



**ORIGINAL RESEARCH PAPER**

**Microbiology**

**A COMPARATIVE STUDY OF DRUG RESISTANCE PATTERNS OF ENTEROBACTERIACEAE AND NFGNBS' IN A TERTIARY CARE HOSPITAL .**

**KEY WORDS:** Drug-Resistance, Enterobacteriaceae , NFGNBs'.

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**ABSTRACT**

**BACKGROUND :** The worldwide emergence of community and hospital acquired drug resistance poses a serious challenge to the clinicians and microbiologists alike. Augmented antibiotic stewardship and effective infection control measures are needed to check the menace of multi-drug-resistance .

**OBJECTIVE :** The aim of the present study is to analyze the patterns of drug resistance by Enterobacteriaceae and non-fermenting Gram Negative Bacilli in a hospital setting and find out the similarities and contrasting features about the same.

**MATERIALS AND METHODS :** A total of 268 clinical isolates from a variety of consecutive clinical specimens in a continuous period of time were recovered. Isolates were identified using standard biochemical tests. Antibiotic susceptibility tests were performed by Kirby Bauer method and antibiograms were used as per CLSI (2017) guidelines.

**RESULTS :** Out of a total of 268 isolates grown in culture , 58.6% (n=157) belonged to family Enterobacteriaceae and 24.3% (n=65) were NFGNB. 17.2% (n=46) were other pathogenic bacteria.

**CONCLUSION :** The members of Enterobacteriaceae family of bacteria and non fermenting Gram Negative Bacilli possess different mechanisms of resistance to antibiotics which necessitate continuous surveillance , strict antibiotic stewardship and prudent therapeutic management .

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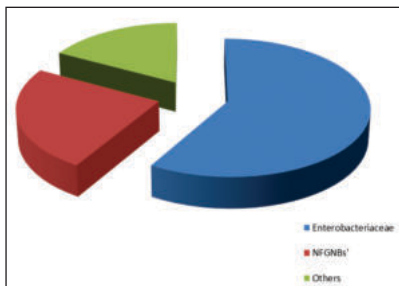
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**MATERIALS AND METHODS :**

A total of 268 clinical isolates from a variety of consecutive clinical specimens over a continuous period of time were recovered . Isolates were identified using standard biochemical techniques. Antibiotic susceptibility tests were performed by Kirby- Bauer method and antibiograms were used as per CLSI (2017) guidelines.

**Observations :**

Out of a total of 268 isolates grown in culture, 58.6 % belonged to family Enterobacteriaceae and 24.3 % (n=65) were NFGNBs'. 17.2 % (n=46) were other pathogenic bacteria. Highest rate of resistance was against cotrimoxazole followed by penicillin group, flourquinolones and third generation cephalosporins Least resistance was shown to Ertepenem.



**Fig.1**

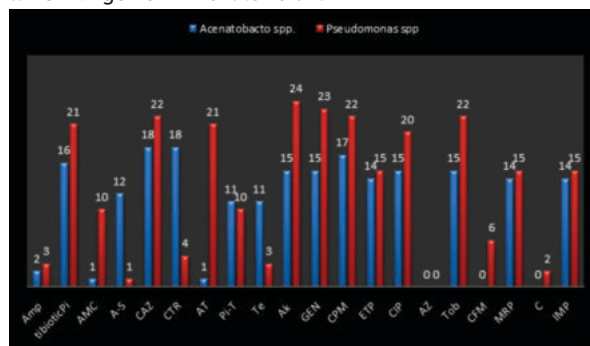
**Antibiotic Resistance Pattern of NFGNBs'**

Study shows that top two non-fermenters which were isolated were Acinetobacter baumannii and Pseudomonas aeruginosa which were multi-drug -resistant to cephalosporins, flourquinolones but were sensitive to Carbapenems.

Most of the NFGNBs' were resistant to penicillins, flourquinolones and cephalosporins, these organisms were least resistant to carbapenams.

Multiple resistance mechanisms are found in these organism that have contributed to the emergence of multidrug and pan drug resistance, causing a serious concern for the microbiologists as well as clinicians.

Non-fementers account for 15% of all bacterial isolates from clinical microbiolgy laboratory. Published studies from various sectors states different rates of isolation of NFGNBs' which range from 2.18% to 45.9%.



**Fig.2**

**Antibiotic Resistance Pattern of Enterobacteriaceae**

58.58% bacteria belonged to family Enterobacteriaceae. E.coli was the most prevalent organism isolated .54.8% of organisms were E.S.B.L. producers. 16.6 % were Carbapenamase producers.

Drug resistance is higher in members of family Enterobacteriaceae as compared to NFGNBs'.

Of the total organisms E.coli was found to be most drug resistant followed by Klebsiella. Which is in concordance with the results of a previous study.

These bacteria are showing alarming trends of resistance towards Ampicillin ,piperacillin, Flouroquinolones and even Amoxycillin-clavulanate and Ampicillin-Sulbactam combination.

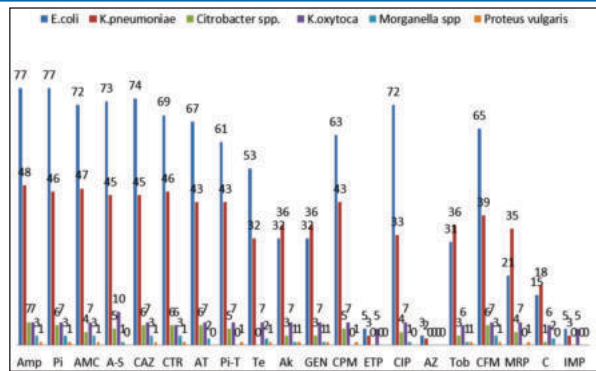


Fig.3

**CONCLUSION:**

There is need to take timely measures to curtail drug resistance in Enterobacteriaceae along with NFGNBs' in order to :-

1. Effectively treat patients,
2. Check the increasing trend of antimicrobial resistance,
3. And formulate new treatment alternatives.

Understanding the resistance mechanism of above two categories of bacteria is necessary to cope up with drug resistant infections.

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