GENOMIC SURVEILLANCE OF INVASIVE STREPTOCOCCUS PNEUMONIAE ISOLATES (SPN) IN BRAZIL, PERIODS PRE-(2008-2009) AND POST-PCV10 (2012-2013) INTRODUCTION (ID 464)

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Abstract

Background

In 2010, Brazil introduced PCV10 into the national children's immunization program. This study describes the genomic population structure of invasive SPN before and after PCV10 introduction.

Methods

As part of Global Pneumococcal Sequencing (GPS) project, 466 (pre-PCV10:n=232, post-PCV10:n=234; <5-year-olds:n=310, ≥5-year-olds:n=156) invasive SPN collected through national laboratory surveillance were whole-genome sequenced.

Results

The study identified 65 GPS clusters (GPSCs): 49 (88%) GPS previously described and 16 (12%) were Brazilian clusters. 36 GPSCs (55%) were non-PCV10 lineages, 11 (17%) PCV10/non-PCV10 and 18 (28%) PCV10. In both periods, the most frequent lineage was GPSC6/CC156/PMEN3/14-9V. Post-vaccine non-PCV10 lineages GPSC16/CC66/9N-15A, GPSC12/CC180/PMEN3/3 and GPSC32/CC218/PMEN24/12F increased; in <5-year-olds, GPSC1/CC320/DLV-PMEN14/19A, GPSC47/CC386/DLV-PMEN20/6C and GPSC51/CC458/3; and ≥5-year-olds GPSC3/CC53/PMEN33/8 were predominant (Figure-1).

SPN penicillin nonsusceptibility was predicted in 40%; 127 PBP combinations were identified (51 predicted MIC≥0.125mg/L); cotrimoxazole (folA+folP alterations), macrolide (mef/ermB/ermB+mef) and tetracycline (tetM/tetO/tetS/M) resistance were predicted in 46%, 13% and 21% SPN, respectively. In <5-year-olds, a penicillin (p=0.0169) and cotrimoxazole (p<0.0001) resistance reduction and an increase in tetracycline (p=0.019) were observed. Post-PCV10, PBP15-12-18(2mg/L) was frequent in lineage GPSC6/CC156/PMEN3/14-9V; among <5-year-olds the PBP13-11-16(4mg/L) in GPSC1/CC320/DLV-PMEN14/19A and PBP2-53-77(0.125mg/L) in GPSC47/ST386/DLV-PMEN20/6C were predominant.

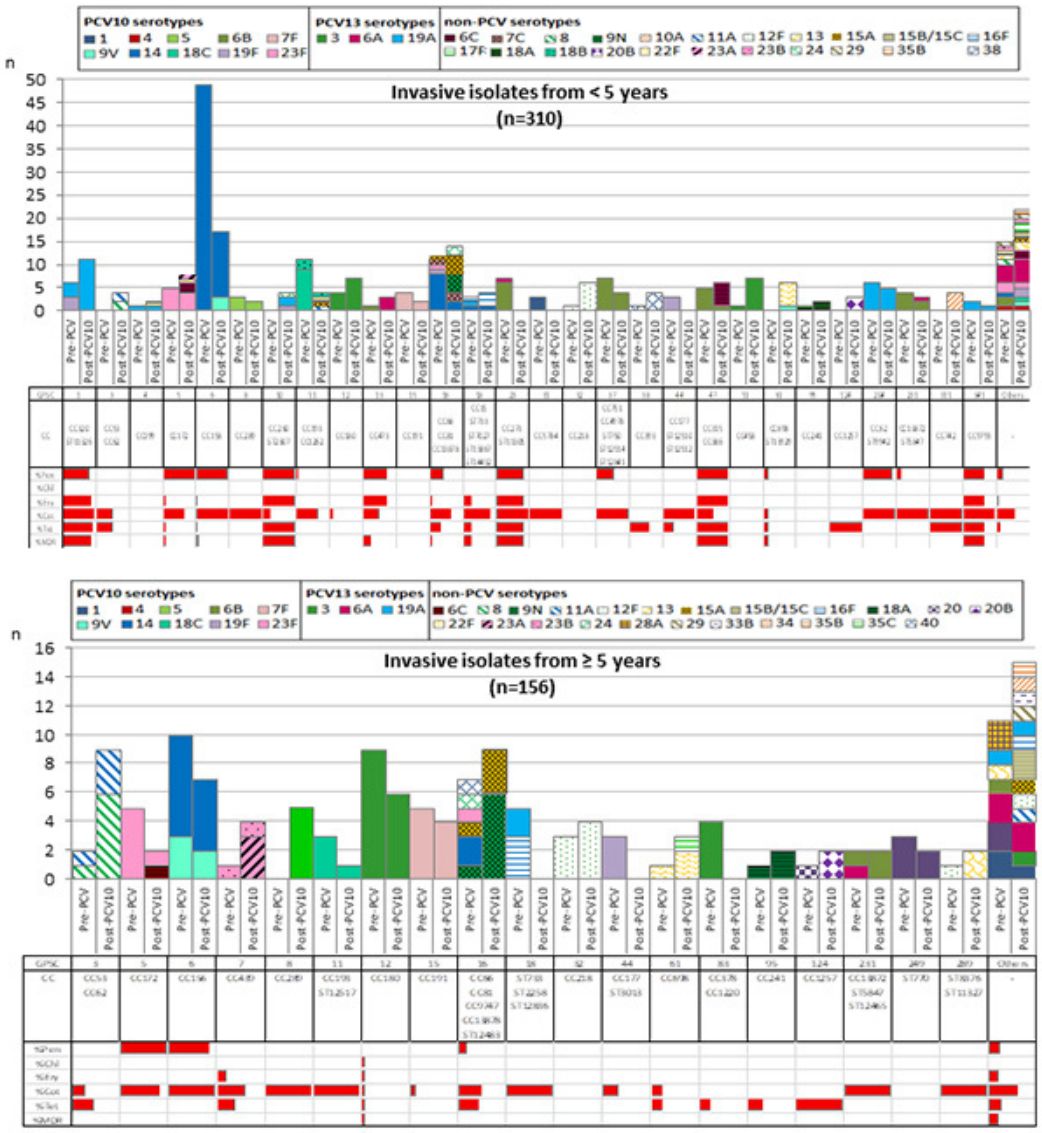

Figure-1. Dynamics of Global Pneumococcal Sequence Clusters (GPSCs) among invasive isolates from children aged <5-year and ≥5-year over vaccine periods in Brazil. The number of invasive pneumococcal disease is plotted by GPSC, with stratification into two vaccine periods (pre-PCV and post-PCV10), MLST clonal complex (CC) and antibiotic resistance pattern; and coloured by serotypes. The PCV10 and PCV13 serotypes are represented by solid fill while non-PCV serotypes by coloured hatched patterns.

Conclusions

Post-PCV10, important non-PCV10 lineages, GPSC1/CC320/DLV-PMEN14/19A and GPSC47/ST386/DLV-PMEN20/6C associated with multidrug resistance and GPSC12/CC180/PMEN31/3, GPSC3/CC53/PMEN33/8 and GPSC32/CC218/PMEN24/12F were identified in Brazil.