Molecular analysis of multidrug resistance in the clinical isolates of *Pseudomonas aeruginosa*

ABSTRACT

Pseudomonas aeruginosa, a Gram-negative aerobic bacterium one of the leading pathogens of nosocomial infections around the world, has been one of the most difficult to treat. As a secondary pathogen, *Pseudomonas aeruginosa* produces several virulence-associated factors and can cause a variety of disease manifestations. *Pseudomonas aeruginosa* remains responsible for a significant number of bacteraemias, ranking third, after *Escherichia coli* and *Klebsiella* species among Gram negative bacteria isolated during nosocomial bloodstream infections, and seventh among all pathogens. In addition to bacteraemia and endocarditis, infection of the urinary tract, respiratory tract, central nervous system, ear, eye, bone, joints and skin are most often reported. *Pseudomonas* species is ranked among the top 10 causes of bacteraemias in hospitals. Despite the recent advances in antimicrobial therapy, *Pseudomonas aeruginosa* infections cause high morbidity and mortality, especially among immunocompromised patients. The emergence of multidrug-resistant (MDR) and extended-spectrum β-lactamase (ESBL) producing *Pseudomonas aeruginosa* poses a serious antibiotic management problem as resistance genes are easily transferred from one organism to another. The current study investigated the prevalence of infection by *Pseudomonas aeruginosa* in three hospitals located in geographically different areas. The 26 clinical isolates of *Pseudomonas aeruginosa* collected from microbiology laboratory, from these hospitals were initially identified by biochemical method. The antibiotic sensitivity test showed that most of the clinical isolates were resistant to more than four antibiotics. Some of the isolates showed intermediary reactions which may develop into resistant strain in due course. Since *Pseudomonas aeruginosa* has intrinsic resistance to several antibiotics and a capability to

acquire resistance during antibiotic therapy, the present study also investigated the presence of ESBL genes such as, TEM, SHV and CTX. The results of ESBL showed that the presence of multiple ESBL genes in all the isolates, thus substantiating the results of antibiotic sensitivity studies. In order to understand the genetic variation among the 26 isolates, ERIC-PCR and RAPD analysis were also carried out. The genetic analysis showed wide variation among the isolated within and among the hospitals. The study found that, the ERIC-PCR is highly discriminatory compared to RAPD-PCR has revealed by the cluster analysis through dendrogram. Variations present among strains from the same hospital and also geographical variations present among the three different hospitals, despite a limited geographic distance and it may change over time according to antibiotic policies or the spread of outbreak strains. Therefore, the monitoring of the resistance rates and the patterns of multi-resistance is required to choose empirical antimicrobial regimens according to local epidemiological factors.