

GENOME-WIDE ASSOCIATION STUDY OF COLONISING NASOPHARYNGEAL PNEUMOCOCCI OBTAINED FROM CHILDREN IN NEPAL TO IDENTIFY GENES ASSOCIATED WITH PNEUMONIA. (ID 729)

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Abstract

Background

Identifying the molecular characteristics of pneumococci associated with disease may inform development of new clinical interventions. We aimed to perform a bacterial genome-wide association study to identify pneumococcal genes associated with carriage among children with pneumonia.

Methods

DNA from nasopharyngeal pneumococcal isolates obtained from Nepalese children admitted to hospital with pneumonia (cases) and healthy community-based children (controls), underwent whole-genome-sequencing on the Wellcome Sanger Institutes core sequencing pipeline. The association of variants from sequences mapped against the *S. pneumoniae* ATCC700669 genome, with cluster of orthologous groups using a fixed effects model, was performed using a python based sequence element enrichment analysis.

Results

245 case and 597 control isolates were sequenced. 405461 variants were identified and 31708 tested after filtering. 20 variants from colonising bacteria had a strong association ($p < 10^{-8}$) with pneumonia. 18/20 of these variants were located within the *lacE2* gene. The variant with the strongest association, presence of an A allele at position 1066739, was identified in 240/597 (40%) of controls and 150/245 (61%) of cases ($p = 10^{-10}$).

Conclusions

In this study in Nepal the pneumococcal gene *lacE2* was associated with colonisation in children with pneumonia. Studies examining the role of *lacE2* in the pathogenesis of pneumococcal pneumonia are needed.