

# ANTIBIOTIC RESISTANCE PATTERNS AND PHYLOGEOGRAPHY OF STREPTOCOCCUS PNEUMONIAE ASSOCIATED WITH PAEDIATRIC MENINGITIS IN PRE- AND POST-PCV-INTRODUCTION WEST AND CENTRAL AFRICA (ID 958)

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## Abstract

### Background

Despite contributing to the heavy disease burden, little is known about the genomic epidemiology of *Streptococcus pneumoniae* causing meningitis among children under 5 in West and Central Africa.

### Methods

We analysed 185 *S. pneumoniae* genomes recovered from suspected paediatric meningitis in West and Central Africa from 2010 to 2016. The phylogeny was reconstructed, accessory genome similarity was computed and antimicrobial resistance (AMR) patterns were inferred from the genome.

### Results

The introduction of PCV significantly perturbed the distribution of serotypes causing paediatric pneumococcal meningitis. Non-PCV13 serotypes increased in prevalence in the post-PCV period ( $c^2= 6.44$ ,  $p$  value 0.011), however, serotype 1 remained the most common serotype in both periods. AMR genes were more common in non-PCV serotypes and this contributed to an increased presence of resistance genes in the post-PCV period ( $c^2= 5.74$ ,  $p$  value 0.057). Resistance genotypes appeared to be conserved within selected sub clades of the phylogenetic tree suggesting clonal inheritance. Phylogeographic clustering was observed within serotypes with isolates from the same sub-region clustering and sharing similar accessory genome content.

### Conclusions

While we note declining trends in vaccine serotypes, the emergence of non-vaccine serotypes and rising antibiotic resistance threat necessitates continued surveillance. Sub regional genotypic differences may be important to study