

Detection of *Streptococcus pneumoniae* non vaccine serotype 12F clone 989 with multidrug antibiotic resistance, circulating globally

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On behalf of all Global Pneumococcal Sequencing project partners. www.pneumogen.net/gps

The Global Pneumococcal Sequencing project (GPS) aims to capture changes in the pneumococcal population through the introduction of pneumococcal conjugate vaccines (PCV).

Background

- Clonal complex (CC)989 is the largest 12F clone in GPS and represents a lineage distinct from the 12F PMEN clone Denmark12F-34.
- CC989 has previously been observed in small numbers; the MLST database includes 55 sporadic isolates, the oldest from 1998 (Kenya).
- Serotype 12F has been reported to be more frequently found in disease than carriage and to be increasing in the PCV era.

Methods

ARIBA for detecting acquired antibiotic resistance genes. Reads mapped to CC989 reference with **SMALT**, **Gubbins** removed recombination, phylogeny with **RAxML**, and **LSD2** for lineage dating. Visualisations with **Microreact**

Results

267 CC989 genomes were available with isolation dates ranging from 2002 -2016. The phylogenetic temporal signal estimates that the clone arose around 1980, tMRCA =1980.634 [1975.858-1983.954]. CC989 has a moderate R/M 7.46 and rho 0.096.

Antibiotic resistance

Tet(M) and chloramphenicol acetyltransferase (*cat*) were detected in >90% of isolates, with concordant phenotypes. 87% of tested (n=26) had a resistant co-trimoxazole MIC ≥ 2 μ g/ml correlating with a *folA* recombination hotspot. 100% of tested (n=56) were phenotypically rifampin resistant MIC ≥ 2 μ g/ml. CC989 is currently penicillin susceptible.

Serotype

Analysis of capsular genotypes and repeat phenotyping suggest that consistently distinguishing 12B and 12F phenotypically may be particularly challenging for this clone, 93% of isolates were designated as 12F/B.

Phylogeography

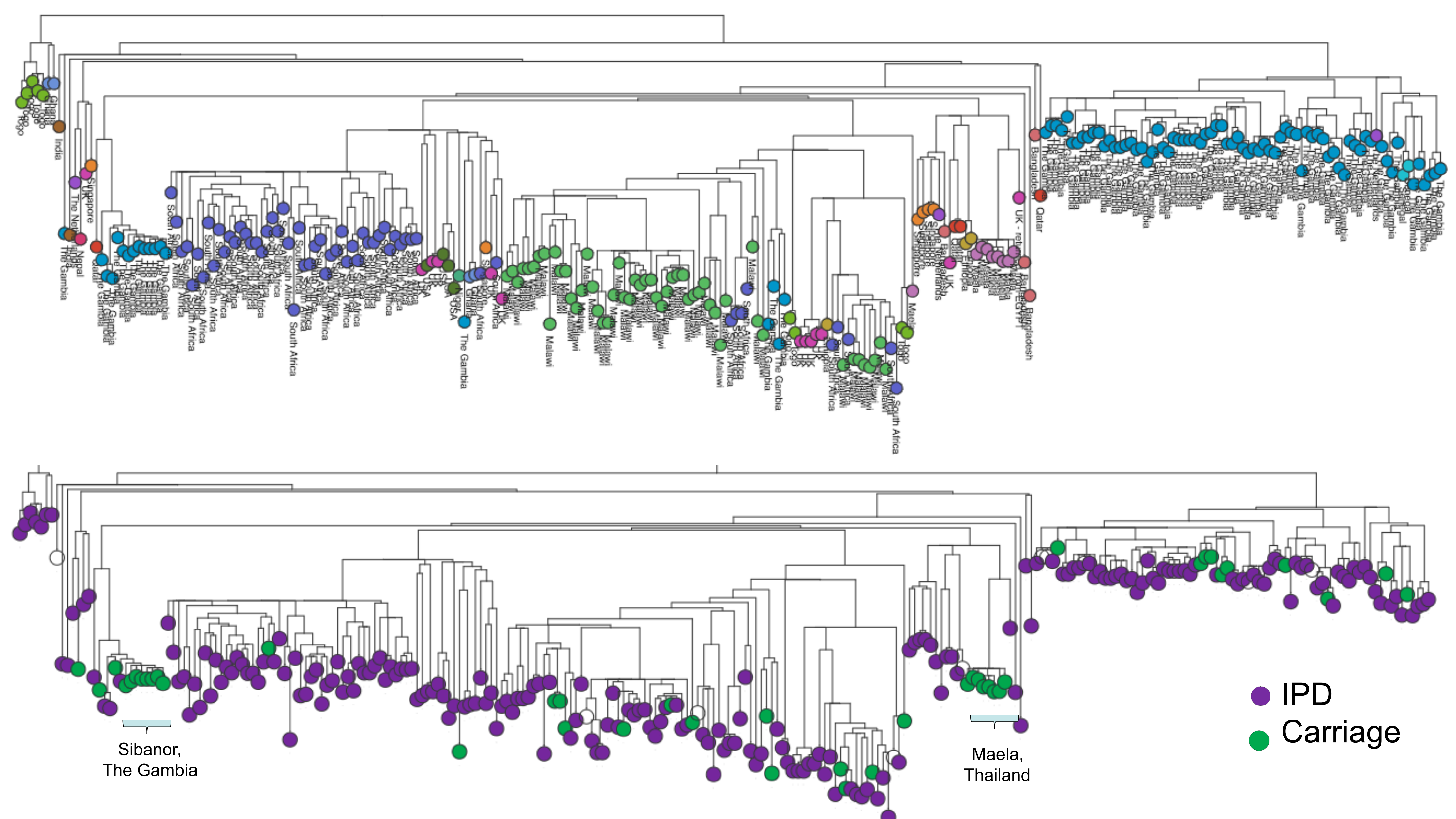
Isolates were from

- The Gambia (91)
- South Africa (58)
- Malawi (53)

and 14 additional countries with clear geographical clustering.

Phylogeny in context of clinical manifestation

79% of the CC989 isolates were from disease, with two small phylogenetic clusters highlighted in the tree accounting for 37% of the carriage isolates; one cluster from Thailand exclusively expressed serotype 46, the other a Gambian 12F cluster.



Conclusions

- CC989 is a intercontinentally disseminated NVT clone with multidrug resistance and expresses disease associated serotype 12F.
- Genomic surveillance allows detection and high resolution description of NVT lineages which pose potential global threats in vaccine replacement.



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