

Analysis of Non-Coding Genome in Streptococcus pneumoniae for Molecular Epidemiology Typing

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Abstract : Streptococcus pneumoniae is the causative agent of pneumonias and meningitids throught all the world. Having high genetic diversity, this microorganism can cause different clinical forms of pneumococcal infections and microbiologically it is really difficult diagnosed by routine methods. Also, epidemiological surveillance requires more developed methods of molecular typing because the recent method of serotyping doesn't allow to distinguish invasive and non-invasive isolates properly. Non-coding genome of bacteria seems to be the interesting source for seeking of highly distinguishable markers to discriminate the subspecies of such a variable bacteria as Streptococcus pneumoniae. Technically, we proposed scheme of discrimination of S.pneumoniae strains with amplification of non-coding region (SP_1932) with the following restriction with 2 types of enzymes of Alu1 and Mn1. Aim: This research aimed to compare different methods of typing and their application for molecular epidemiology purposes. Methods: we analyzed population of 100 strains of S.pneumoniae isolated from different patients by different molecular epidemiology methods such as pulse-field gel electrophoresis (PFGE), restriction polymorphism analysis (RFLP) and multilocus sequence typing (MLST), and all of them were compared with classic typing method as serotyping. The discriminative power was estimated with Simpson Index (SI). Results: We revealed that the most discriminative typing method is RFLP (SI=0,97, there were distinguished 42 genotypes). PFGE was slightly less discriminative (SI=0,95, we identified 35 genotypes). MLST is still the best reference method (SI=1.0). Classic method of serotyping showed quite weak discriminative power (SI=0,93, 24 genotypes). In addition, sensivity of RFLP was 100%, specificity was 97,09%. Conclusion: the most appropriate method for routine epidemiology surveillance is RFLP with non-coding region of Streptococcus pneumoniae, then PFGE, though in some cases these results should be obligatory confirmed by MLST.

Keywords : molecular epidemiology typing, non-coding genome, Streptococcus pneumoniae, MLST

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