

Global population structure of serotype 12F pneumococci

Thi N M Huynh^{1,2}, Kate C Mellor², Stephanie W Lo², Rebecca A Gladstone³, Lesley McGee⁴, Paulina A. Hawkins⁴, Stephen D Bentley², The Global Pneumococcal Sequencing Consortium⁵.



¹Hughes Hall, University of Cambridge, CB1 2EW, UK; ²Parasites and Microbes Programme, The Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, UK; ³Department of Biostatistics, Institute of Basic Medical Sciences, Faculty of Medicine, University of Oslo, Oslo, Norway; ⁴Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA; ⁵<https://www.pneumogen.net/gps/>.

Objectives

Characterise pneumococcal **serotype 12F lineages globally** and their **antimicrobial resistance profiles**.

Background

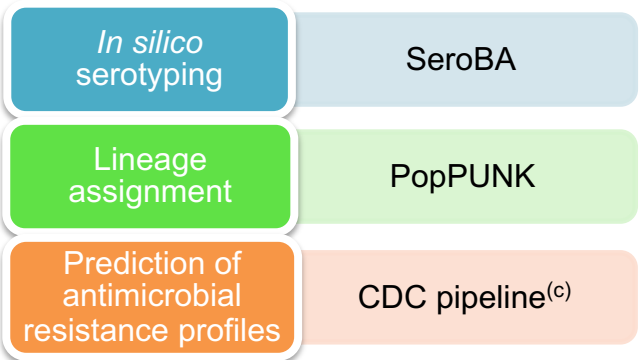
- Serotype replacement** following pneumococcal conjugate vaccine (PCV) introduction.
- Serotype 12F** is **emerging** in many countries post vaccine introduction.^{(a),(b)}
- Increase in multidrug-resistance (MDR)** (resistance to ≥ 3 antimicrobial classes) among non-PCV serotypes has been detected post vaccine introduction.

Methods

Study population

- We whole genome sequenced **407** pneumococcal isolates, **both disease cases (n=374)**, **carriage (n=28)** and **unknown (n=5)**, from **1998 to 2016** in **17** countries, as a part of the Global Pneumococcal Sequencing project (n=26,100).

Analysis for each genome



Phylogenetic Analysis

- To create alignments, sequence reads were mapped to reference genome ATCC700669 using BWA.
- Phylogenies were built using FastTree 2.1.10

Results

- Seven pneumococcal lineages (GPSCs) were identified.
- GPSC26 was observed across 12 countries, while some serotype 12F lineages were regional-specific.

GPSCs	Africa	Asia	Europe	North America	South America	Grand Total
26	158	25				183
32	2		1	45	28	76
55		89		1		90
56	54					54
289					1	1
334			2			2
575					1	1
Grand Total	214	114	3	46	30	407

Figure 1: Population structure of serotype 12F in different regions.

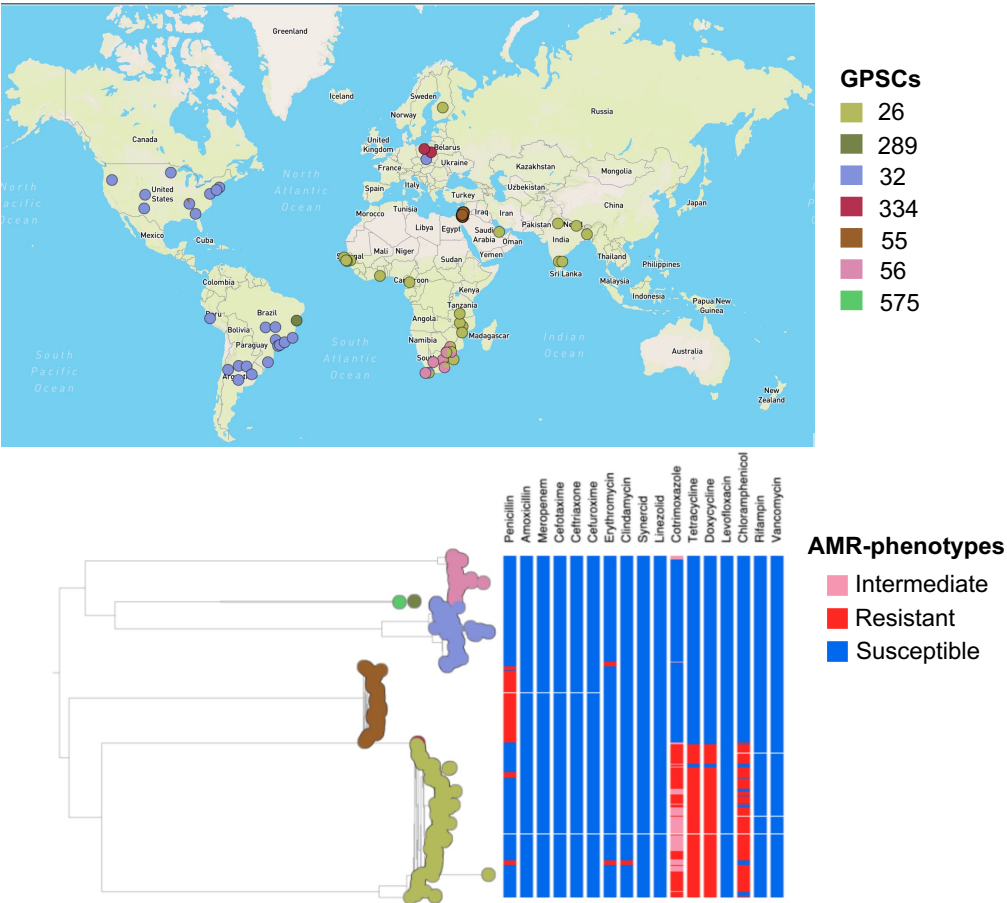


Figure 2: Antimicrobial resistance profiles of 407 pneumococcal isolates.

- MDR was only observed in GPSC26 and 58.5% (107/183) of this lineage was MDR.
- 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

- Some GPSCs expressing serotype 12F were found in **multiple countries** whereas other lineages were only associated with a **single country**.
- GPSC26** accounted for **all serotype 12F MDR isolates** in this study.

References:

(a) Rokney A. *et al.* Emergence of streptococcus pneumoniae serotype 12F after sequential introduction of 7- and 13-valent vaccines, Israel. *Emerging Infectious Diseases*. 2018;24(3):453-461. DOI:10.3201/eid2403.170769
(b) Almeida SCG. *et al.* Genomic surveillance of invasive streptococcus pneumoniae isolates in the period pre-pcv10 and post-pcv10 introduction in Brazil. *Microbial Genomics*. 2021;7(10). :000635. DOI: 10.1099/mgen.0.000635.
(c) CDC pipeline. Available at: https://github.com/BenJamesMetcalf/Sanger_SPN_Scripts-Ref (Accessed: 22 Feb 2022).

Acknowledgements:

This study was co-funded by the Bill & Melinda Gates Foundation (grant code OPP1034556), the Wellcome Sanger Institute (core Wellcome grants 098051 and 206194), and the US Centers for Disease Control and Prevention. We would like to thank all members of the Global Pneumococcal Sequencing Consortium for their collaborative spirit and determination, for the monumental task of sampling and extracting data. We also acknowledge the Wellcome Sanger Institute Sequencing Facility and Pathogen Informatics team for their technical support.

