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

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**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**

i. 72 Sg19 isolates of *S. pneumoniae* strains collected across India from 2009-2017 were sequenced

ii. Isolates were sequenced on Illumina HiSeq 2500 platform as a part of GPS study

iii. Population structure, STs, resistotypes, were analyzed

iv. The phylogenetic tree was built with FastTree after mapping to ATCC700669

**RESULTS**

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

![Distribution of Sg-19 isolates - Serotypes](image1)

![Distribution of Sg-19 isolates – Carriage/Disease](image2)

![Diverged clonal lineages of Sg-19](image3)

ii. Population structure analysis of serogroup 19 showed high level heterogeneity.

iii. 19F, 19A and 19B serotypes showed 17, 13 and 2 diverged specific clonal lineages respectively

![Population snapshot of Sg-19 isolates](image4)

![Geographic Distribution of Sg-19 isolates](image5)

iv. MLST resolved 72 isolates - 18 known & 11 novel STs.

v. Prevalent clones : ST236, ST271 & ST320

vi. Multi-drug resistance was present in 36% of isolates

vii. 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