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


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

### 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 12F 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 has been increasing in the PCV era.

### Methods
ARIBA detected acquired antibiotic resistance genes. Reads were mapped to CC989 reference, Gubbins removed recombination and phylogeny produced using RAxML with Path-O-Gen for lineage dating. Visualisations with Phylocanvas.org and Microreact.org

### Results
212 CC989 genomes were available with Isolation dates ranging from 2005 - 2015. The phylogenetic temporal signal estimates that the clone arose around 1971.

### Antibiotic resistance
* Tet(M) * and chloramphenicol acetyltransferase (*cat*) were detected in > 85% of isolates. 29% had a resistant co-trimoxazole MIC of ≥ 2 µg/ml correlating with a *folA* recombination hotspot. All isolates were penicillin susceptible from phenotype or inferred from *pbp* allele profile.

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

**Phylogeny in context of clinical manifestation**
80% of the CC989 isolates were from disease, with two small phylogenetic clusters accounting for 48% of the carriage isolates; one exclusively serotype 46 from Thailand.