

# MOLECULAR EPIDEMIOLOGY OF PNEUMOCOCCUS ISOLATED FROM INVASIVE PNEUMOCOCCAL DISEASES BEFORE INTRODUCTION OF PCV-10 IN BANGLADESH, 2002-2015 (ID 1037)

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## Abstract

### Background

Bangladesh has been generating pneumococcal data since last 30 years to make an evidence-based data for vaccine introduction. This study is aimed to make a genomic characterization of pneumococcus isolated from pre-vaccine period.

### Methods

Whole-genome sequencing data of total 525 pneumococcus isolated from IPD, during 2002 to 2015, were analyzed using previously established methods.

### Results

Overall, 57 serotypes were identified, and most predominant serotypes were 2, 1, 14, 23F, 5, 19F, 12A and 45 which accounted for 50% of isolates. Serotype coverage were 47% for PCV10+6A, 50% for PCV13 and 58% for PCV20. The population was genetically diverse with 108 known and 61 new Sequence Types (STs), encompassing in 89 GPSCs. Among them, GPSC96 (serotype 2, n=66, 11.6%), GPSC 2 (serotype 1, n=48, 9%), GPSC 9 (serotype 14, n=32, 6%) were most predominant. Significant increase in resistance has observed for Erythromycin (0%-60%). Resistance is commonly seen in GPSC 10, 43, 101 and 482 mainly among serotype 19F, 23F, 6B and 7B, respectively.

### Conclusions

Pneumococcus in Bangladesh is diverse and different in respect of serotype, ST and GPSC. This data will work as the baseline population to monitor vaccine induced changes in molecular epidemiology.