

SEROTYPE, GENOTYPE AND ANTIBIOTIC RESISTANCE OF NON-VACCINE TYPE INVASIVE PNEUMOCOCCAL ISOLATES FROM PRE-VACCINE ERA (BEFORE 2018) - AN INDIAN STUDY (ID 1125)

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Presenter

Shincy M R, India

Authors

Shincy M R, India AKSHATA KRISHNA PRABHU, India Sravani Dharmavaram, India Nagaraj Geetha, India Stephen D. Bentley, United Kingdom Rebecca Gladstone, Norway Stephanie Lo, United Kingdom Robert F. Breiman, United States of America Lesley McGee, United States of America KL Ravikumar,

Abstract

Background

Pneumococcal Conjugate Vaccine (PCV) use has resulted in decrease of vaccine serotypes (VTs) and emergence of non-vaccine types (NVTs). We applied whole genome sequence (WGS) to predict serotype, sequence type (ST) and antibiotic resistance of NVT invasive pneumococcal isolates collected during the pre-vaccine era from Indian population.

Methods

96 NVT invasive isolates (2009-2017) collected across the country were sequenced on Illumina platform. Bioinformatic pipelines SeroBA and CDC pneumococcal pipeline for AMR calls were used for data analysis.

Results

Serotypes 15B (n=11), 24 (n=9) were dominant NVT types followed by 8 (n=8) and 34,10A,11A,16F (n=5). MLST resolved strains into 67 known STs. ST13727 (n=6) and ST2234 (n=5) were most common. Strains clustered in 45 clonal complexes and 16 singletons. The dominant clonal complex CC230 (n=12) was from serotypes 15B,15C,24,10A and 11A. 78(81%) of isolates were multidrug-resistant. Resistance genes for tetracycline (n=44), cotrimoxazole (n=41), erythromycin (n=34), penicillin (n=13) and chloramphenicol (n=2) were identified.

Conclusions

With the introduction of PCV in 2018 in national immunization program our data provides information for post-vaccination assessments. With higher valency vaccines coming to market by Indian manufacturers, knowledge of PCV13 NVT disease is important to identify serotypes to expand vaccine coverage in India.