

Zmpb allelic variation in *Streptococcus Pneumoniae* isolates causing Meningitis in Indian population

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Background:

Streptococcus pneumoniae is a leading cause of meningitis. The organism produces several virulence factors that are involved in the disease process. Intense inflammatory response observed in meningitis is partially attributed to zinc metalloprotease encoded by *zmpB* in pneumococcal strains. We aimed to study allelic variations of *zmpB* among isolates obtained from Meningitis patients in India.

Materials and methods:

36 cerebrospinal fluid (CSF) isolates collected across the country from 2009-2016 were sequenced on Illumina platform. The CRL in-house bioinformatics pipeline was used to extract gene sequences, alignment and phylogeny analysis. SeroBA was used to determine serotype. Allelic variations of *zmpB* gene was analyzed by comparing the identity with the virulent strain *S. pneumoniae* TIGR4. The phylogenetic tree was visualized using Microreact (<https://microreact.org/>).

Results:

36 pneumococcal isolates belong to 24 serotypes with 19F (n=5) as dominant type. Non-PCV13 vaccine serotypes constituted 50% of the isolates (n=18). The isolates were assigned to 28 different sequence clusters, among them GPSC10 (n=4) & GPSC2 (n=3) were predominant. 32 of 36 isolates showed 21 to 88% of sequence variation, while remaining 4 isolates showed sequence similarity of 98% with the TIGR4. Allelic variations did not affect the protein coding region analysis and conserved domains of ZmpB protein was identified in all isolates.

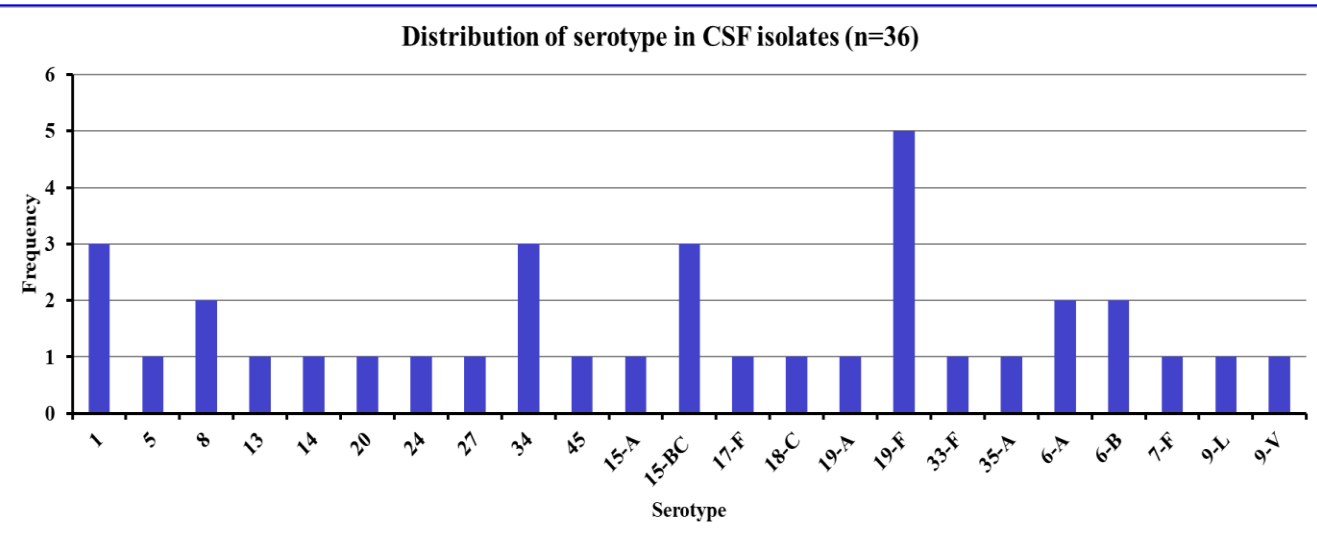


Figure 1. Frequency distribution of Serotypes of invasive *S. pneumoniae* (n=36) isolates.

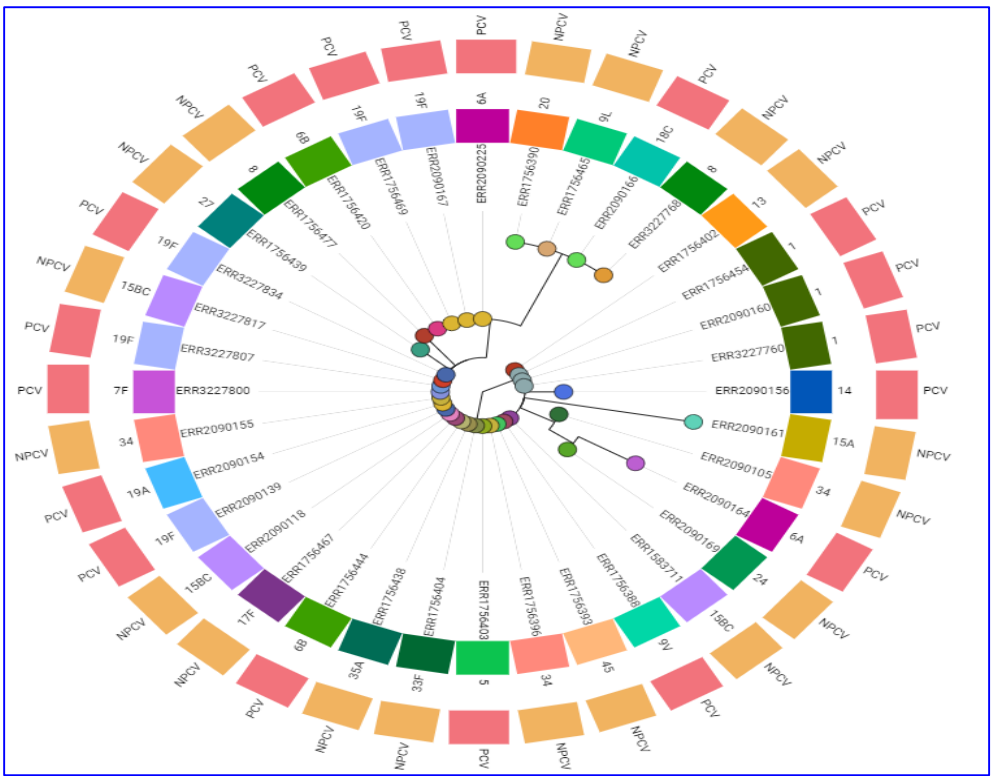


Figure 2. Phylogenetic tree representing the serotype distribution and PCV vaccine coverage with respect to the *zmpB* variation.

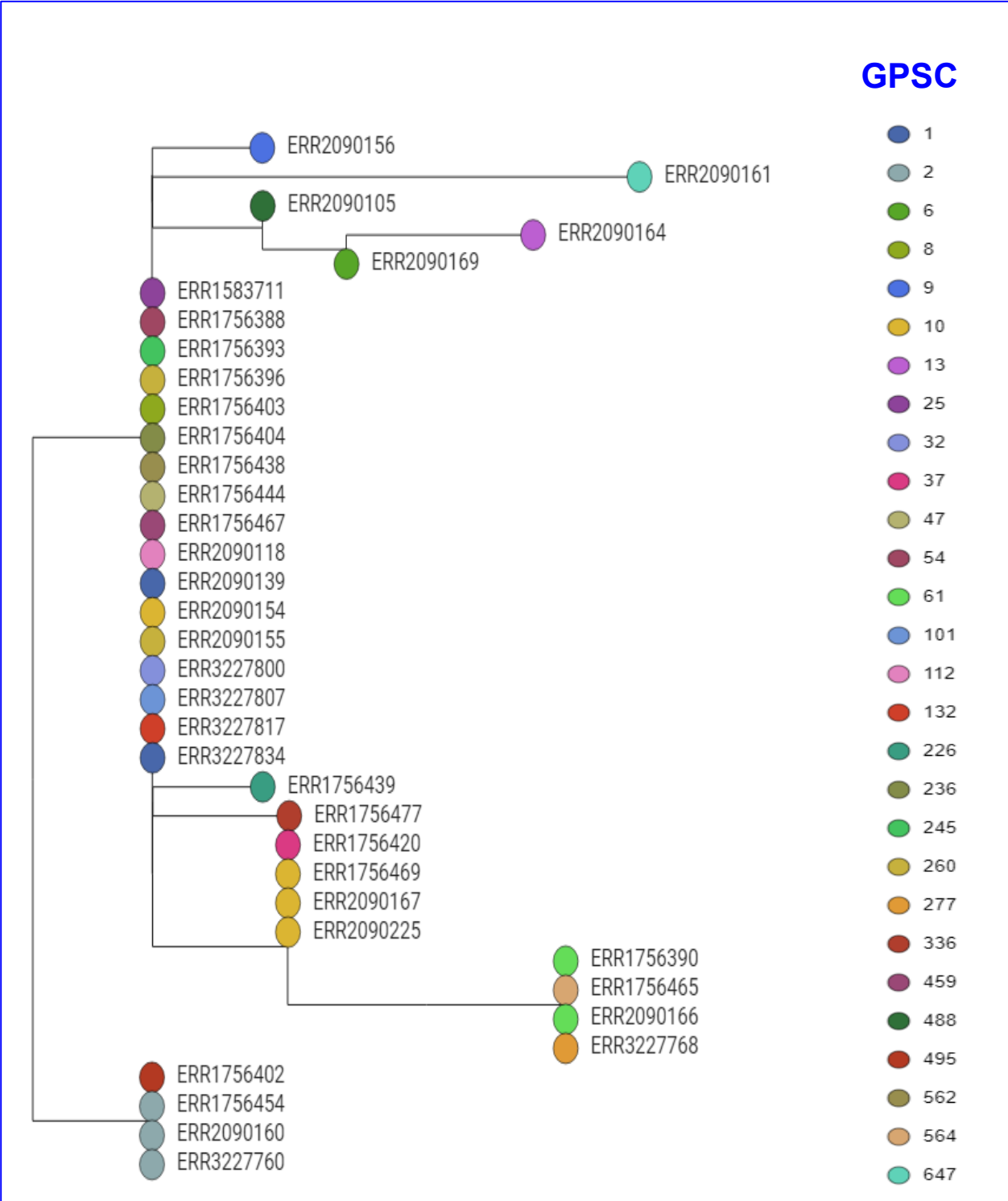


Figure 3. Phylogenetic tree based on *zmpB* gene variation by using the minimum evolution algorithm. Bootstrap values, based on 1000 replicates, are shown for major allelic variation in *zmpB* gene. The node representation is based on GPSC and the color for each GPSC is indicated by colored dots.

Conclusion:

The findings provide insight on the allelic variations of *zmpB*, indicating there is a high degree of polymorphism in the sequence of *zmpB* in pneumococci causing meningitis.

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