



Genomic diversity of
Streptococcus pneumoniae serotype 1
across sub-Saharan Africa



WHO

The PAGe Consortium represents a collaboration between several African centres utilising cutting edge whole genome sequencing in partnership with the Wellcome Trust Sanger Institute to answer some of the key biologically relevant pneumococcal questions of Africa importance.

WHAT

PAGe1 is the first consortium led sequencing project and we are asking for any interested group which has pneumococcal serotype 1 isolates available for this exciting African led project to contact the consortium to discuss how we might collaborate.

WHY

Streptococcus pneumoniae serotype 1 is an important vaccine target in sub-Saharan Africa. It exhibits a strong association with invasive disease and is known to occur in outbreaks or epidemics. Understanding the genetic traits that underpin this association and contribute towards its epidemic potential will help to refine vaccine target discovery and guide the development process.

The PAGe1 study will address the following specific questions:

- A) Define the genomic diversity of serotype 1 isolates and establish the relative contributions of sequence variation, gene content, and genome organization to this diversity.
- B) Establish the relationship of this diversity to clinical presentation, epidemic potential, disease versus carriage, and establish whether epidemic, disease and carriage characteristics (such as pneumonia, bacteremia or meningitis) are associated with particular genes or lineages.
- C) Establish the extent of regional serotype 1 temporal and geographic variation.



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