GENETIC VARIATION ASSOCIATED WITH SEROTYPE 19A VACCINE FAILURES IN IRELAND (ID 1139)

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Abstract

Background

Ten of sixteen (62.5%) vaccine failures from IPD surveillance in Ireland, after PCV introduction, were serotype 19A. We aimed to identify genetic features that might explain the vaccine failures.

Methods

Serotype 19A IPD isolates from 2007-18 in Ireland were illumina sequenced. Genomes (n=302) were assigned to Global Pneumococcal Sequence Clusters (GPSCs) and MLST. The pangenome was defined using Roary, and genes associated with phenotype identified with Scoary. Pyseer was used to test for lineage effects and association of phenotype with sequence variation. Irish isolates of GPSC1 (n=48) were mapped with international GPSC1 isolates of ST320 (n=204) to produce a recombination free tree with Gubbins.

Results

Most 19A vaccine failures (8/10) were in the predominant 19A GPSC post-PCV13 - GPSC1. There was a significant lineage effect ($p<0.05$) for GPSC1 and vaccine failures. Twenty-five of the Irish GPSC1 isolates shared a common ancestor within the international GPSC1 isolates, including 5/8 of the GPSC1 vaccine failures. A specific allele of GalE was associated with this sub-cluster.

Conclusions

GalE encodes for UDP-galactose 4-epimerase which has been reported to affect CPS production. The association of a GalE allele with the clade containing the most vaccine failures offers a plausible explanation for these 19A vaccine failures, worthy of further investigation.