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Molecular biology, including diagnostics: Molecular typing

Using of multilocus sequence typing of *S. pneumoniae* strains gained in aged patients in far east of Russia

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Background: despite of the gained results in diagnostic and treatment, *Streptococcus pneumoniae* remains the important reason of lower respiratory tract morbidity in aged patients of our region. Unfortunately, epidemiological characteristics of pneumococcal isolates are not well-documented and molecular sequence typing (MLST) could be valuable instrument to define epidemiologically significant isolates. As there were no any attempts of multilocus sequence typing in our region, we conducted this method in strains of *S.pneumoniae*, isolated in aged patients. AIM of our project was to perform MLST in a group of aged patients with pneumococcal community-acquired pneumoniae (50 patients) and in carriers of *S.pneumoniae* of the same age (30 patients). Materials and methods: mlst was conducted with housekeeping genes on standard method on recommendations of MC Enright (1998) et al. with previous study of antimicrobial agents resistance and serotyping. Results: Isolates from patients ( 50 strains) included 24 serotypes ( 26 of non-typable) and 22 sequence types ( ST) according to MLST of which 7 were novel, 8 were of Taiwanese clones (TW-28,19,26) of 19F serotype, 3 were of R6, EU38, SP95. The most prevalent serotype of 6B included 3 newly identified STs. In 30 strains from carriers 17 sequence types, and here are prevailing the strains with similarity to TW50-9V, TW82-14. In strains from patients there were isolated 18% resistant to erythromycin, 16% tetracycline, 4 % chloramphenicol. In strains from carriers there were isolated 16,6% resistant to erythromycin, 10% to tetracycline. Conclusion: multilocus sequence typing allows us to suggest the epidemiological significance of Taiwanese isolates of *S.pneumoniae* in our region.