

PCV10 IMPACT ON PNEUMOCOCCAL LINEAGES ISOLATED FROM HEALTHY NEPALESE CHILDREN. (ID 736)

Presenter

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Abstract

Background

The 10-valent pneumococcal conjugate vaccine (PCV10) was introduced into the Nepalese infant immunisation schedule in August 2015. We aimed to examine how PCV10 introduction in affected pneumococcal lineages.

Methods

DNA from randomly selected nasopharyngeal pneumococcal isolates of healthy community-based Nepalese children in the Kathmandu valley pre- (2009-2014) and post-PCV10 (2017-2018) introduction, underwent whole-genome-sequencing on the Wellcome Sanger Institutes core sequencing pipeline. Isolates were clustered into lineages based on shared sequence and gene content using Population Partitioning Using Nucleotide K-mers (PopPUNK) software.

Results

313 and 284 pre- and post-PCV10 isolates were sequenced. There was a significant reduction in the proportion of PCV10 serotypes when comparing pre 73/313 (23.3%) with post 37/284 (13%) PCV10 samples ($p=0.0014$). Overall 122 distinct lineages were identified, 98 pre- and 74 post-PCV10. Simpson's index of diversity for the lineages was 0.992 and 0.987 pre- and post-PCV10 respectively. Within the 3 largest PCV10 serotype lineages there were no examples of non-PCV10 serotype isolates pre-vaccination, whereas all 3 lineages contained non-PCV10 serotypes post-vaccination.

Conclusions

PCV10 serotype prevalence significantly declined following PCV10 introduction. However, strain diversity remained high post-PCV10 and there is evidence suggestive of vaccine escape via capsular-switching among lineages possessing predominantly vaccine-covered capsules prior to PCV10 introduction.