Evaluation of Antimicrobial Resistance and Bacterial Spectrum of Infections at a Tertiary Care Teaching Hospital: A Retrospective Analysis

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ABSTRACT

Introduction: It is essential to study the antimicrobial resistance and spectra of activity of bacteria time to time to provide data for the rational use of antibiotics, henceforth the present retrospective study was taken into consideration.

Materials and Methods: The present study was conducted over total 500 samples of bacterial culture that comprised of blood samples, swabs from ear, nose, throat, skin and wound infections and urine samples. Bacterial isolates were identified using standard laboratory methods. Identification of isolates was confirmed by PCR. Data so obtained was analyzed using the SPSS Version 17 software and was arranged according to characteristics and represented as a number and percentage.

Results: Staphylococcus aureus was found in 36% cases, Enterococcus faecalis in 26%, Escherichia coli 18%, Streptococcus pneumonia in 11%, Salmonella enteric in 5% cases, Klebsiella pneumonia in 9%, Pseudomonas aeruginosa in 6%, Salmonella enteric in 5%, Enterococcus faecium in 5%, and Proteus mirabilis in 4% cases. 38% were Methicillin-resistant S aureus.

Conclusion: The bacterial spectrum of infection and antimicrobial resistance of various strains should be evaluated time to time to monitor antibiotic resistance as well as prevalence of multidrug resistant strain as it is important to plan treatment strategy.

KEYWORDS: Antibiotic resistance, Methicillin-resistant Staphylococcus aureus, Microbiology.

INTRODUCTION

Antimicrobial resistance is not a novel concern, however the number of resistant organisms, the geographic locations affected by drug resistance, and the breadth of resistance in single organisms are unparalled and mounting.[1] The knowledge of the infection epidemiology and the antibiotic resistance patterns is important to guide optimal empiric treatment in critically ill patients.[2] Diseases and disease agents that were once thought to be controlled by antibiotics are returning in new leagues resistant to these therapies.[1] In view of this, it is essential to study the antimicrobial resistance and spectra of activity of bacteria time to time to provide data for the rational use of antibiotics, henceforth the present retrospective study was taken into consideration.

MATERIALS AND METHODS

The present retrospective study was conducted in Department of Microbiology, Chintpurni Medical College & Hospital, Bungal, Pathankot, Punjab (India) over total 500 samples of bacterial culture that comprised of blood samples, swabs from ear, nose, throat, skin and wound infections and urine samples. Samples were randomly selected from the data of patients with age from 18 to 50 years from microbiological laboratory over a period of one year. Ethical clearance was taken for the commencement of the study.

Commercial blood cultures were used to study blood infections. Sterile cotton swabs were used for the collection of samples from ear, nose, throat, skin and

wound infections. Sterile single-use pots were used for collection of urine samples for microbiological culture. Bacterial isolates were identified using standard laboratory methods. Identification of isolates was confirmed by PCR.

Disk-diffusion method was used for antimicrobial susceptibility testing as described according to guidelines for laboratory detection of Clinical and Laboratory Standards Institute (CLSI). PBP2a-agglutination test was used for assessing methicillin-resistance for all cefoxitin-resistant Staphylococcus aureus.

Data so obtained was analyzed using the SPSS Version 17 software and was arranged according to characteristics and represented as a number and percentage.

Table 1: Bacterial spectrum of infection in present study.

Pathogen	Patients n (%)
Staphylococcus aureus	36%
Salmonella enteric	5%
Streptococcus pneumonia	11%
Enterococcus faecalis	26%
Enterococcus faecium	5%
Escherichia coli	18%
Klebsiella pneumoniae	9%
Proteus mirabilis	4%
Pseudomonas aeruginosa	6%

Table 2: Resistance rate of Methicillin resistant Staphylococcus aureus to various antibiotics

Staphylococcus aureus	Antibiotics	Resistance rate
	Methicillin	38%
Methicillin resistant	**Erythromycin**	100%
Staphylococcus aureus	**Fluoroquinolones**	62%
	Clindamycin	71%
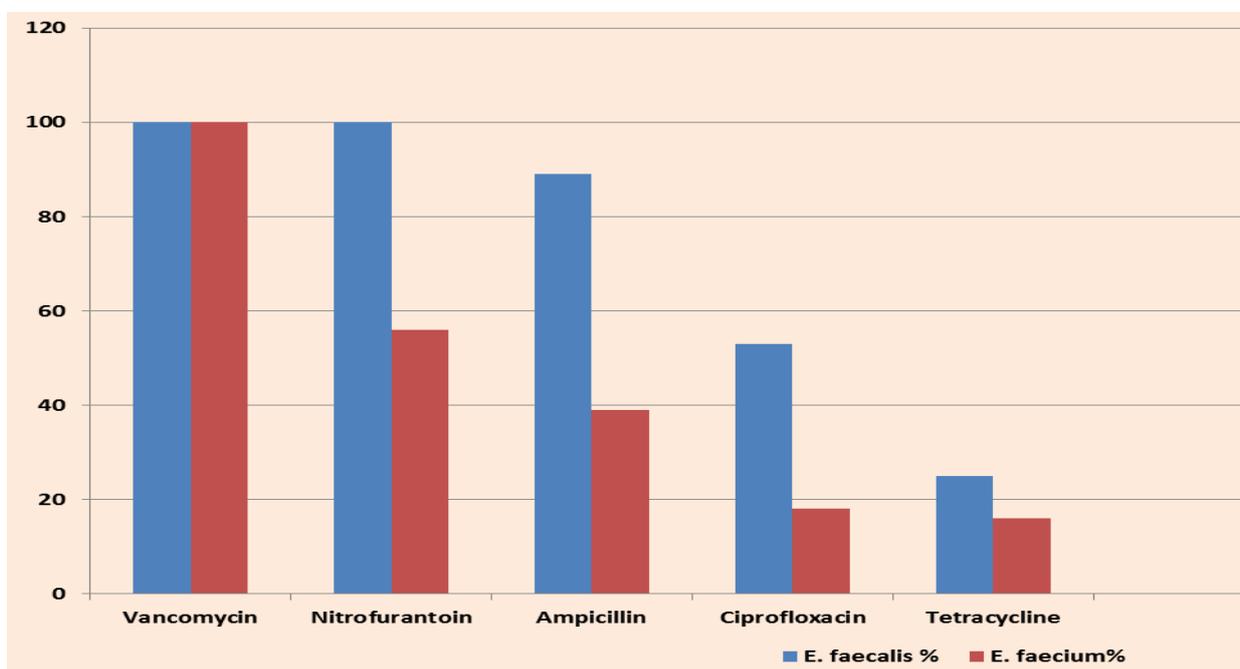
Graph 1: Antibiotic sensitivity of Enterococcus faecalis and Enterococcus faecium

RESULTS

Staphylococcus aureus was found in 36% cases, Enterococcus faecalis in 26%, Escherichia coli 18%, Streptococcus pneumonia in 11%, Salmonella enteric in 5% cases, Klebsiella pneumonia in 9%, Pseudomonas aeruginosa in 6%, Enterococcus faecium in 5%, and Proteus mirabilis in 4% cases (table 1).

From the Staphylococcus aureus isolates, 38% were Methicillin-resistant S aureus (MRSA) with 100% of them showed resistance to erythromycin, 62 % fluoroquinolones and 71% to clindamycin (table 2).

All isolated strains of E. faecalis were sensitive to vancomycin and to nitrofurantoin, 89% strains were sensitive to ampicillin, 53% to ciprofloxacin and 25% to tetracycline. All strains of E. faecium were sensitive to vancomycin, 56% to nitrofurantoin, 39% were sensitive to ampicillin, 18% to ciprofloxacin and 16% to tetracycline.

DISCUSSION

The most prevalent pathogen found in present study was Staphylococcus aureus followed by Enterococcus faecalis and Escherichia coli. Similarly, Alabi AS et al[2] conducted a study retrospective analysis of microbiological findings from a secondary care hospital in South Africa and reported Staphylococcus aureus as the most prevalent. Orsini J et al[3] conducted a prospective observational study among adult patients with clinical signs of sepsis in hospital in New York and reported that Staphylococcus aureus was found in 20.8% patients, Enterococcus spp in 16.6% and Streptococcus pneumoniae in 11.1%.

Staphylococcus aureus is one of the most considerable human pathogens responsible for nosocomial and community-acquired infections. It can cause a range of infectious diseases from mild conditions, such as soft tissue infections, to severe life-threatening debilitation, such as endocarditis.[4] Methicillin-resistant Staphylococcus aureus is a major pathogen worldwide; MRSA infections are associated with increased morbidity and mortality, in comparison with other S. aureus infections. Over the past decade, the changing pattern of resistance in S. aureus has underscored the need for new antimicrobial agents.[5]

In the present study, from the Staphylococcus aureus isolates, 38% were Methicillin-resistant S aureus. Chapin KC et al[6] conducted a study to identify Methicillin-Resistant Staphylococcus aureus from blood cultures and found that of the 70 blood cultures positive for S. aureus, 44 had methicillin-resistant S. aureus and 26 had methicillin-susceptible S. aureus as determined by the oxacillin screen agar method using isolated colonies. Shitu AO et al[7] studied antibiotic resistance and molecular epidemiology of Staphylococcus aureus in Nigeria and reported that ermA gene was identified in all erythromycin-resistant MRSA isolates, while two erythromycin-resistant MSSA isolates possessed the msrA gene. All the gentamicin-resistant isolates carried the aacA-aphD gene. Methicillin resistance has become an important problem among hospital isolates as these strains are also often resistant to other antibiotics such as aminoglycosides, tetracyclines and quinolones.[4] Methicillin resistance in S. aureus involves an altered target site due to an acquired penicillin-binding protein (PBP 2a) with decreased affinity to b-lactams. The mecAgene encodes this protein and is located on a mobile SCCmec cassette chromosome. This genetic element confers resistance to most currently available b-lactam antibiotics.[8] Zahid KF et al[9] evaluated bacterial spectrum and susceptibility patterns of pathogens in adult febrile neutropenic patients and reported that 33% strains of Staphylococcus aureus were methicillin resistant and Escherichia coli was the pathogen found in 23.1% of patients, followed by Staphylococcus epidermidis in 13.9%, Pseudomonas aeruginosa in 12.5% and Staphylococcus aureus in 7.9%.

The importance of the genus Enterococcus clinically is directly related to its antibiotic resistance, which contributes to the risk of colonization and infection. The species of the greatest clinical importance are Enterococcus faecalis and Enterococcus faecium.[10] Enterococci show natural resistance to many antibiotics as well as also acquire easy resistance to antibiotics. Infections caused by multiresistant strains are difficult to treat, are chronic and recurrent as well as are fatal sometimes.[11]

Enterococcus faecalis, while normally a gut commensal, is a frequent cause of many serious human infections, including urinary tract infections, endocarditis, bacteremia, and wound infections. Among the diseases that E. faecalis causes, urinary tract infections are the most common, responsible for approximately 110,000 cases yearly, many of which are nosocomial. Infections with E. faecalis can be especially troublesome to treat because of their frequent resistance to multiple antibiotics, including vancomycin, a drug of last resort for many gram-positive infections.[12] However, in the present study, all isolated strains of E. faecalis were sensitive to vancomycin and to nitrofurantoin, 89% strains were sensitive to ampicillin, 53% to ciprofloxacin and 25% to tetracycline. All strains of E. faecium were sensitive to vancomycin, 56% to nitrofurantoin, 39% were sensitive to ampicillin, 18% to ciprofloxacin and 16% to tetracycline.

A major cause behind the survival of these organisms in hospital environment is the intrinsic resistance to several commonly used antibiotics and, possibly more importantly, their ability to acquire resistance to all presently available antibiotics, either by receipt of foreign genetic material through the transfer of plasmids and transposons or by mutation. The emergence of vancomycin-resistant enterococci is a matter of concern,

as it is very difficult to control when once established. Moreover, there can be transfer of resistant gene from enterococci to Staphylococcus aureus thereby posing a threat to the patient safety and also challenges for the treating physicians.[13]

CONCLUSION

The present study concludes that bacterial spectrum of infection and antimicrobial resistance of various strains should be evaluated time to time to monitor antibiotic resistance as well as prevalence of multidrug resistant strain. It is also of importance as epidemiological profile varies place to place and the knowledge of the infection epidemiology and the antibiotic resistance patterns is important to plan treatment strategy.

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