

GENETIC DIVERSITY OF CBPA AMONG INVASIVE STREPTOCOCCUS PNEUMONIAE ISOLATES FROM INDIA (ID 1152)

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Abstract

Background

Streptococcus pneumoniae is a human opportunistic pathogen responsible for morbidity and mortality worldwide. Pneumococcal surface protein, Choline-binding protein A (CbpA) plays a key biological role in nasopharyngeal colonization and modulating the immune response to pneumococci. We have analyzed the genetic diversity of *cbpA* in invasive isolates.

Methods

264 invasive *S.pneumoniae* isolates collected from 2010-2018, were sequenced on Illumina Platform. The CRL in-house bioinformatics pipeline was used to extract gene sequences, alignment and phylogeny analysis. Allelic variations of *CbpA* gene was analyzed by comparing the identity with a well-defined virulent strain of *S. pneumoniae* TIGR4.

Results

Gene *cbpA* was identified in 261(99%) of the 264 genomes. The sequences were highly polymorphic at both nucleotide and amino acid levels. Similarity of *cbpA* gene ranged from 65 – 98%, while 80- 99% homology was observed at amino acid level. Amino acid residues with similar physicochemical properties aligned allowing the identification of broadly conserved *CbpA* domains.

Conclusions

Due to high polymorphism at the *cbpA* locus, analysis of this loci from different isolates highlights how sequence diversity correlates with structural variation. The conserved epitope regions of the *CbpA* protein fragments can be exploited to develop more efficacious serotype-independent vaccines.