

POPULATION GENETIC STRUCTURE, SEROTYPE DISTRIBUTION AND ANTIBIOTIC RESISTANCE OF STREPTOCOCCUS PNEUMONIAE ISOLATES COLLECTED IN MOSCOW IN 2011-2015 (ID 446)

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Abstract

Background

The invasive pneumococcal disease remains one of the leading causes of morbidity and mortality worldwide. In this study, we investigated high-resolution population genetic structure of *S. pneumoniae* isolates in Moscow, using the genomic definition of pneumococcal lineages (Global Pneumococcal Sequence Clusters (GPSCs)), serotypes and antimicrobial resistance patterns.

Methods

Eighty-seven pneumococcal isolates were recovered from cerebrospinal fluid and nasopharyngeal swabs of patients with meningitis and upper respiratory tract infections, ages one to 93 years in Moscow between 2011-2015. The serotypes and multilocus sequence types (MLSTs) were derived from whole-genome sequencing data using ARIBA and MLSTcheck. GPSCs were assigned by popPUNK. Antibiotic susceptibility was predicted based on genotypes.

Results

Sixty-seven sequence types identified in the collection belonged to 39 clonal complexes (CCs) and 10 singletons. Overall, 42 GPSCs were identified. The two prevalent lineages were GPSC1 (CC320) and GPSC7 (CC437). Twenty-two serotypes were found and their associated GPSCs are shown in Figure 1. The major GPSC contributing to multidrug resistance was GPSC1, which expressed 19F/19A serotypes (Figure 2).

Conclusions

The pneumococcal collection showed high diversity in population structure. Ongoing surveillance is needed to monitor the dynamics of the pneumococcal population in Russia following the introduction of PCV13 immunization in 2014