Population genomics reveals vaccination-induced genotypic changes in carried pneumococcal population

Christina CHAGUZA1,2, Ellen HEINSBROEK2,3, Maaske ALAERTS2,3, Rebecca A. GLADSTONE1, Chikondi PENO2,3, Jennifer E. CORNICK2,3, Patrick MUSICA2,4,7, Naor BAR-ZEEV2,3, Arox KAMINGONA1,2,3, Aras KADIOGLU1,2, Lesley MCGEE4,5, Robert F. BREIMAN1,6, William P. HANGSEG, Robert S. HEYDERMAN1,5, Neil FRENCH2,3, Stephen D. BENTLEY1,2,4,5, & Dean B. EVERETT2,3,5,7,*

1Wellcome Sanger Institute, 2University of Liverpool, 3Malawi-Liverpool-Wellcome Trust Clinical Research Programme, 4Public Health England, 5University of Antwerp, 6Mahidol Oxford Tropical Medicine Research Unit, 7University of Oxford, Johns Hopkins Bloomberg School of Public Health, 8University of Malawi College of Medicine, 9Centers for Disease Control and Prevention, 10University College London, 11Emory University, 12Harvard T.H. Chan School of Public Health, 13The University of Cambridge, 14The University of Edinburgh

† Joint Senior Authors.  * Correspondence: Chrispin.Chaguza@sanger.ac.uk

Recent clinical trials globally have increasingly demonstrated the effectiveness of PCV13 Streptococcus pneumoniae (Spn) vaccine but population-wide vaccine-induced perturbations in Spn populations remain poorly understood. To assess the vaccine-driven epidemiological, genomic and ecological changes in healthy Spn carriers following PCV13 introduction in a previously naïve setting in northern Malawi, we characterised the genetic population structure, strain type and lineage diversity, antibiotic resistance and accessory genome dynamics of whole genome sequenced carried Spn strains sampled pre- and post-PCV13 introduction. Because carriage remains largely unchanged post-PCV, ‘frequency’ means proportion among carriers.

Key Findings & Conclusions

1. Significant fluctuation of strain types and lineages among Spn carriers pre- and post-vaccination (Fig. 1a-b).
2. Significant reduction in frequency of VT strains in under-fives consistent with findings in Fig1. Majority of the changes occurred in mobile genetic elements and bacteriocin associated genes consistent with recent findings in carried Spn in the USA3.
3. These findings reveal high-resolution insights into the genotypic changes in Spn carriage post-vaccination but continued surveillance remain crucial to monitor population changes such as expansion of replacement NVT serotypes.

References