POPULATION STRUCTURE AND ERYTHROMYCIN RESISTANCE OF STREPTOCoccus PNEUMONIAE ISOLATES COLLECTED IN MOSCOW BETWEEN 2011-2015
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Introduction
It was reported that resistance of pneumococci to macrolides have increased in recent years in Russia. In current study, we aimed to explore genetic sequences of pneumococci in order to evaluate the distribution of sequence clusters especially as they relate to erythromycin resistance.

Methods and Materials
A total of 90 isolates were investigated, and were recovered from CSF samples of patients with meningitis (n=56) and nasopharyngeal swabs of both asymptomatic carriers (n=15) and patients with nasopharyngitis (n=19). The isolates were collected during 2011-15 in Moscow from adults (n=43), and children under 5 years (n=42) and between 5 and 18 years (n=5). Whole genome sequencing (WGS) was done as a part of the Global Pneumococcal Sequencing project. Phylogenetic analysis was carried out using the PHYLOViZ software. Antimicrobial susceptibility of erythromycin was determined by disk diffusion method.

Results
Among the investigated isolates 62 STs were revealed. The results of goeBURST Full MLST analysis identified 4 major sequence clusters (SC) in all groups (Fig.1). Twenty erythromycin-resistant isolates were identified, 12 (60%) of them were from patients with meningitis and belonged to CC 320 (Fig.2).

Conclusions
The study highlighted substantial variety of STs among pneumococcal isolates. Ongoing surveillance will be helpful to monitor the further emergence and spread of antimicrobial resistance and the genetic evolution of pneumococci following the introduction of PCV13 immunization of children in Russia in 2014.

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