

## Genomic characterisation of *Streptococcus pneumoniae* vaccine serotypes pre- and post-PCV introduction in The Netherlands.

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**Background:** In 2006, PCV7 vaccine was introduced in the Netherlands paediatric immunization programme and replaced by PCV10 in 2011. This study characterises *Streptococcus pneumoniae* blood isolates recovered from patients from Nijmegen, the Netherlands before PCV (n=191;2000-2005), and when PCV7 (n=226;2006-2010) and PCV10 (n=563;2011-2020) were introduced.

**Methods:** Genome sequences of 1004 *S. pneumoniae* isolates were clustered into Global Pneumococcal Sequence Clusters (GPSC) using PopPUNK. Serotype and antibiotic susceptibility were predicted using SeroBA and CDC AMR pipeline, respectively. A phylogeny was generated using FastTree.

**Results:** Before PCV introduction frequent GPSCs included GPSC15 (9.4%), GPSC995;3 (9.4%) and GPSC27 (7.9%). In the post-PCV7 period GPSC31 (12.8%), GPSC15 (12.4%) and GPSC995;3 (9.7%) were the most frequent. GPSC3 (20.2%), 15 (9.2%) and 995;3 (7.8%) were the most common after PCV10 introduction.

After PCV introduction, PCV7 and PCV10 serotypes percentages (59.6%) decreased when comparing post-PCV7 (56.1%) and post-PCV10 (18.8%) percentages. In the post-PCV7 period, PCV7 serotypes (30%) decreased in comparison to the pre-PCV period (41.3%). And PCV10 serotypes 7F (13.3%) and 1 (12.8%) became more frequent when compared with the pre-PCV period (9.9% and 6.3%, respectively). PCV7 serotypes decreased further in the post-PCV10 period to 4.3%. PCV10 serotype 7F decreased to 9.4%, and serotype 1 decreased to 4.4%.

Antibiotic susceptibility to beta-lactams and macrolides was high among the *S. pneumoniae* population studied pre- and post- PCV introduction (pre-PCV 91.1% to 100%, post-PCV7 and PCV10 92.7% to 100% and 96.1% to 100%, respectively).

**Conclusions:** Pneumococcal serotypes and GPSCs have changed over time suggesting that PCV introduction has impacted the invasive *S. pneumoniae* population in the Netherlands.