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Original Research Article

Antimicrobial resistance among common clinical isolates from Wayanad district

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ABSTRACT

Introduction: The emerging multi-drug resistant variants in different clinical isolates is leading to increased morbidity and mortality, due failure in treatment. The paucity of an accurate data of antimicrobial resistance from different geographical areas is a major setback to its control and management. The aim of this study was to analyse the occurrence of drug resistant organisms from different clinical samples in the district of Wayanad, and also to determine the most prevalent and emerging bacterial pathogens among them.

Materials and Methods: A seven-month retrospective study of different bacterial isolates from various clinical samples was conducted in a tertiary care hospital in Wayanad district. Clinical samples taken for the study included urine, pus, sputum and blood.

Results: Data from 2125 clinical samples were studied, in which 661 were urine samples, 910 were pus samples, 225 were blood samples and 339 were sputum samples. The predominant bacteria identified from urine sample was *E. coli* among which the prevalence of extended spectrum beta lactamase (ESBL) producing *E.coli* was 40.61%, and the metalobetalactamase (MBL) producers 3.45%. *Staphylococcus aureus* was the predominant bacteria in the pus samples, in which Methicillin resistant *Staphylococcus aureus* (MRSA) was found to be 3.92%. *Acinetobacter* was the most predominant bacteria in the blood samples, in which ESBL producing *Acinetobacter* was noted as 3.57%. Klebsiella species were the predominant bacteria in the sputum samples, in which ESBL producing *Klebsiella* was 16.79% and MBL producers were 3.82%.

Conclusion: The study helped to identify the most predominant antibiotic resistant strains from each of the clinical samples in a resource limited setting like Wayanad. Similar studies would help in successfully formulating treatment strategies against bacterial infections, thereby reducing morbidity and mortality in patients.

1. Introduction

Antimicrobial resistance has now become a global health concern. The advent of antibiotics was a major milestone in the field of medicine and has not only saved countless lives but also have played a pivotal role in achieving significant advances in medicine and surgery and effectively combating and managing infections in patients.[1,2] However, the unregulated use of antibiotics has resulted in the development of multi-drug resistant organisms.[2]

Microbes develops various mechanism to counter act the antimicrobial agents through adaptation and therefore resulting in resistance to antimicrobmulti-drug.[3,4] The emerging multi-drug resistant variants in different clinical isolates has led to increased morbidity and mortality, due to failure in treatment.[5,6] Factors contributing to the emerging resistant organism include overutilization of antibiotics in human medicine, agriculture, and animal husbandry,

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release of unmetabolized residues of antibiotics through faeces to environment, inadequate management of antibiotic disposal as well as poor hygiene and sanitation.[7] The threat of antimicrobial resistance poses a broader risk beyond the diminished efficacy in treatment of acute infection, as it undermines the protective benefits of antimicrobial prophylaxis, rendering patients vulnerable to potential infections.[8]

Emergence of resistant organisms can pose a great economic burden to the community as the conventional antibiotics becomes ineffective in the treatment of common infectious diseaases.[6,9] Extended hospitalization periods in surgical patients due to heightened risk of surgical site infection have contributed to escalated healthcare expenditure.[9]

The objective of this study is to determine the prevalence of bacterial pathogens in different clinical samples. It also aims to identify the most common pathogenic bacterial isolates causing infection and their antimicrobial resistance, and thereby contributing to the development of effective strategies for infection control and antimicrobial stewardship in this area of study in the district of Wayanad.

2. Aim

1. To study the prevalence of bacterial isolates in various clinical samples.
2. To determine the antimicrobial resistance among common pathogenic bacterial species isolated from different clinical samples.
3. To find out the incidence of infections in both genders.
4. To study the risk groups in different age categories.

3. Materials and Methods

3.1. Study sample and design

A seven-month retrospective study of different bacterial isolates from various clinical samples was conducted in a tertiary care and teaching hospital in Wayanad district, Kerala.

3.2. Sample collection, bacterial culture and identification

The study included clinical samples like urine, pus, sputum and blood samples. The study was conducted after getting ethical clearance from the institute. The specimens were collected by standard microbiological techniques.[10] Depending on the clinical sample, urine and sputum samples were inoculated into MacConkey agar, Blood agar and Chocolate agar, blood samples were platted into MacConkey agar and blood agar, and pus samples were inoculated into MacConkey agar, Blood agar, Chocolate agar and thioglycolate broth. Inoculated plates were incubated at 37ºC overnight and the colonies grown on the plates were identified using biochemical tests. All the identified pathogenic bacterial species were then subjected to antimicrobial susceptibility testing to find out the drug resistance.

3.3. Antimicrobial susceptibility testing

The antimicrobial susceptibility of the isolated colonies was done using Kirby- Bauer, disk diffusion method on Muller-Hinton agar[11] and the pattern of resistance and susceptibility was measured using standards of CLSI guidelines.[12]

3.4. Statistical analysis

The data were stored and processed using WHONET software, and statistically analysed using Microsoft Excel 2019 and SPSS 26.0 version. Categorical variables were analysed to derive descriptive statistics such as frequency counts and percentages. Bivariate comparisons using Chi-square logistic regression were employed to assess the association between variables. A p-value of less than 0.003 was considered statistically significant. The aims of the study were clearly analysed using the software the results are as follows.

4. Results

Out of 7694 clinical samples collected from patients with suspected infection, 2125 samples showed bacterial growth (27.61%). Data from 2125 clinical samples were studied, in which 661 were urine samples, 910 were pus samples, 225 were blood samples and 339 were sputum samples.(Figure 1) The predominant bacteria identified from urine sample was *E. coli*, among which the prevalence of extended spectrum beta lactamase (ESBL) producing *E.coli* was 40.61%, and the metallo-beta-lactamase (MBL) producers were 3.45%. *Staphylococcus aureus* was the predominant bacteria in pus sample, in which Methicillin resistant *Staphylococcus aureus* (MRSA) was found to be 3.92%. *Acinetobacter* was the most predominant bacteria isolated from blood samples, in which ESBL producing *Acinetobacter* was noted as 3.57%. *Klebsiella* species were the predominant bacteria in the sputum samples, in which ESBL producing *Klebsiella* was 16.79% and MBL producers were 3.82%. (Figures 2, 3, 4 and 5)

Out of the total 2125 samples studied, 1034 were females and 1091 were males. Urine samples studied were predominantly females with incidence of 60.51%. The pus, blood and sputum samples were predominantly males with incidence of 55.38%, 50.22%, 64.74% respectively.

Most of the patients identified with urinary tract infection were in the age group of 70-79 years (%). Soft tissue infection and respiratory tract infection were mostly noted in the age group of 60-69 years. Two age groups showed increase of incidence of blood stream infections. The age group identified were, children with day 1 age and upto 9 years (28%) and also in patients in the age group of 60-61 years (20.89%) (Figures 2, 3, 4 and 5)

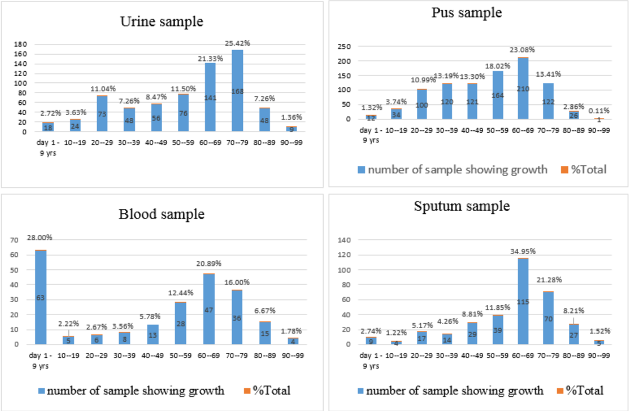

Fig. 1:

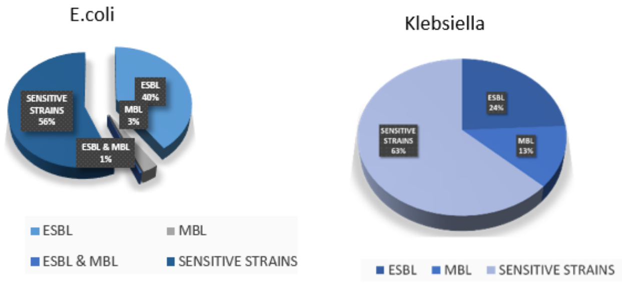

Fig. 2: Drug resistance in most prevalent uropathogens

5. Discussion

The emergence and spread of drug resistant pathogen is a major challenge faced by health sector. The successful management of bacterial infection require the proper selection of antimicrobials effective against the organism. The present study was conducted to find out the resistance profile of microorganism from different kinds of clinical specimens in a resource limited setting in Wayanad.

In the present study, the most notable findings that we made was Gram negative organisms which were more frequent than Gram positive bacteria. These findings were in accordance with those reported earlier.[13] In our study we noted that *staphylococcus aureus* is one of the most common bacterial pathogen isolated from skin and soft tissue infections. It is known that *S. aureus* is one of

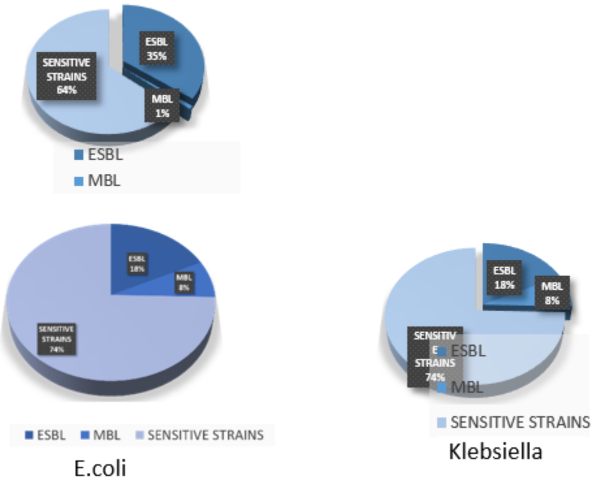

Fig. 3: Drug resistance in pathogens isolated from skin and soft tissue infection -*Staphylococcus*

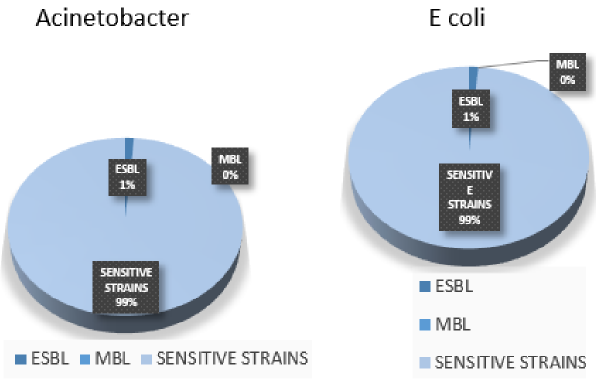

Fig. 4: Drug resistance in pathogens isolated from Blood samples

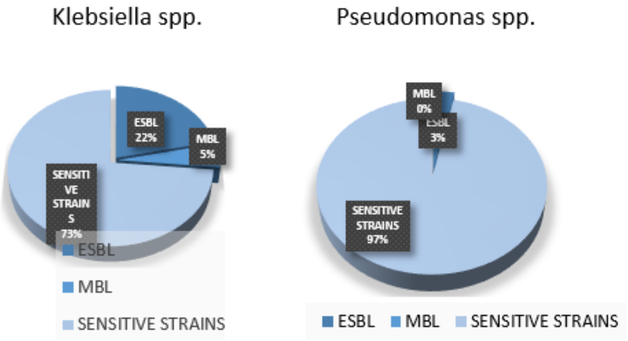

Fig. 5: Drug resistance in pathogens isolated from Sputum samples

the most common bacterial pathogens in most settings and it is a well-known multi-drug resistant pathogen causing different kinds of infections.[14] The overall burden of staphylococcal disease particularly that caused by methicillin resistant *S. aureus* is increasing in many countries in both healthcare and community settings.[10,15] The study identified infections in different age categories, urinary tract infection were mostly found in the age group of 70-79 years (%) this finding was similar with a study conducted by Theresa A Rowe.[16] Soft tissue infection and respiratory tract infection were mostly noted in the age group of 60-69 years. Many studies are showing significant difference in age categories. The present study identified two age categories with increase of incidence of blood stream infections. The age group identified were, children with day 1 of age and upto 9 years (28%) and also in elderly patients in the age group of 60-69 years (20.89%). Two extremes of age always carries risk of infections due to immuno suppression and hormonal variations. A study conducted by Noah Obeng Nkrumah showed significant blood culture positivity in infants as compared to children, adults and the elderly.[17] In addition, infections caused by ESBL-producing pathogens are problematic due to the co-existing of resistance determinants to other antimicrobial agents. Because of this reason they cause major and severe challenges to public health practitioners due to the reduced treatment options and failure of therapy with broad-spectrum antibiotics.[18] Our study reports mainly focuses on Antimicrobial resistance by clinical isolates and it was observed that most of the isolates are β-lactamase and metalo-betalactamase producers. These isolates may worsen the situation, leading to reduced therapeutic options and ultimately treatment failure.

6. Conclusion

There is paucity of data on AMR due to lack of surveillance system in the study area, regular monitoring of the etiologic agents and their antibiotic resistance profile should be evaluated for formulating a drug profile for treatment and better patient management. Moreover, actions to contain the impact of AMR should be evaluated and strengthened in the study area. The present study helped to identify the most predominant antibiotic resistant strains from each of the clinical samples in a resource limited setting like Wayanad. Similar studies would help in successfully formulating treatment strategies against bacterial infections, thereby reducing morbidity and mortality in patients.

7. Source of Funding

None.

8. Conflict of Interest

None.

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