

GENOME ANALYSIS OF INVASIVE SEROTYPE 1 STREPTOCOCCUS PNEUMONIAE ISOLATES FROM INDIA (ID 768)

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Abstract

Background

Serotype 1 *Streptococcus pneumoniae* is a common cause of IPD in India. The present study describes the phylogeny, clonality and antimicrobial susceptibility pattern of the isolates collected in the pre-PCV era in India.

Methods

21 invasive serotype 1 pneumococcal isolates collected across India during 2009-2016, were sequenced on Illumina platform. Phylogenetic tree was built with REALPHY 1.12. Abricate software with VFDB was used to analyse virulence genes and CDC Pneumococcal specific pipeline was used for antimicrobial resistance gene identification.

Results

Population structure analysis of the strains showed that 20 of them belong to sequence cluster GPSC2 and one to GPSC31. MLST resolved the isolates to 8 known STs and four clonal complexes CC217, CC5191, CC5316 and CC303. CC217 (n=16) was the most prevalent clonal complex, followed by CC5191 (n= 3). 90% (n=19) of the isolates harboured the virulence factors, *lytA*, *nanA*, *hasC*, *pspA*, *srtG1*, *srtG2*. Phenotypic and genomic analysis demonstrated sensitivity to penicillin, erythromycin and vancomycin of all 21 isolates; six isolates were resistant to cotrimoxazole and one to tetracycline.

Conclusions

With the introduction of pneumococcal vaccine in the national immunization programme in 2017, this study provides baseline data for future analyses.