A RETROSPECTIVE STUDY OF COMMON BACTERIAL ISOLATES AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERN FROM SKIN INFECTIONS IN A TERTIARY CARE HOSPITAL IN GOA

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ABSTRACT

BACKGROUND
The aim of this study is to analyse the pattern of common bacterial isolates and to study the antimicrobial susceptibility pattern of these isolates from skin infections.

MATERIALS AND METHODS
This observational study was conducted using the skin swab culture and sensitivity reports collected retrospectively from the records maintained in the Department of Dermatology, Venereology and Leprosy over a period of one year from January 2015 to December 2015 in our hospital.

RESULTS
During the study, 361 non-repeat culture positive reports were analysed. Staphylococcus aureus (55.1%) was the most common organism isolated followed by Pseudomonas aeruginosa (11.9%). Other isolates include the species of CONS, Beta haemolytic Streptococcus, Escherichia coli, Acinetobacter, Enterobacter, Klebsiella, Proteus and Serratia. High sensitivity rates were observed against Linezolid (98.4%) in case of gram positive cocci and against Meropenem (80.1%) for gram negative bacilli in our study.

CONCLUSION
In order to prevent resistance against antibiotics, antibiotic stewardship program should be an integral part of every hospital setting.

KEYWORDS
Skin Swab Culture, Skin Infections, Antibiotic Susceptibility.


BACKGROUND
In recent years, skin infections particularly due to multidrug resistant pathogens are increasingly being encountered in a hospital setting.⁴ Skin infections contribute to increase in the cost of medical care, longer hospital stay, increase in morbidity and have a significant role in the development of antimicrobial resistance.⁶

The superficial skin infections commonly encountered are of bacterial origin and the examples include folliculitis, cellulitis, carbuncle, furuncle, impetigo and erysipelas.⁶ These infections are frequently treated with either topical or oral antibiotics.⁶⁴ The commonly prescribed antibiotics are rendered resistant due to emergence of Methicillin Resistant and Vancomycin Resistant Staphylococcus aureus as well as ESBL producing and multi-drug resistant gram negative organisms in the community.

It is crucial to monitor the changing trends in bacteria causing skin infections and their antimicrobial susceptibility pattern to provide suitable antimicrobial therapy for curbing infection, reducing morbidity and ameliorate the quality of life.⁵

The present study was undertaken to analyse the pattern of bacterial pathogens isolated from patients attending the O.P.D. as well as admitted to the ward and their antimicrobial susceptibility from skin swab culture reports in a tertiary care hospital.

MATERIALS AND METHODS
This retrospective study was conducted in the Department of Dermatology, Venereology and Leprosy. The records of 361 non-repeat culture positive samples were retrieved from the Department of Microbiology of this Institution over a period of one year from January 2015 to December 2015.

Inclusion Criteria
Single and mixed (only two organisms) growth showing Gram positive as well as Gram negative organisms were included in this study.

Exclusion Criteria
Mixed growth showing three or more organisms were excluded from the study.

All the bacterial isolates were identified and studied according to the standard procedures followed in the Microbiology Laboratory.⁵
Antimicrobial susceptibility testing was performed according to the Clinical and Laboratory Standards Institute (CLSI) guidelines using the Kirby-Bauer disk diffusion technique. The antibiotics evaluated were Linezolid (30 μg), Trimethoprim-Sulfamethoxazole (1.25/23.75 μg), Clindamycin (2 μg), Azithromycin (15 μg), Ampicillin (10 μg), Levofloxacin (5 μg) and Vancomycin (30 μg) for gram positive cocci, whereas Gentamicin (10 μg), Amikacin (30 μg), Piperacillin/Tazobactam (100/10 μg), Meropenem (10 μg), Ceftazidime (30 μg) and Cefepime (30 μg) for gram negative bacilli. The data was analysed using SPSS software version 22.0 and the results were obtained as percentages.

RESULTS
Out of the 361 samples yielding bacteria on culture, 85.6% i.e. 309 samples had monomicrobial etiology, while in 52 cases (14.4%), more than one organism was obtained on culture. The most frequent bacterial combination in polymicrobial etiology cases was one gram positive coccus and one gram negative bacilli.

As depicted in [Figure 1] gram positive cocci accounted for 70.1%, while Gram Negative Bacilli (GNB) accounted for 29.9% of the total. The predominant bacterial pathogen isolated was Staphylococcus aureus (55.12%) followed by Pseudomonas aeruginosa (11.9%).

The sensitivity of Staphylococcus aureus was 98.4% for Linezolid, 82.1% for Clindamycin, 45.8% for Trimethoprim/Sulfamethoxazole and 25% for Azithromycin [Table 1].

The overall sensitivity of the GNB was maximum against Meropenem (80.1%) followed by Piperacillin/Tazobactam (68.5%), whereas a low level of sensitivity was noted against the cephalosporins i.e. 36.4% for Ceftazidime and 41% for Cefepime [Table 2].

![Number of bacterial isolates](image)

**Figure 1: Bacterial Pathogens Isolated**

<table>
<thead>
<tr>
<th>Bacterial Isolate</th>
<th>Linezolid</th>
<th>Clindamycin</th>
<th>Azithromycin</th>
<th>Trimethoprim/Sulfamethoxazole</th>
<th>Ampicillin</th>
<th>Vancomycin</th>
<th>Levofloxacin</th>
</tr>
</thead>
<tbody>
<tr>
<td>St. aureus*</td>
<td>98.4</td>
<td>82.1</td>
<td>25</td>
<td>45.8</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>CONS**</td>
<td>96.8</td>
<td>76.7</td>
<td>30</td>
<td>40.7</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Beta Haemolytic Streptococci</td>
<td>100</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>64.3</td>
<td>100</td>
</tr>
</tbody>
</table>

*CONS = Coagulase Negative Staphylococcus

*Staphylococcus aureus * ** Coagulase Negative Staphylococcus.
**Table 2. Antibiotic Susceptibility Pattern of Gram Negative Bacilli**

<table>
<thead>
<tr>
<th>Bacterial Isolate</th>
<th>Amikacin</th>
<th>Gentamicin</th>
<th>Levofloxacin</th>
<th>Ceftazidime</th>
<th>Cefepime</th>
<th>Piperacillin/Tazobactam</th>
<th>Meropenem</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pseudomonas aeruginosa</td>
<td>50.1</td>
<td>52.3</td>
<td>57</td>
<td>28.1</td>
<td>30.5</td>
<td>60.2</td>
<td>78.1</td>
</tr>
<tr>
<td>E. coli*</td>
<td>72.8</td>
<td>70.4</td>
<td>68.2</td>
<td>50.2</td>
<td>50.3</td>
<td>80.4</td>
<td>90.2</td>
</tr>
<tr>
<td>Acinetobacter species</td>
<td>40.6</td>
<td>42.4</td>
<td>37</td>
<td>22</td>
<td>22.5</td>
<td>38</td>
<td>47</td>
</tr>
<tr>
<td>Enterobacter species</td>
<td>73.7</td>
<td>73.9</td>
<td>66.1</td>
<td>32.9</td>
<td>48.4</td>
<td>82.1</td>
<td>91.3</td>
</tr>
<tr>
<td>Others**</td>
<td>71.9</td>
<td>72</td>
<td>69.5</td>
<td>48.8</td>
<td>53.3</td>
<td>81.6</td>
<td>93.7</td>
</tr>
<tr>
<td>Total</td>
<td>61.8</td>
<td>62.2</td>
<td>59.6</td>
<td>36.4</td>
<td>41</td>
<td>68.5</td>
<td>80.1</td>
</tr>
</tbody>
</table>

‘Escherichia coli,’ ‘others include species of Klebsiella, Proteus and Serratia.’

**REFERENCES**


