Title: A preliminary epidemiological analysis by phenotypic and genotypic characterization of *Pseudomonas aeruginosa* strains isolated from nosocomial infections

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Abstract:

Pseudomonas aeruginosa (Pa) commonly causes nosocomial infections and the emergence of multidrug-resistance strains (MDR) is worrying. Some virulence factors can favor the pathogen's infection and cross-infection, such as the production of bacteriocins, of Extendspectrum beta-lactamase (ESBL), and the abilities to adapt to a variety environments and to colonize wide range of hosts. Objectives: The purposes of this study were to type seventy Pseudomonas aeruginosa isolated from 50 patients of three public hospitals of Maceió, AL by antibiotic susceptibility patterns, bacteriocin production profile and genotypic diversity by random amplified polymorphic DNA (RAPD-PCR). These techniques were used to preliminary epidemiological analysis. In addition, was detected the frequency of ESBL production in isolates resistant to carbapenems and cephalosporins. Methodology: Seventy Pa isolates were biochemically identified. The antibiotic susceptibility to 17 antibiotics was determine by Kirby-Bauer test (CLSI) and the bacteriocin production was tested by antagonism technique against 21 indicator strains. The genotyping was performed with the RAPD technique using the arbitrary primer OPA-02. The Simpson's index of diversity was used to test the discriminatory index of each technique. ESBL production was detected by phenotypic method of approach-disks. Results: There was a high frequency of strains resistant to cephalexin (100%) and fluoroquinolones (56,86%). All isolates showed sensitivity to polymyxin. Only 9 (12,85%) strains showed resistance to carbapenems and 22 strains (31,42%) were classified as MDR and resistant to 4 or more antibiotic class. Among the 18 strains resistant to carbapenems and cephalosporins, 11 (61,1%) produced ESBL. Among the 70 isolates, there were 49 bacteriocin production profiles and 33 different genotypes. The discriminatory index of genotypic method (0,97) was higher than bacteriocin typing (0,93). Epidemiological unrelated individuals share AP-PCR similar types, although these genotypes showed distinct phenotypic profiles. Conclusion: There is a high frequency of MDR and ESBL producing strains among nosocomial Pa. There were high genetic and phenotypic diversity among clinical isolates. The association of the phenotypic and genotypic typing methods showed that although there were self infection cases, there were not cross-infection cases in these hospitals.

Key words: antibiotic resistance – nosocomial infections – bacteriocin - ESBL – *Pseudomonas aeruginosa*

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