

DETECTION OF MULTIDRUG RESISTANCE IN *KLEBSIELLA* SPECIES BY PHENOTYPIC AND GENOTYPIC METHODS IN A TERTIARY CARE HOSPITAL

ABSTRACT

BACKGROUND

Infections caused by multidrug-resistant microorganisms have become a major threat for the human health. Especially nosocomial infections when hospitalized give problems with antibiotics susceptibility, because the hospital environment gives a constant selective pressure that favours resistance. Nosocomial infections are often caused by multidrug-resistant Gram-negative microorganisms.

One of these Gram-negative bacteria is *Klebsiella* species, which is naturally found in the gut microbiota of both humans and animals. *Klebsiella* species is a Gram negative opportunistic nosocomial pathogen and is known to cause community acquired infections. *Klebsiella* is known to produce bacterial pneumonia, urinary tract infection, wound infections, blood stream infections and infections in the intensive care unit. This study is aimed to know the resistant pattern of multi drug resistant *Klebsiella* species in various clinical samples received in microbiological laboratory in Rajiv Gandhi government general hospital.

AIMS:

To detect the Multidrug resistant *Klebsiella* species among various clinical specimens and to determine its resistance pattern by phenotypic and genotypic methods.

MATERIALS AND METHODS:

A total of 200 clinically significant, consecutive, non-duplicate isolates of *Klebsiella* spp. were included in this study. The isolates were tested by bacteriological culture, biochemical identification and antibiotic susceptibility testing. ESBL, AmpC beta-lactamase (AmpC), Metallo-beta-lactamase (MBL), and *Klebsiella pneumoniae* carbapenemase (KPC) producers were screened and confirmed by phenotypic methods based on guidelines given in CLSI 2016 and EUCAST 2016. Molecular characterisation was analysed for bla KPC gene by RT-PCR.

RESULTS

200 Multidrug resistant *Klebsiella* strains were isolated mainly from Intensive care unit (29%) followed by Orthopaedic ward (16.5%). Among these 200 Multidrug resistant *Klebsiella* isolates, *Klebsiella pneumoniae subsp aerogenes* (48%) was the most common species isolated followed by *Klebsiella oxytoca* (46%) and *Klebsiella pneumonia subsp pneumoniae* (6%). Among these 200 isolates 119 (59.5%) showed ESBL production, 16 (8%) showed Metallo-beta-lactamases, 13 (6.5%) showed AmpC production and 12 (6%) showed KPC production and 25 (12.5%) were enzyme co-producers. All resistance mechanisms were most common in *Klebsiella pneumoniae* and Metallo-beta-lactamase production were more common in *Klebsiella oxytoca*.

CONCLUSION

In view of controlling these resistant strains of *Klebsiella* isolates, early and simultaneous detection of these resistance patterns (ESBL, AmpC, MBL and KPC) and strict adherence to antibiotic policies by curtailing injudicious use of antibiotics and implementation of antimicrobial Stewardship would prevent the emergence and the cross transmission of multidrug resistant organisms.