

MECHANISMS OF RESISTANCE AND CLONALITY AMONG GRAM NEGATIVE BACTERIA ISOLATED FROM RESPIRATORY SECRETIONS OF PATIENTS ADMITTED TO AN INTENSIVE CARE UNIT

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Respiratory infections particularly ventilator associated infections are one of the common infections that can occur in patients admitted to intensive care units (ICUs). The organisms responsible are likely to derive from the surrounding environment. Due to the high antibiotic pressure, most organisms in the ICUs are likely to be resistant to commonly used drugs. Additionally, there is high possibility of within unit spread of such organisms in developing countries due to the difficulty in implementing infection control methods. Therefore, this study was conducted with the objective of characterizing the organisms derived from respiratory tract secretions of patients admitted to an ICU and to identify their clonality.

Isolates obtained from respiratory specimen of patients being admitted to the given study unit were identified using routine biochemical tests following standard methods. Antibiotic sensitivity testing was performed and interpreted using the Clinical and Laboratory Standards Institute (CLSI) guidelines for 2013. Genetic relatedness of the isolates was assessed by using Random Amplified Polymorphic DNA (RAPD) analysis.

Seventy Gram negative isolates collected over a period of 6 months was used in the study. Of them seven isolates (10%) were *Escherichia coli*, 14 were *Klebsiella pneumoniae* (20%), 15 were *Pseudomonas aeruginosa* (21%), 30 were *Acinetobacter* spp. (43%). The rate of extended spectrum β lactamase production was 100% among the *E.coli* and 93% for *K.pneumoniae*. The carbapenem non-susceptibility rates for *E.coli*, *K.pneumoniae*, *Pseudomonas aeruginosa* and *Acinetobacter* spp. were 29%, 43%, 20% and 100% respectively. Of the carbapenem non-susceptible isolates 50% of the *E.coli*, 100% of *K.pneumoniae*, none of the pseudomonads and 67% of the acinetobacters were found to produce carbapenemases. The multi drug resistance rates defined as being resistant to three or more classes of antibiotics, were 100% for *E.coli*, *K.pneumoniae* and *Acinetobacter* spp. while it was 13% for the pseudomonads. Both *K.pneumoniae* and *Acinetobacter* spp. had a single predominant cluster comprising of 78.6% and 73.3% of the isolates respectively.

These findings highlight a high prevalence of antibiotic resistance contributed by mostly single genotypes in the given study unit highlighting the importance of establishing strict infection control regimes.