Phenotypic and genotypic characterization of Pseudomonas aeruginosa isolates from Egyptian hospitals

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Abstract

Pseudomonas aeruginosa (P. aeruginosa) is an opportunistic pathogen and a leading cause of hospitalacquired infections. Characterization of the isolates from different infection sites might help to control infections caused by the pathogen. The aim of the present work is to characterize P. aeruginosa isolates recovered from different clinical specimens at two hospitals in Cairo with regard to their antibiogram, genotypes and virulence factors. The highest antimicrobial resistance pattern was exhibited by isolates from sputum. Resistance rate recorded for sputum samples to different in- use antibiotics was 80, 80-100, 36, 54 and 54% for Penicillins, Cephems, Carbapenems, Aminoglycosides and Fluoroquinolones, respectively. Phenotypic detection of virulence factors in P. aeruginosa isolates included detection of protease, lecithinase, DNase, hemolysin and pyocyanin revealed that, each isolate had at least one virulence factor. Protease and lecithinase were the most commonly detected, where 68 and 66% of the isolates showed positive protease and lecithinase activities respectively. Random amplified polymorphic DNA (RAPD) genotyping using 2 random primers revealed 22 and 14 different genetic profiles. Phylogenetic trees based on genetic distances showed 3 clusters with obvious similarity between some isolates, indicating common sources of infection. No association could be found between clustering pattern of the isolates, their antibiogram and virulence.

Key words: Pseudomonas aeruginosa, antibiogram, genotypes, random amplified polymorphic DNApolymerase chain reaction (RAPD-PCR).

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