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

Ngwa D¹, Kwambana-Adams BA¹, Senghore M¹, Worwui A¹, Tientcheu PE¹, Odoi C¹, Salaudeen R¹, Lo SW², Gladstone RA², McGee L³, Breiman RF¹, Bentley SD², Mwenda JM³, Roca A¹, Mackenzie G¹, Antonio M¹

1Medical Research Council Unit The Gambia at The London School of Hygiene and Tropical Medicine, Atlantic Road, Fajara, The Gambia. 2The Welcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, UK. 3Respiratory Diseases Branch, Centre for Disease Control and Prevention, Atlanta, GA, USA. 4Global Health Institute, Emory University, Atlanta GA, USA. 5WHO Regional Office for Africa.

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

- Total = 122
- 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 era
- A novel genotype with unique recombination patterns, ST12311, emerged in the post PCV13 era

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.](image)

![Figure 3: A map of The Gambia with pie charts showing the proportions of the STs in Western and Eastern Gambia.](image)

Accessory genome

- Isolates with the same genotype had more similar accessory genome content (Figure 5)

![Figure 4: A phylogenetic tree of 112 serotype isolates from The Gambia alongside 10 isolates from West Africa. ST and Vaccine Era Sequence Type](image)

![Figure 5: A scattered diagram showing similarity in accessory genome content. The distance between dots is relative to similarity in accessory genome content.](image)

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

Many thanks to all the study participants and their families. Thanks to all the members of the clinical microbiology team at Basse and Fajara and the field workers. Many thanks also go to the core sequencing facility at Medical Research Council Unit The Gambia at London School of Hygiene and Tropical Medicine.

References