SPATIAL DISTANCE IS A KEY DETERMINANT OF PNEUMOCOCCAL STRAIN SHARING AND THE SUSTAINED CARRIAGE OF SHARED STRAINS (ID 957)

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Abstract

Background

We sought to understand the dynamics of Streptococcus pneumoniae strain sharing among rural Gambian infants followed up longitudinally during the first year of life.

Methods

We implemented a reference free phylogenetic method to compute whole genome pairwise genetic differences between 1074 pneumococcal nasopharyngeal isolates from 102 healthy infants recruited from 21 villages. We studied the role of spatial distance between villages as a determinant of strain sharing and the relationship between sharing and prolonged colonization.

Results

Approximately 70% of strains were shared by multiple infants. The pairwise SNP distances between strains from a close geographic proximity were significantly lower compared to strains recovered over longer distance distances (p-value <0.005). Infants were significantly more likely to both sustain a shared strain if they resided in villages within a 5km radius of each other (p-value < 0.0005, OR 3.742, 95% CI 1.874-7.596). Conversely, if the infants were both transiently colonized by the shared strain they were significantly more likely to reside in villages separated by over 15 km (p-value < 0.05, OR 1.501, 95% CI 1.061 to 2.098).

Conclusions

Spatial distance is an important determinant of strain sharing and our data suggests repeated exposure may play a role in sustained carriage of a shared strain.