

**Abstract title:** Global population structure of serotype 12F pneumococci

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**Background:**

Serotype replacement of *Streptococcus pneumoniae* can occur following the introduction of pneumococcal conjugate vaccine (PCV), with a consequent increase in disease caused by pneumococci expressing non-PCV serotypes. Serotype 12F has high invasive disease potential and is emerging in many countries post vaccine introduction. The increase in prevalence of multidrug-resistance (MDR) (is defined as resistance to  $\geq 3$  antibiotic classes) has also been a concern for public health.

**Methods:**

Genomic sequences from both invasive and non-invasive 407 serotype 12F pneumococcal isolates collected from 1998 to 2016 in 17 countries, as a part of the Global Pneumococcal Sequencing project (n=26,100), were analysed to infer sequence type, serotype and antimicrobial resistance profiles. Pneumococcal lineages (Global Pneumococcal Sequence Clusters, GPSCs) were assigned, and lineage-specific phylogenies were constructed.

**Results:**

Among the 407 pneumococcal serotype 12F isolates, nine GPSCs were identified, with GPSC26 being the most common (183/407, 45.0%). MDR was only observed in GPSC26 and 58.5% (107/183) of this lineage was MDR. GPSC26 was observed across 12 countries across five continents, while some serotype 12F lineages were regional-specific. For example, GPSC 334 was only detected in Poland. Overall, the MDR rate of all 12F isolates was 26.3% (107/407). The prevalence of resistance against tetracycline was 44.0%, chloramphenicol 38.8%, cotrimoxazole 27.8%, penicillin 24.3%, erythromycin 2.7% and clindamycin 1.2%.

**Conclusions:**

GPSC26 was the most common lineage, detected in multiple regions and accounting for all MDR isolates among the whole collection of serotype 12F pneumococci in this study.