

Euclidian distances (EuD) of each OG tree with the ribosomal protein encoding tree resulted in three distributions of distances. To reach an alignment with high phylogenetic resolution, the sequences from OGs whose phylogenies were similar to the ribosomal phylogeny ($\text{EuD} \leq 0.03$) were concatenated to the ribosomal alignment to give a single reduced 'core' super-alignment. Finally, polymorphic regions of this super-alignment were extracted and re-analyzed with RAXML using a general time-reversible (GTR) nucleotide substitution model. Core OG diversity was determined by comparing the average of the pairwise distances between the isolates per year. The reduced core super-alignment was also analyzed using BAPS; Bayesian Analysis of Population Structure software⁴⁶ to determine the sequence clusters. Two runs of 40 and 50 maximum clusters were performed, each creating 12 largely monophyletic sequence clusters and an extra 'sink' cluster that incorporated all unclassified isolates. Visualization of the tree was performed using iTOL⁴⁷.

Analysis of the population structure. Core genomes and whole genomes of strains with a capsule switched serotype were separately aligned in Mauve⁴⁸, along with their closest neighbors (Supplementary File 1). SNP coordinates were isolated and characterized in Artemis⁴⁹.

Genomic diversity and dynamics. The genomic diversity was determined based on the strains' accessory genomes. For each OG a binary measure of presence (1) or absence (0) of a representative protein from a given strain was generated. The contribution of each strain to an OG was therefore denoted by a single numeric value (1 or 0) to represent the presence or absence of a gene, or a group of paralogs in a certain strain. This information was collated into a gene presence/absence matrix (Supplementary File 2). Using the method described by Dutilh *et al.*⁵⁰, the genomic variations among strains collected within each year were calculated. Core OGs (those constituted of a single gene from each of the analyzed isolates) were excluded from this analysis.

The time frames applied to detect changes in the proportion of strains carrying a certain OG post PCV7 compared to before were 2001 to 2006; pre-vaccine, and 2008 to 2011; post-vaccine respectively.

Statistical analysis. The difference in phylogenetic distance among strains collected between 2001 to 2006 and 2007 was tested by an unpaired t-test. Differences in pre- and post-vaccine gene frequencies were tested by Fisher Exact test. For all analyses, the significance level was set at 0.05.

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