Detection of virulence factors and β lactamase encoding genes among the clinical isolates of *Pseudomonas aeruginosa.*

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Abstract

Background: Pseudomonas aeruginosa has emerged as a significant opportunistic bacterial pathogen that causes nosocomial infections in healthcare settings resulting in treatment failure throughout the world. This study was carried out to compare the relatedness between virulence characteristics and β-lactamase encoding genes producing Pseudomonas aeruginosa.

Methods: A total of 120 P. aeruginosa isolates were obtained from both paediatric and adult patients of Selayang Hospital, Kuala Lumpur, Malaysia. Phenotypic methods were used to detect various virulence factors (Phospholipase, Hemolysin, Gelatinase, DNAse, and Biofilm). All the isolates were evaluated for production of extended spectrum beta-lactamase (ESBL) as well as metallo β-lactamase (MBL) by Double-disk synergy test (DDST) and E-test while AmpC β-lactamase production was detected by disk antagonism test.

Results: In this study, 120 Pseudomonas aeruginosa isolates (20 each from blood, wounds, respiratory secretions, stools, urine, and sputum samples) were studied. Among Pseudomonas aeruginosa isolates, the distribution of virulence factors was positive for hemolysin (48.33%), DNAse (43.33%), phospholipase (40.83%), gelatinase (31.66%) production and biofilm formation (34%) respectively. The prevalence of multiple β-lactamase in P. aeruginosa showed 19.16% ESBL, 7.5% MBL and 10.83% AmpC production respectively.

Conclusion: A regular surveillance is required to reduce public health hazard and the spread of virulence factors and β-lactamase genes among clinical isolates of Pseudomonas aeruginosa

Keywords: *Pseudomonas aeruginosa*; ESBL; MBL; Virulence factors