Profile of genes coding for Carbapenemases among resistant acinetobacter species from a tertiary care centre: A laboratory based study

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Background: Acinetobacter species are being increasingly reported to be associated with infections among seriously ill individuals. These infections are difficult to treat due presence of genes coding for resistance to most of the available antibiotics. The study was conducted to identify the presence of commonly described genes coding for carbapenemases among the isolates.

Methods & Materials: The study was a cross-sectional laboratory based observational study from a tertiary care hospital. 89 consecutive (single isolate per patient) isolates of Acinetobacter species were included. Study period: isolates collected during 2011-2012 from clinical samples and molecular studies done in 2013. Organisms identified as Acinetobacter baumanii complex(Acb complex) using biochemical tests were included in the study. Antibiotic susceptibility test was done by Kirby Bauer Disc diffusion. Resistance to carbapenems was confirmed by Microbroth dilution. PCR was done to identify the presence of the following genes using published primers, Oxa(23like,24like,51like,NDM,VIM and IMP). PCR was done to identify if there was any clonal similarity among these isolates.

Results: The isolates demonstrated resistance to nearly all antibiotics tested except for Netilmicin for which 11%(10/89) were susceptible.

The samples from which the Acb complex were isolated: Respiratory secretions(n = 60,67%), pus samples(n = 25,28%), urine (n = 10,11%) blood 2 and other fluids 3 isolates. 53,(60%) of the samples were from patients admitted to the intensive care unit.

The common mechanisms of Resistance for carbapenemases were found to belong to the OXA carbapenemases(23) in 92% of isolates,followed by VIM(65%). Around 82% also had AmpC beta-lactamases.NDM detected in 12.

ERIC PCR: Isolates showing >90% of similarity were grouped into 4 different clusters, genetic heterogeneity was noticed among each cluster.

Conclusion: Acinetobacter species though previously thought to be contaminants have now gained notoriety as multidrug resistant, hospital acquired pathogens due to acquisition of a number of resistance genes. Genes coding for Carbapenem resistance identified commonly in our study were the OXA 23like and VIM.NDM was also detected. Considerable heterogeneity was noted by ERIC PCR.

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