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

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Introduction

• The nasopharynx 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 nasopharynx
• 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)

1. Carriage surveillance in Eastern Gambia
2. Nasopharyngeal swabs from all age groups
3. Specimens grown on gentamycin blood agar
4. Colonies confirmed by Optochin disk test
5. Whole genome sequencing Illumina HiSeq
6. 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

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

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