiology key points for clinical practice. International Journal of General Medicine.2019; 12: 437.
[6] Yong D, Toleman MA, Giske CG, Cho HS, Sundman K, Lee K, Walsh TR. Characterization of a new metallo-β-lactamase gene, bla NDM-1, and a novel erythromycin esterase gene carried on a unique genetic structure in Klebsiella pneumoniae sequence type 14 from India. Antimicrobial agents and chemotherapy.2009 Dec; 53 (12): 5046-54.
[7] World Health Organization. Prioritization of pathogens to guide discovery, research and development of new antibiotics for drug-resistant bacterial infections, including tuberculosis. World Health Organization; 2017.
[8] Fukuoka T, Ohya S, Narita T, Katsuta M, Iijima M, Masuda N, Yasuda H, Trias J, Nikaido H. Activity of the carbapenem panipenem and role of the OprD (D2) protein in its diffusion through the Pseudomonas aeruginosa outer membrane. Antimicrobial agents and chemotherapy.1993 Feb; 37 (2): 322-7.
[9] Konman EW, Allen SD, Janda WM, Schreckenberger PC, Winn Jr WC. Color atlas and textbook of Diagnostic Microbiology, 5th Ed. Philadelphia: Lippincott-Raven; 1997.
[10] Debnath S, Bhaumik D, Chakraborty M, Ghosh R, Das L, Bhattacharjee P. Antibiotic sensitivity pattern of bacterial isolates from sputum samples of admitted patients with acute lower respiratory tract infections in a tertiary care teaching hospital of Tripura: a hospital record-based study. Int J Basic Clin Pharmacol 2020; 9: 254-8.
[11] Ahmed SMA, Abdelrahman SS, Saad DM, Osman IS, Osman MG, Khalil EA. Etiological Trends and Patterns of Antimicrobial Resistance in Respiratory Infections. Open Microbiol J.2018; 12: 34-40.
[12] Promite S, Ahsan S, Akhter MZ, Saha SK. Characterization and Antibiotic Sensitivity Profile of Bacteria Isolated from Patients with Respiratory Tract Infections in Bangladesh. Dhaka Univ J Pharm Sci.2017; 16: 235-44.
[13] Manikandan C, Amsath A. Antibiotic susceptibility of bacterial strains isolated from patients with respiratory tract infections. Int J Pure Appl Zool.2013; 1: 61-9.
[14] Ali I, Butt MA. Antibiotic Susceptibility Pattern of Bacterial Isolates from Patients of Respiratory Tract Infection at 43 Centers in Punjab, Pakistan. Clin Exp Pharmacol.2017; 7: 1-7.
[15] Agarwal R, Gupta D, Ray P, Agarwal AN, Jindal SK. Epidemiology, risk factors and outcome of nosocomial infection in a respiratory intensive care unit in North India. J Infec.2006; 53: 98-105.
[16] Nepal R, Singh A, Shrestha B, Shrestha S, Joshi DM, Joshi RD. Antibiotic susceptibility pattern of gram-negative isolates of lower respiratory tract infection. J Nepal Health Res Counc.2018; 16: 22-6.
[17] Thomas B, Sukumaran P, Oommen S, Midhun M, George D. Antimicrobial resistance of Acinetobacter baumannii infection of lower respiratory tract and mortality-A cross sectional study from a tertiary care teaching hospital in Kerala. Indian J Immunol Respiratory Med.2018; 3: 183-7.