



Prevalence of Penicillin Resistance Determinants in Streptococcus pneumoniae Strains Isolated from ICU Ptients by Real-Time PCR

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Background & Objectives: The appearance and dissemination of penicillin resistant Streptococcus pneumoniae strains has caused increasing concern worldwide. In order to provide data for antibiotic therapy and resistance control, routine monitoring of antibiotic resistance and corresponding genes is necessary. The aim of this study was to assess the prevalence of pbps gene in penicillin resistance in *S. pneumoniae* strains isolated from Intensive Care Unit (ICU).

Methods: This cross – sectional study was carried out on 50 streptococcal cultures isolated from patients who admitted to ICU of southwest of Iran. At first, S. pneumoniae strains were confirmed based on presence of lytA gene by Real-time PCR Methods. After that, Antibiotic resistance was performed according to CLSI guidelines and a minimum inhibitory concentration (MIC) of penicillin was determined by the E-test methods. Finally, presences of altered pbp1a, pbp2b and pbp2x genes were evaluated by Real-time PCR.

Results: All 50 strains was confirmed as *S. pneumoniae* by presence of lytA gene. Drug resistance of the isolates was 56% to erythromycin and ampicillin, 48%, to trimethoprim-sulfamethoxazole and clarithromycin, 44%, 40%, 16%, 10% and 4% to zithromycin, penicillin, nalidixic acid, tetracycline and levofloxacin. All isolates were sensitive to chloramphenicol, amikacin, streptomycin and gentamicin. MIC of penicillin resistant strains were $\geq 10\mu$ g/ml. Prevalence of altered pbp1a, pbp2b and pbp2x were 20% (6/50), 0% (0/50) and 3.3% (1/50) respectively.

Conclusion: Results showed that resistance to penicillin is mainly due to an increase in the proportion of isolates carrying the altered pbp1a gene. Regarding to low frequency of pbps resistance genes, monitoring of other kinds of mechanisms of penicillin resistance is recommended.

Keywords: S. pneumoniae; Penicillin Binding Protein; ICU

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