





Diversity of pneumococcal carriage in the Upper River Region of The Gambia in 2009 prior to the introduction of pneumococcal conjugate vaccines

Cham MA¹, Kwambana-Adams BA¹, Senghore M¹, Usuf E¹, Worwui A¹, Salaudeen R¹, McGee L², Bentley SD³, Breiman RF⁴, Roca A¹, Mackenzie G¹, Antonio M¹

1 Medical Research Council Unit The Gambia at The London School of Hygiene and Tropical Medicine, Atlantic Road, Fajara, The Gambia 2 Respiratory Diseases Branch, Centre for Disease Control and Prevention, Atlanta, GA, USA 2 Centre for Respiratory Diseases and Meningitis, National Institute for Communicable Diseases of the National Health Laboratory Service Johannesburg, South Africa; 3The Wellcome Trust Sanger Institute, Wellcome Campus, Hinxton, Cambridge CB10 1SA, UK 4 Global Health Institute, Emory University, Atlanta GA, USA

Introduction

- The nasopharnyx serves as a reservoir for the carriage of Streptococcus pneumoniae (the pneumococcus), a leading cause of invasive disease in The Gambia
- Pneumococcal conjugate vaccines (PCV) are known to alter the ecology of the pneumococcal population in the nasopharnyx
- Here we present baseline genomic data on the epidemiology of pneumococcal carriage in rural Gambia prior to PCV7 introduction

Methods and workflow

Whole genome sequencing was performed on isolates recovered from the 2009 pneumococcal carriage study (Figure 1)



- Carriage surveillance in Eastern Gambia
- Nasopharyngeal swabs from all age groups
- Specimens grown on gentamycin blood agar
- Colonies confirmed by Optochin disk test
- Whole genome sequencing Illumina HiSeq
- Phylogenetic analysis

Figure 1: Flowchart summarising the workflow specimen collection, laboratory testing and whole genome sequencing analysis for the study

Results summary

- •Study participants included 51% males and 46% females
- •The most commonly carried serotypes in our dataset were 6E(6B), 6A, 3, 19F (Figure 2)
- •PCV serotypes recovered from the same ethnic group clustered together on the phylogenetic tree respectively (Figure 3)
- There was a high level of diversity amongst 6A isolates forming divergent clades with distinct clustering
- •Serotypes 3 and 23B were widespread across the villages (Figure 4)

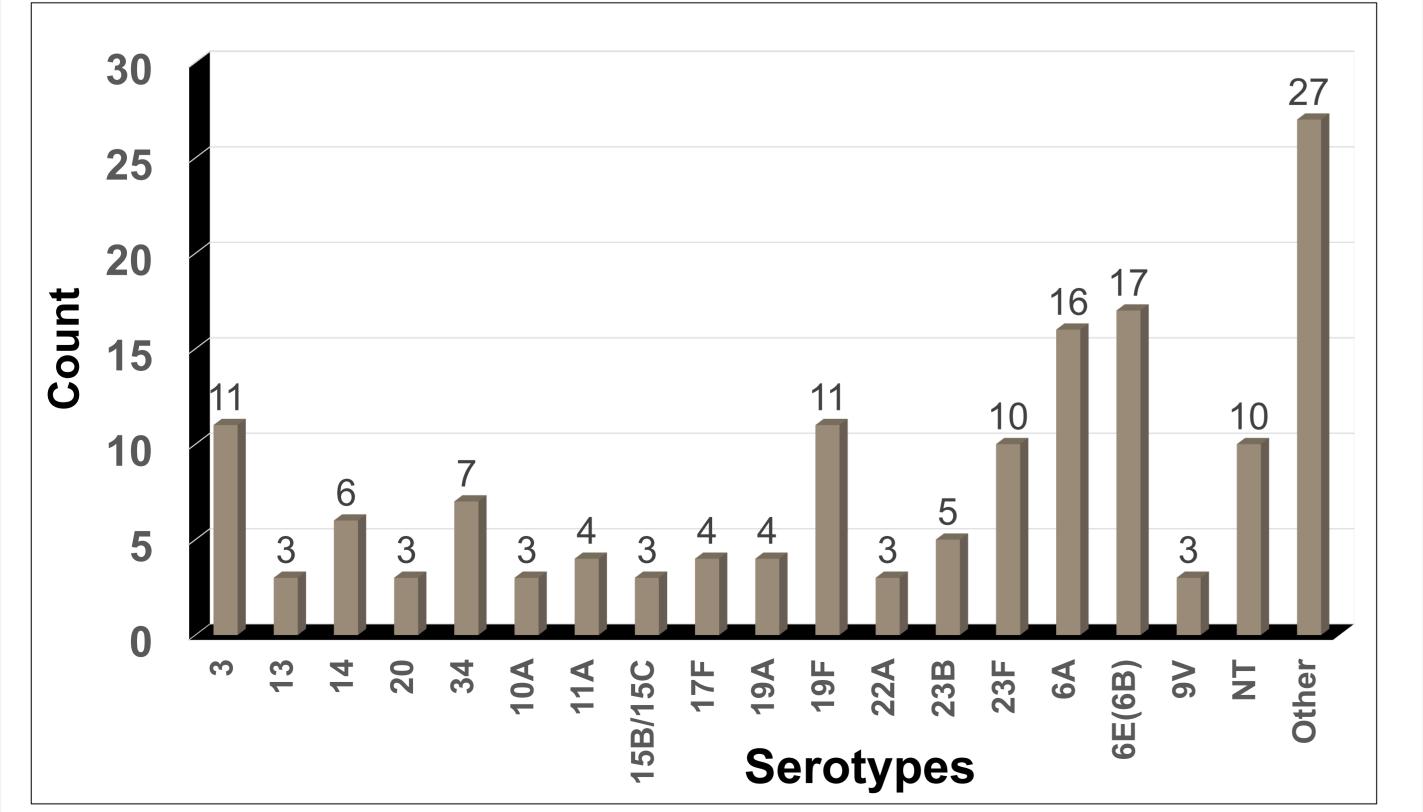


Figure 2: Bar chart showing the distribution of the most common serotypes detected in carriage among study participants

Results phylogeny and geographic diversity

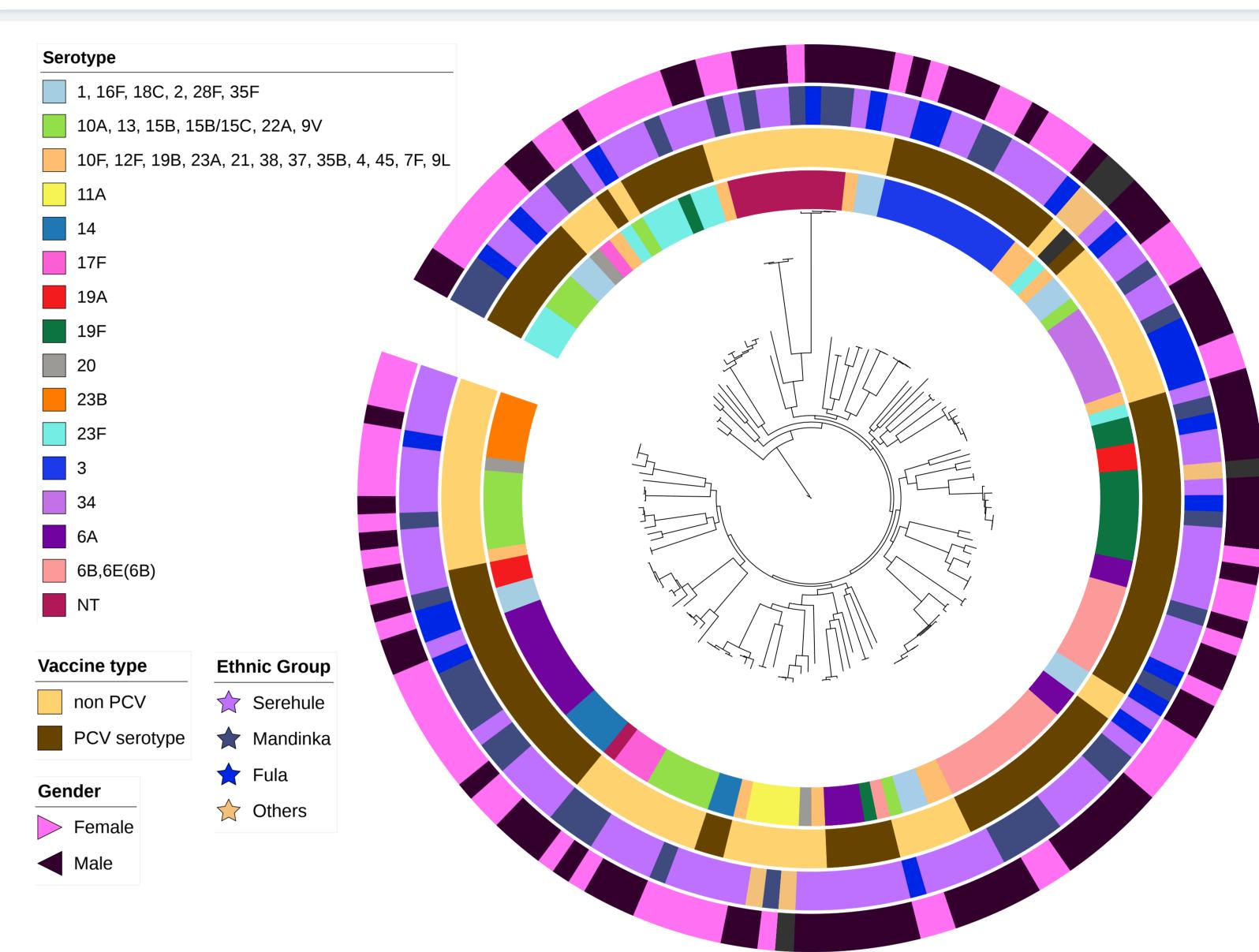


Figure 3: Whole genome phylogeny of pneumococcal carriage isolates reconstructed from core genome single nucleotide polymorphisms. Metadata rings show serotype, serotypes covered by PCV, subject ethnicity and gender.

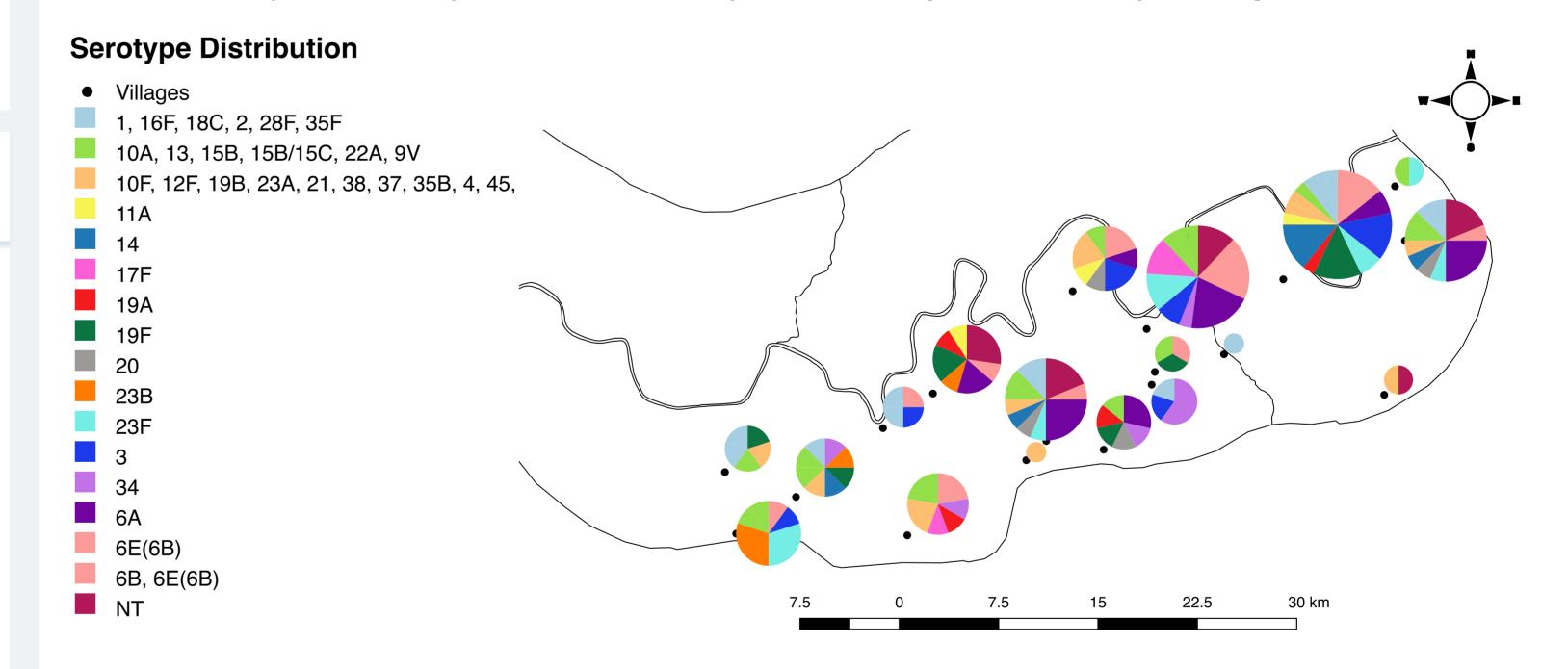


Figure 4: A map of the surveillance region with pie charts showing serotype distribution across the villages in the south bank of the upper river region.

Discussion

- •There was high level of diversity between and within serotypes
- •The impact of PCV13 on the evolution of pneumococcal carriage in Basse can be determined based on this data and on-going carriage surveillance
- •This baseline data is crucial in understanding how PCV13 has affected the nasopharyngeal pneumococcal ecology in rural Gambia

Acknowledgements

We thank the study participants, the MRC Unit the Gambia at LSHTM, the demographic surveillance system team and the health workers for carrying out the surveillance. Whole genome sequencing was performed at the Wellcome Trust Sanger institute through the Global Pneumococcal Sequencing project.