

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

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Background

The PCV7 vaccine was introduced in the Netherlands paediatric immunization in 2006 and was replaced by PCV10 in 2011.

This study characterised 1004 *S. pneumoniae* blood isolates recovered from patients from four different hospitals in the Netherlands. This collection included 980 isolates that were from the Nijmegen area and 24 penicillin-resistant isolates were selected from the Dutch Reference Laboratory for Bacterial Meningitis.

The collection was recovered from patients across age groups: 0-13 years old (n=44), 16-50 years old (n=168), and >50 years old (n=767)

Aim

We aimed to investigate the changes in serotype and relate it to lineages during the introduction of PCVs

Methods

Each pneumococcal genome was assigned a pneumococcal lineage or Global Pneumococcal Sequence Clusters (GPSC) using PopPUNK, serotype using SeroBA, antimicrobial susceptibility using an AMR pipeline developed by the US CDC. A phylogeny was generated using FastTree.

The isolates were grouped into Pre-PCV period (n=191; 2000-2005), and PCV7 period (n=226; 2006-2010) and PCV10 period (n=563; 2011-2020). Changes in serotype groups were detected using the Fisher's Exact Test.

Results

The PCV10 serotypes have significantly reduced in PCV10 period, as compared with pre-PCV (60% vs 19%, p value < 0.05) while significantly increasing in NVTs serotypes (40% vs 81%, p value < 0.05, Figure 1)

After the PCV10 introduction, the top-five serotypes were serotype 8 (n=135, 24%), 7F (n=53, 9.4%), 3 (n=43, 7.6%), 19A (n=48, 8.5%) and 1 (n=25, 4.4%) (Figure 2).

Among them, serotype 8, 3 and 19A were not included in the current PCV10, but serotype 3 and 19A were included in PCV13, and serotype 8 in PCV20 (only approved for adult use at present).

In the PCV10 period, GPSC3 (n=158, 28.6%) was the major pneumococcal lineage accounting for 95% of the serotype 8 (n=128) isolates.

The majority of serotype 3 isolates belonged to GPSC12 (93%; n=40) with two isolates belonging to GPSC35 (4.7%) and one isolate to GPSC83 (2.3%)

Serotype 1 isolates were all expressed by GPSC31.

Serotype 19A isolates were expressed by 11 GPSCs, including GPSC4 (48%, n=23), GPSC18 (2%, n=1), GPSC10 (3%, n=3), GPSC1 (2%), GPSC197 (8%, n=4), GPSC146 (12.5%, n=6), GPSC109 (12.5%, n=6), GPSC17 (2%, n=1), GPSC11 (2%, n=1), GPSC99 (2%, n=1) and GPSC5 (2%, n=1)

Serotype 7F isolates belonged to two GPSCs. GPSC15 (98%, n=52) and GPSC32 (1.8%, n=1) (Figure 3).

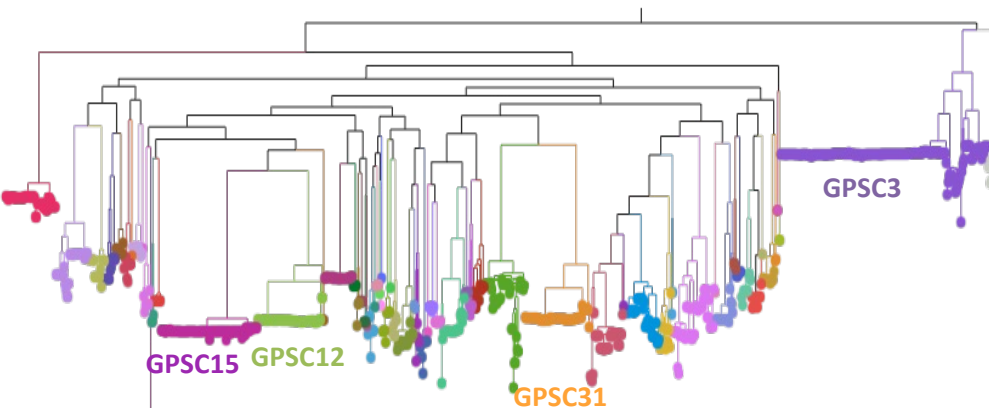


Figure 3: Maximum likelihood phylogeny of the population with the different colours indicating different GPSCs. The major GPSCs expressed by the top-five serotypes in the PCV10 period are indicating in the labels.

Serotype Percentage per PCV period

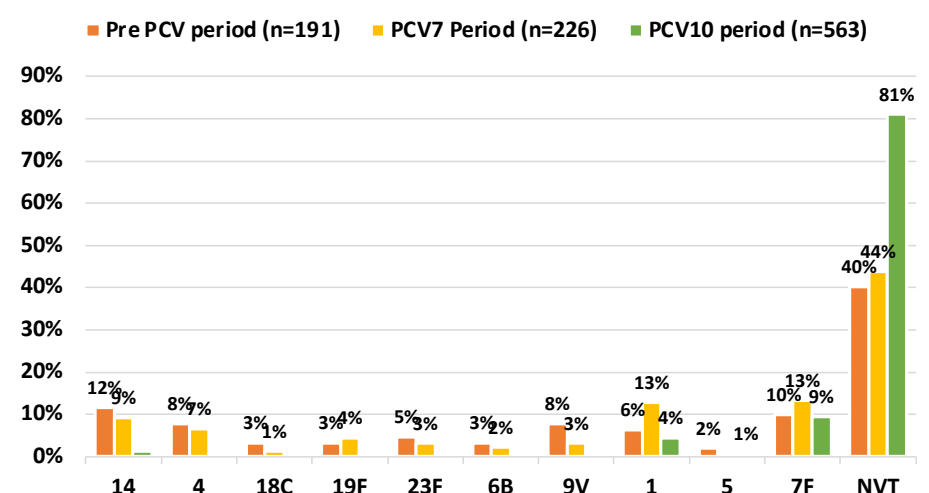


Figure 1: Distribution in percentage of vaccine serotypes and non vaccine serotypes (NVTs).

PCV10 period Serotype Distribution

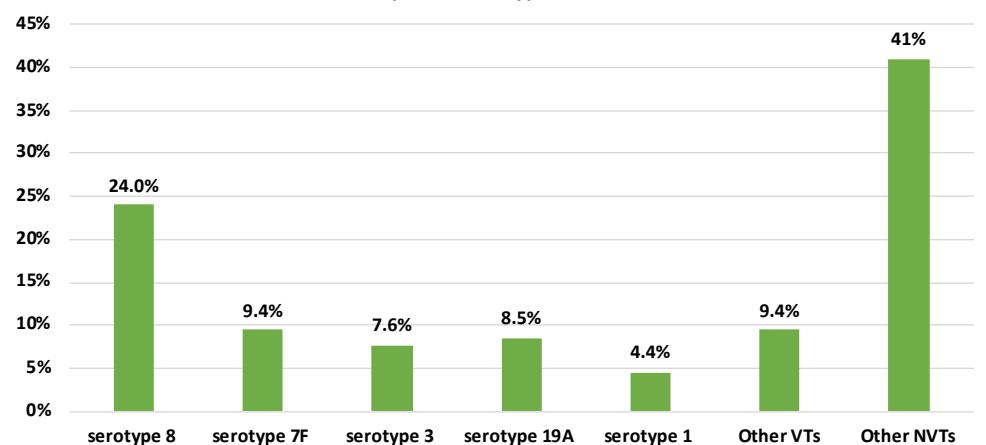


Figure 2: Distribution in percentage of the top-five serotypes found after introduction of the PCV10 and percentage of other vaccine serotypes (VTs) and non vaccine serotypes (NVTs) in this period.

Conclusion:

We observed early signals of vaccine-driven perturbation in the disease-causing pneumococcal population. Serotype 8 is the emerging serotype in the Netherlands, similarly to findings also observed in other European countries.