

Whole genome sequencing of *Streptococcus pneumoniae* serogroup 19 isolates before the introduction of vaccine in the National Immunization programme of India (NIP)

Geetha N¹, Vandana G¹, Avid H¹, Feroze G¹, Ravikumar KL¹, Stephen D. Bentley², Rebecca A. Gladstone², Stephanie W. Lo², Robert F. Breiman³, Lesley McGee⁴ and the Global Pneumococcal Sequencing Consortium

¹Central Research laboratory, KIMS H&RC, Bangalore; ²Infection Genomics, The Wellcome Trust Sanger Institute, ³Emory University, Atlanta, USA, ⁴Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, USA

BACKGROUND AND AIMS

Infection caused by *S. pneumoniae* is a major cause of morbidity and mortality worldwide. Introduction of PCV13 in NIP is bound to have impact on the epidemiology of disease in India. Serogroup-19 is among the most prevalent serotype in India. We performed phylogenetic analysis of Sg19 strains to understand the larger impact.

METHODS

- 72 Sg19 isolates of *S. pneumoniae* strains collected across India from 2009-2017 were sequenced
- Isolates were sequenced on Illumina HiSeq 2500 platform as a part of GPS study
- Population structure, STs, resistotypes, were analyzed
- The phylogenetic tree was built with FastTree after mapping to ATCC700669

RESULTS

- Majority of the isolates belonged to 19F (n=43) followed by 19A (n=23) and 19B (n=3).

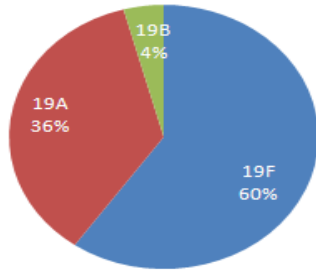


Fig 1a: Distribution of Sg-19 isolates - Serotypes

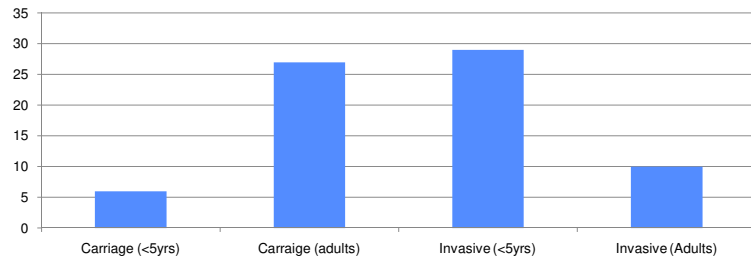


Fig 1b: Distribution of Sg-19 isolates – Carriage/Disease

- Population structure analysis of serogroup 19 showed high level heterogeneity.
- 19F, 19A and 19B serotypes showed 17, 13 and 2 diverged specific clonal lineages respectively

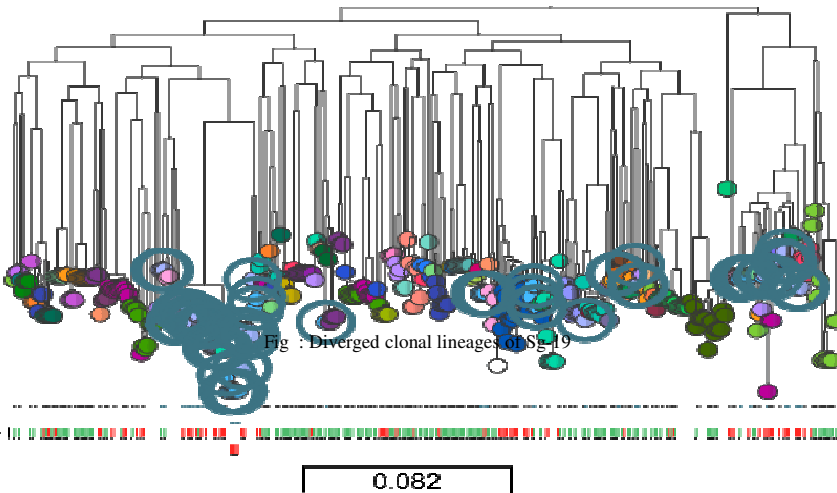


Fig 2 : Population snapshot of Sg-19 isolates

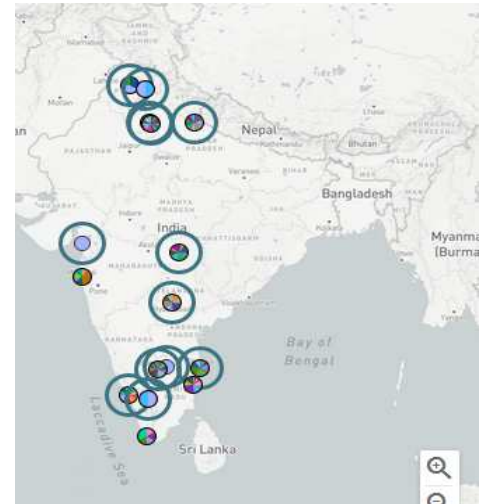


Fig 3 : Geographic Distribution of Sg-19 isolates

- MLST resolved 72 isolates - 18 known & 11 novel STs.
- Prevalent clones : ST236, ST271 & ST320

- Multi-drug resistance was present in 36% of isolates
- 30.5 % Penicillin resistant isolates belonged to 19F

CONCLUSIONS:

Whole genome sequencing of serogroup 19 identified a genetically diverse collection with novel clones and lineages associated with antimicrobial non-susceptibility

