STUDY OF PHENOTYPIC AND GENOTYPIC CHARACTERISATION OF KLEBSIELLA SPECIES ISOLATED FROM WOUND INFECTION WITH SPECIAL REFERENCE TO CARBAPENEM RESISTANCE

INTRODUCTION

Wound infection is one of the most important cause of health care related problem because the resulting wound is being colonised by pathogenic microorganism(1) Infection is major cause of morbidity and mortality in hospitalized patients(2) Gram positive bacteria which was the predominant organism in wound infection is being replaced by gram negative bacteria in recent years(3)A nd *Klebsiella species is showing rising trend in wound infection among gram negative bacteria* (4). Its prevalence in burns is 34.40%(2),in surgical site infecion 18.08% and in diabetic foot ulcer it is 8%(3)

AIM & OBJECTIVES:

AIM: To find the prevalence of *Klebsiella species* from wound infection and to find its molecular characterisation with special reference to carbapenem resistance

OBJECTIVE

- To isolate, characterize and speciate Klebsiella from wound infection.
- To identify the antibiotic sensitivity pattern of the klebsiella species isolated.
- To detect the Exetended spectrum beta lactamase(ESBL), Amp C and carbapenemase production among the identified Klebsiella species.
- To do molecular characterisation of the resistant Klebsiella isolates.

MATERIALS AND METHODS

The present study was conducted in the Department of Microbiology, Kilpauk medical college and hospital, Chennai from JUNE 2017 TO MAY 2018. 800 wound samples was processed by standard microbiolobical techniques to speciate Klebsiella species .Antimicrobial susceptibility pattern was identified by Kirby bauer disk diffusion test.ESBL,AMPC and Carbapenemase lactamases was identified by both screening method and confirmatory test.Molecular characterization of carbapenemase resistant Klebsiella species was done by PCR.

RESULTS:

Out of 800 wound samples ,113 Klebsiella species was isolated.103 was *Klebsiella pneumoniae* and 10 was *Klebsiella oxytoca.* out of 103 *Klebsiella pneumoniae* isolated from wound infection, 52 (46.01%) was ESBL producer, 23(20.35%) AMPC and 9(7.96%) was carbapenemase producers.Molecular study showed all 9 strains to carry blaNDM. Out of these 9MBL, 4 strains showed co –existence of ESBL and they carried all 3 gene(blaSHV,blaTEM,bla CTX-M) and another 4 strain carried AMPC lactamases all carrying the AMPC gene.

CONCLUSION

This study shows increased prevalence of Klebsiella pneumoniae in wound infection carrying multi drug resistant strain leading to multi drug resistant strain.This could be prevantad by by performing screening and confirmatory test routinely in microbiological laboratories, and also by following simple measures like hand washing and strict adherence to hospital antibiotic policy the occurrence and spread

of resistant strains can be prevented in wound infection . This will enable in better wound healing, there by preventing mortality and morbidity.

KEYWORDS:Klebsiellapneumoniae,ESBL,AMPC.,Carbapenemase,MBL,blaNDM,blaSHV,blaTEM and blaCTX-M

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