

Genomic epidemiology of *Streptococcus pneumoniae* serotype 5 pre and post introduction of PCV13 in The Gambia

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Introduction

- *Streptococcus pneumoniae* serotype 5 is the second leading cause of Invasive Pneumococcal Disease (IPD) in The Gambia
- Pneumococcal Conjugate Vaccine (PCV), PCV7 was introduced in The Gambia in August 2009 and PCV13 in May 2011
- Despite the introduction of PCV13, serotype 5 pneumococcal burden remains high (1)
- *S. pneumoniae* serotype 5 Multilocus Sequence Type (ST289) and ST3404 are associated with invasive disease (2,3)
- This study aims to determine the effect of PCV13 introduction on the genomic epidemiology of *S. pneumoniae* serotype 5 in The Gambia

Methods

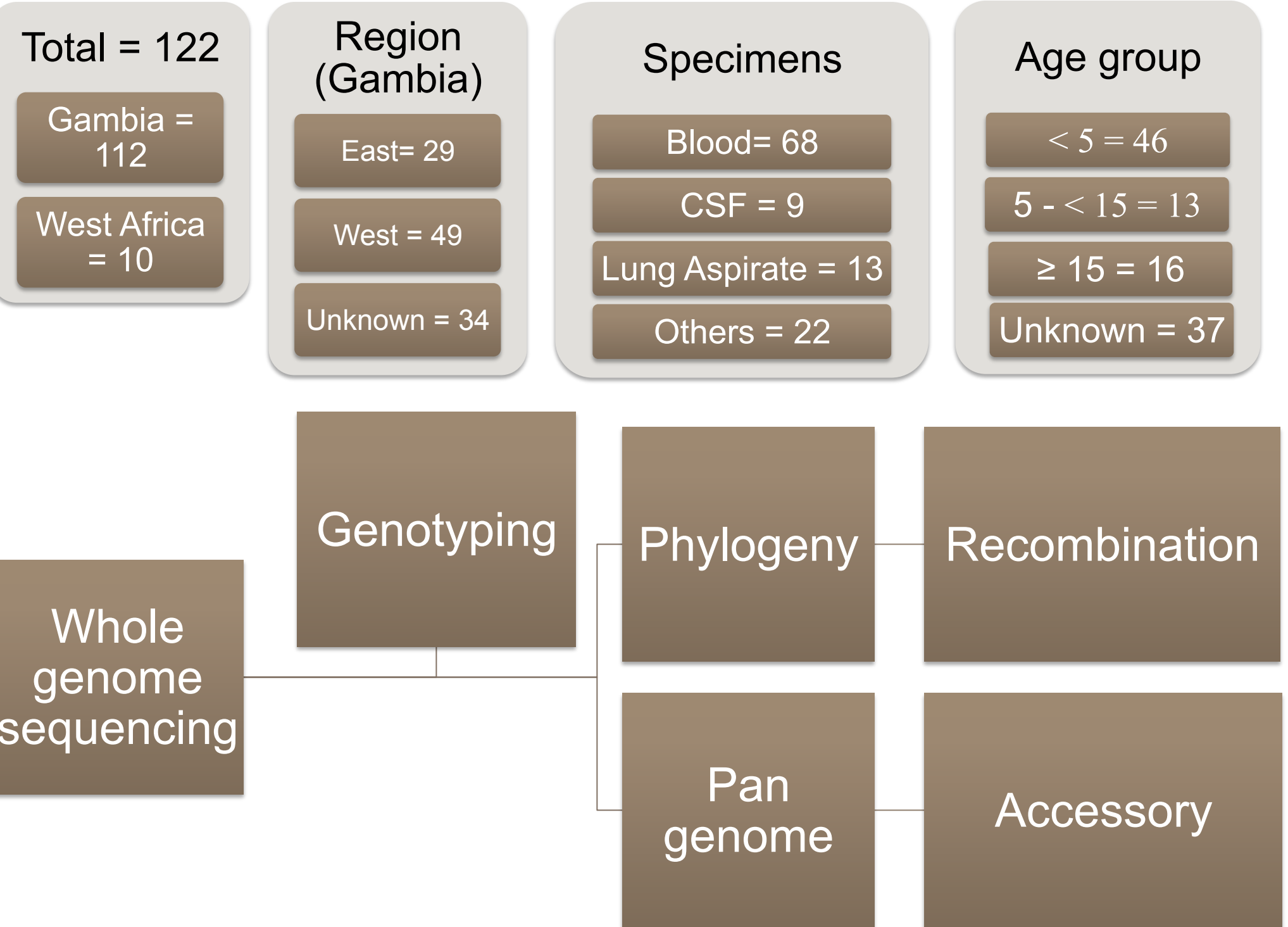


Figure 1: A flowchart showing the methods implemented in the whole genome analysis of serotype 5 isolates between May 1995 to April 2016.

Genotype distribution

ST289 and ST3404 were dominant in the post PCV era across The Gambia (Figure 2 and 3).

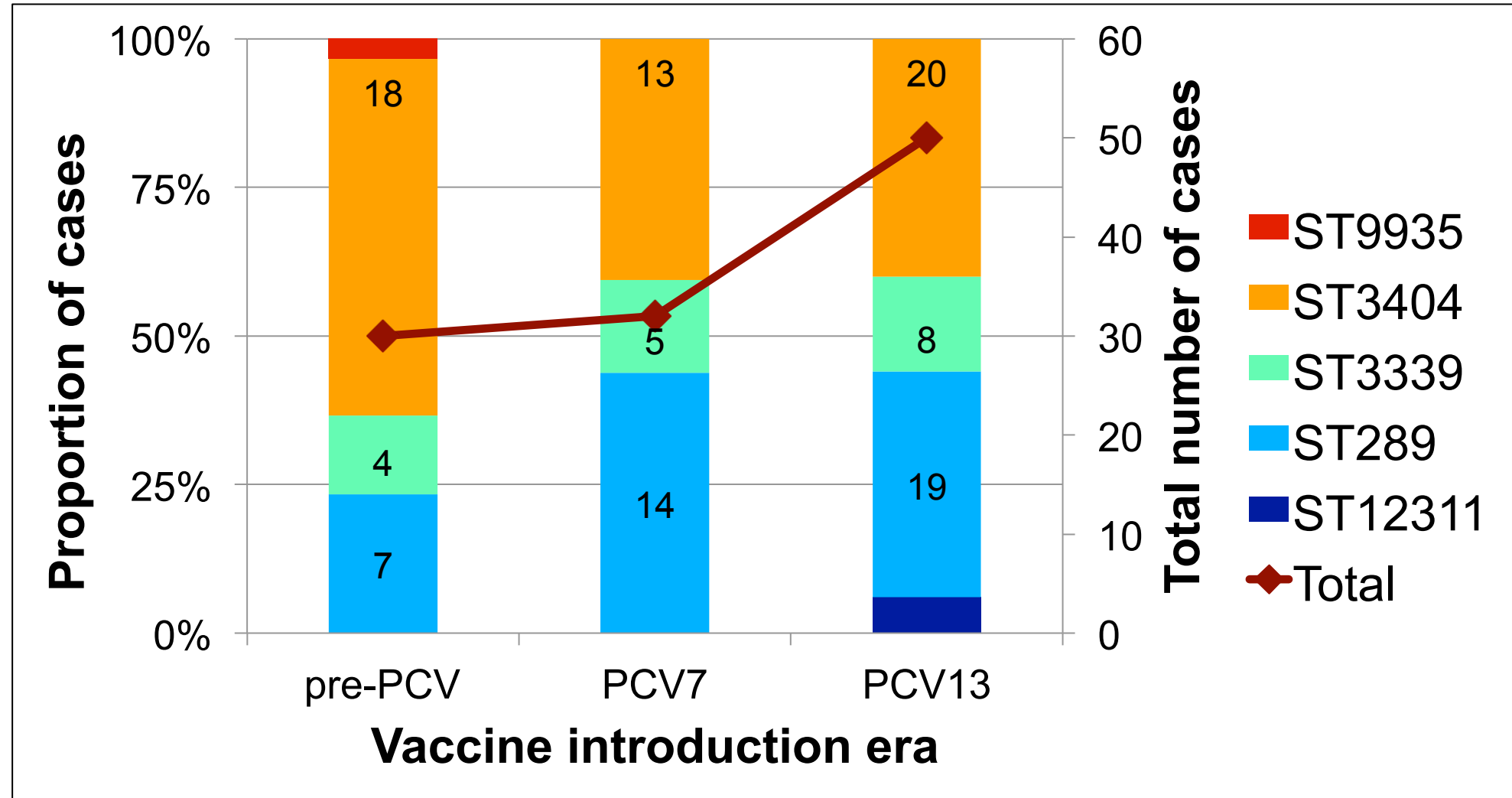


Figure 2: A bar chart showing the proportions of STs in The Gambia based on the vaccine introduction eras.

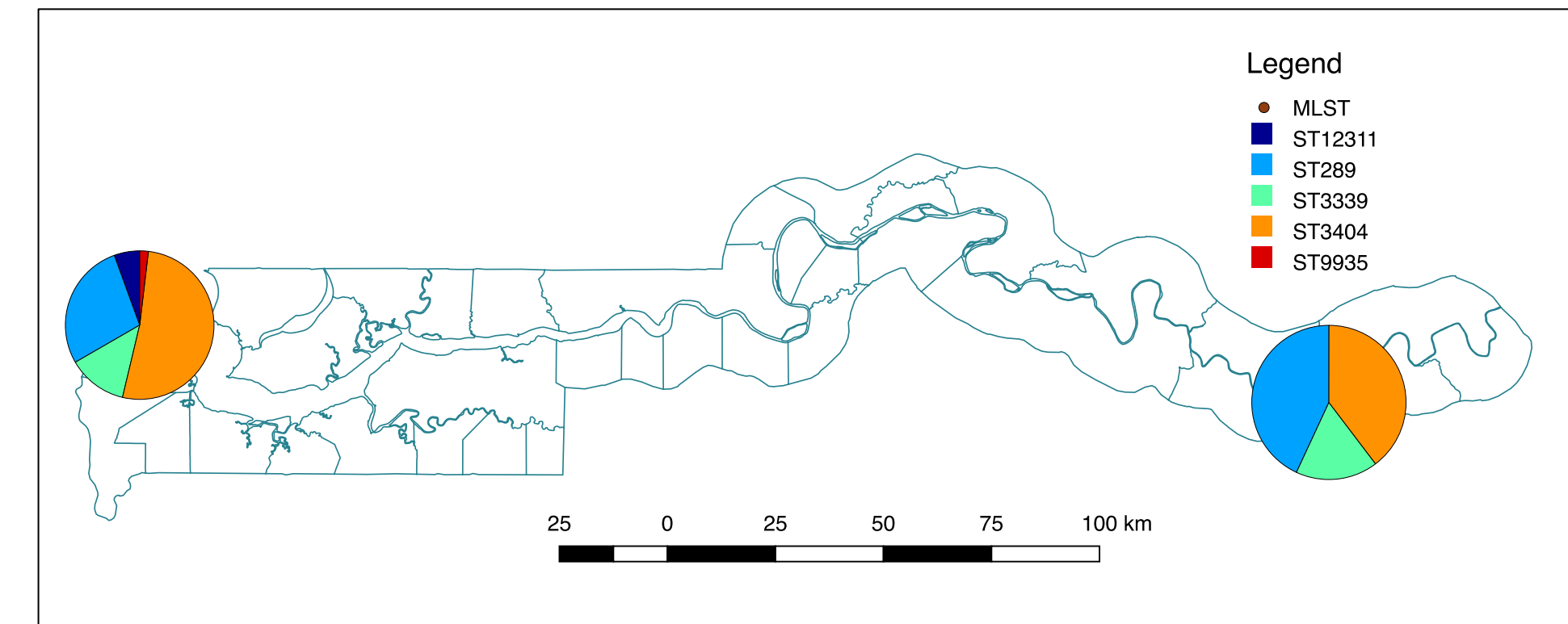


Figure 3: A map of The Gambia with pie charts showing the proportions of the STs in Western and Eastern Gambia.

Phylogeny and recombination

- Isolates clustered by ST into monophyletic clades that had unique recombination patterns (Figure 4)
- ST289 evolved through large-scale genetic recombination and was predominant in the post PCV13
- A novel genotype with unique recombination patterns, ST12311, emerged in the post PCV13 era

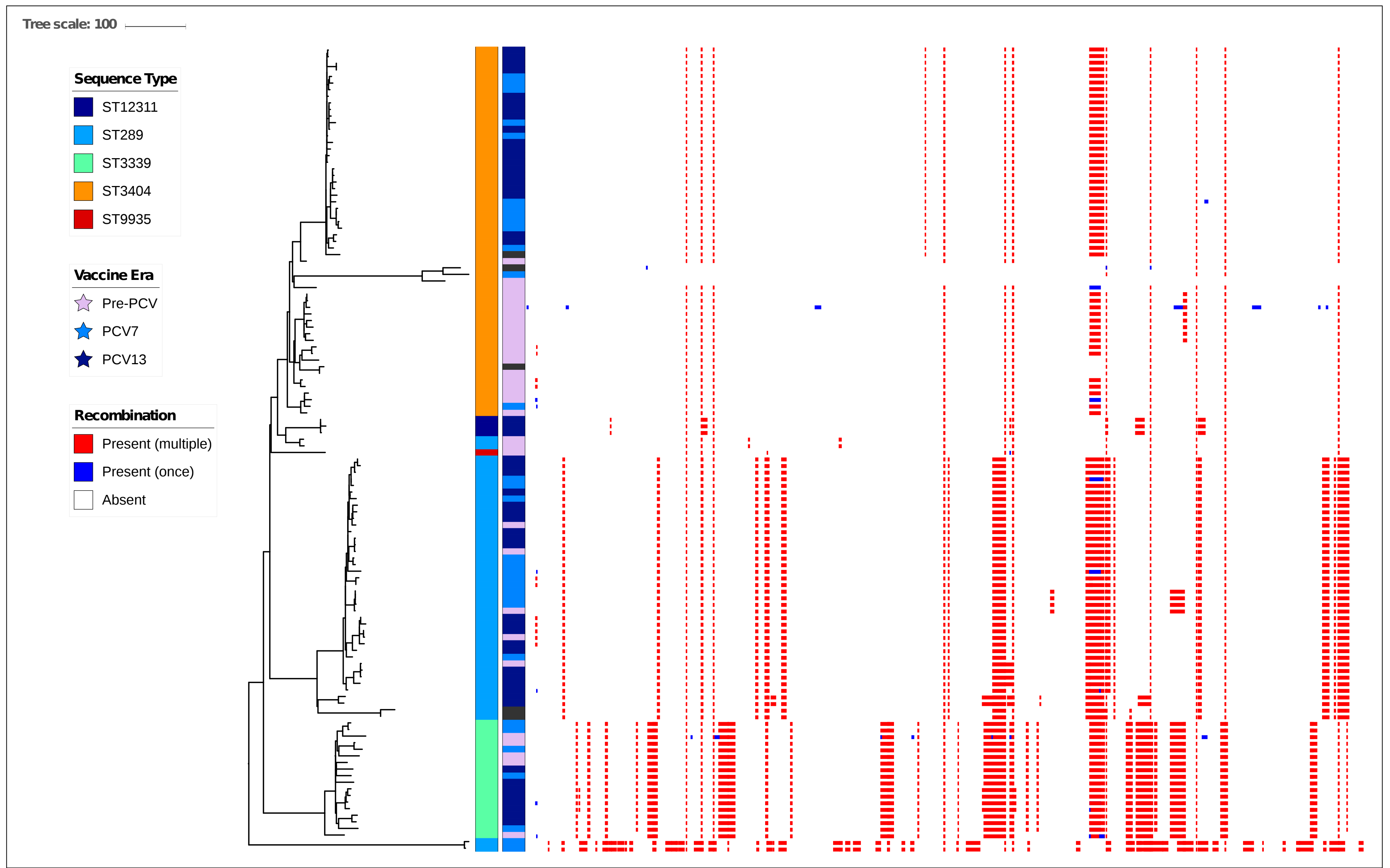


Figure 4: A phylogenetic tree of 112 serotype isolates from The Gambia alongside 10 isolates from West Africa. ST and vaccine introduction era are shown alongside the tree as colored metadata blocks. A heatmap showing presence (red or blue) and absence of recombination blocks is also shown alongside the phylogenetic tree.

Accessory genome

- Isolates with the same genotype had more similar accessory genome content (Figure 5)
- ST 289 had unique accessory gene variants including *blpH*, *blpC*, *manY*, *manZ*, *fucA*, *fucU*, *fucK*, *cbpF*, *levE*, *gspA* and PTS-E11

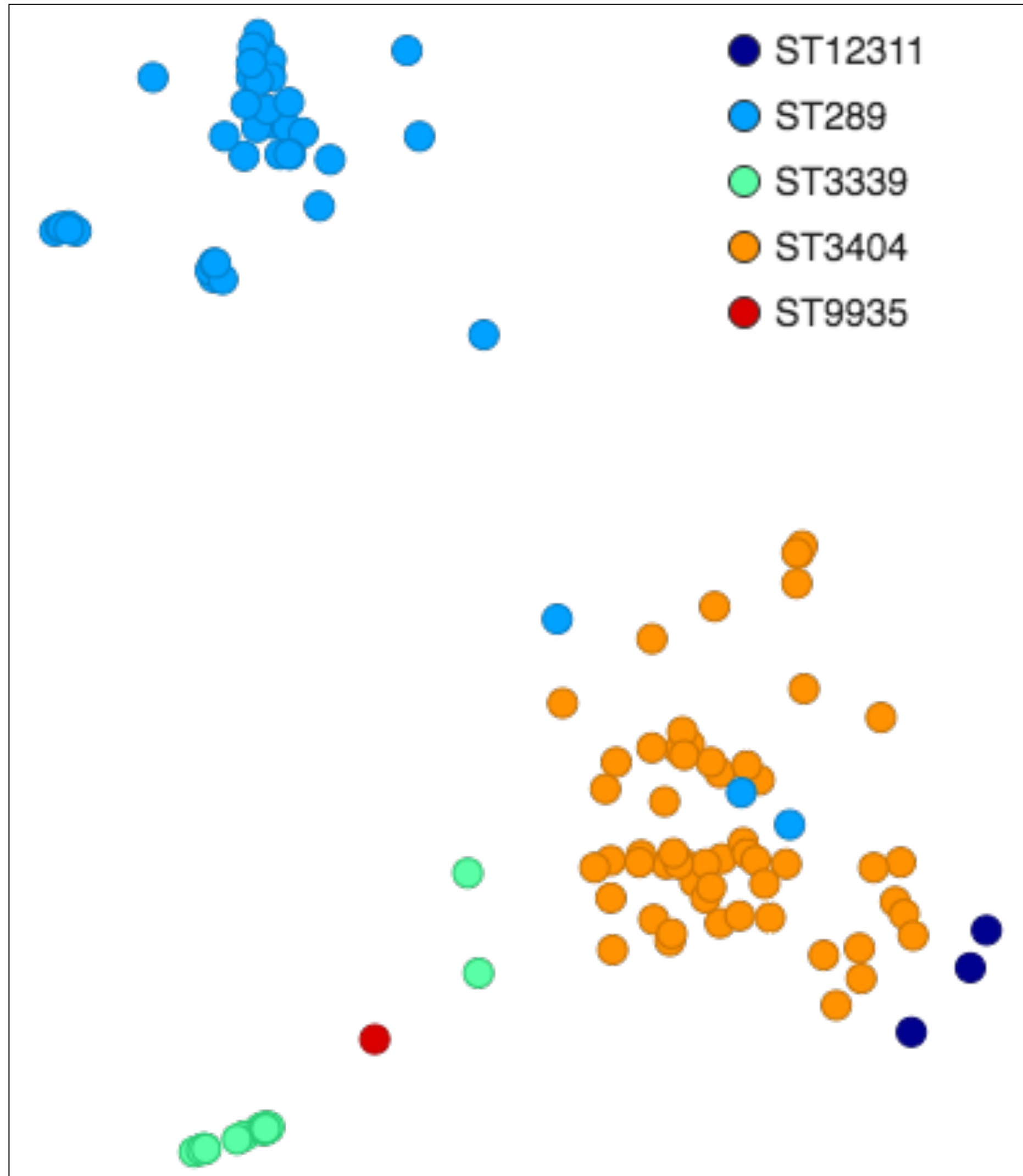


Figure 5: A scattered diagram showing similarity in accessory genome content. The distance between dots is relative to similarity in accessory genome content.

Key findings

- ST3404 remained dominant from the pre-PCV era to the post PCV13 era in the Gambia
- The proportion of isolates belonging to ST289 increased from 23% the pre-PCV era to 40% in the post PCV13 era
- ST289 had unique recombination patterns and unique accessory genome variants
- It remains unclear why ST289 and ST3404 continue to cause disease in the post PCV13 era

Acknowledgements

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