

# New Adventures in NTHi

David W. Cleary<sup>1,2</sup>, Vanessa T. Devine<sup>1,3</sup>, Denise E. Morris<sup>1</sup>, Karen L. Osman<sup>1</sup>, Rebecca A. Gladstone<sup>4</sup>, Stephen D. Bentley<sup>4</sup>, Saul N. Faust<sup>1,2,5</sup> and Stuart C. Clarke<sup>1,2,6</sup> (<sup>1</sup>Faculty of Medicine and Institute for Life Sciences, University of Southampton <sup>2</sup>NIHR Southampton Biomedical Research Centre; <sup>3</sup>Northern Ireland Centre for Stratified Medicine and Clinical Translational Research Innovation Centre, Ulster University; <sup>4</sup>Pathogen Genomics, Wellcome Trust Sanger Institute; <sup>5</sup>NIHR Southampton Clinical Research Facility, University Hospital Southampton Foundation NHS Trust; <sup>6</sup>Global Health Research Institute, University of Southampton)

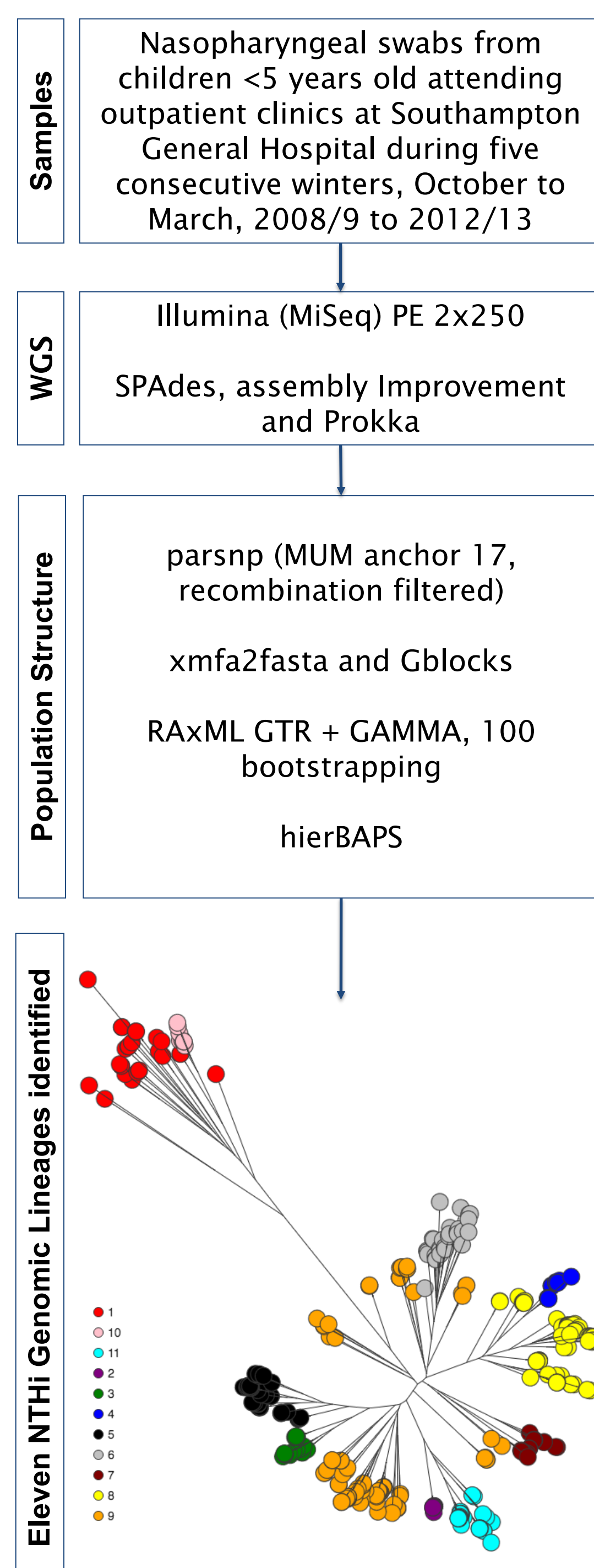
## Pneumococcal vaccine impacts on the population genomics of non-typeable *Haemophilus influenzae*

Background: Widespread use of pneumococcal conjugate vaccines (PCVs) have reduced the disease burden from *Streptococcus pneumoniae* and altered the epidemiology of circulating serotypes. The indirect impacts on other members of the respiratory niche in which pneumococci reside have been less well studied. There is evidence that one such effect has been the increased carriage of non-typeable *Haemophilus influenzae* (NTHi), an opportunistic pathogen capable of causing both invasive and non-invasive disease. Although not ubiquitous, this outcome has been seen with PCV vaccines rather than those with a *Haemophilus*-protein conjugate.

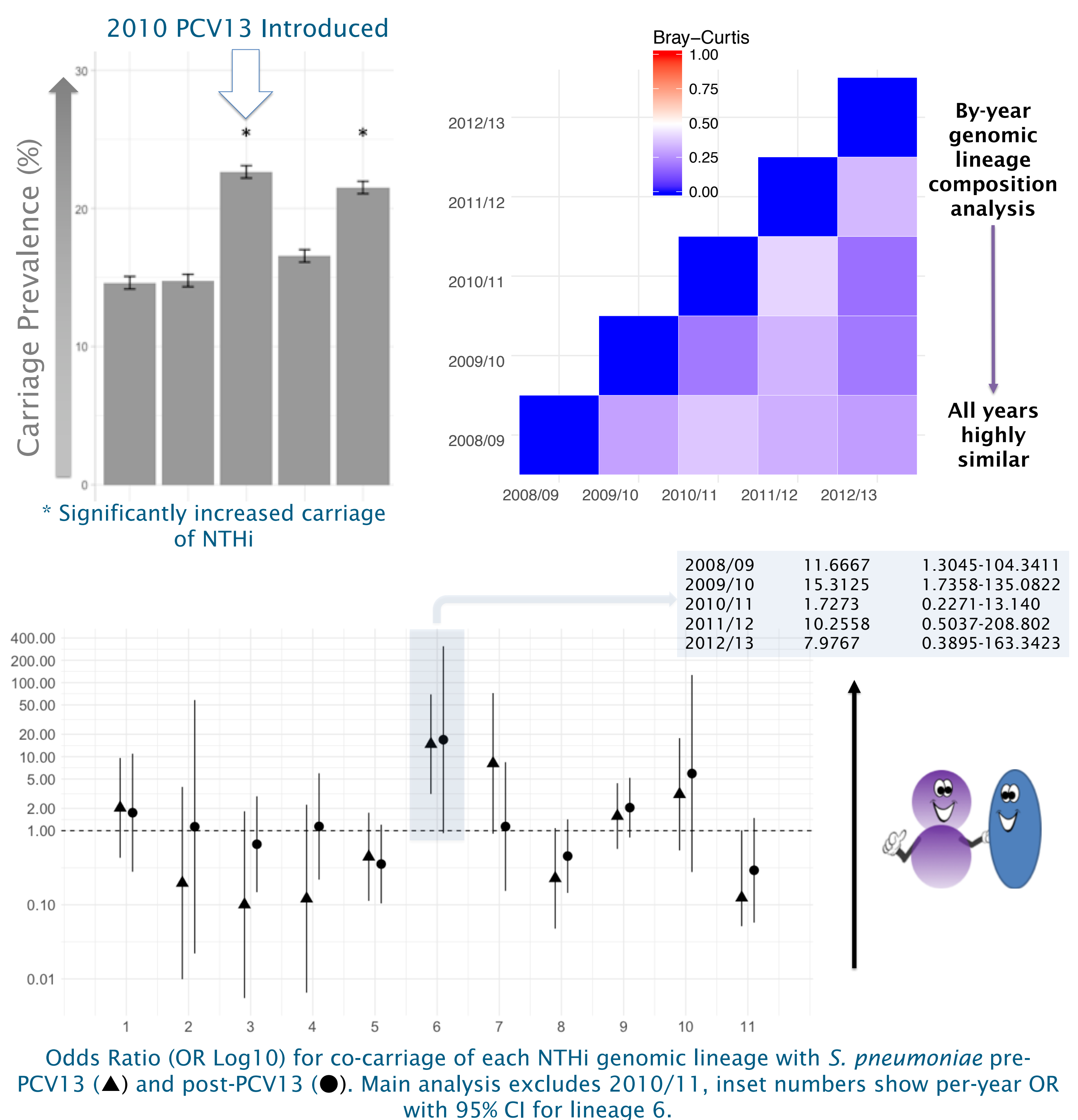
### Aims

Determine the population epidemiology of NTHi before, during and after the implementation of PCV13.

### Methods



### Results



### Conclusions

- NTHi were characterised into eleven discrete, temporally stable lineages.
- Significantly increased carriage in post-PCV13 years was observed. Increase could not be linked to the expansion of a particular clone.
- Lineage-specific associations with *S. pneumoniae* were observed.