



## International links between *Streptococcus pneumoniae* vaccine serotype 4 sequence type (ST) 801 in Northern European shipyard outbreaks of invasive pneumococcal disease



R.A. Gladstone<sup>a,b,\*</sup>, L. Siira<sup>c</sup>, O.B. Brynildsrud<sup>d</sup>, D.F. Vestrheim<sup>d</sup>, P. Turner<sup>e,f</sup>, S.C. Clarke<sup>g,h,i,j,k</sup>, S. Srifuengfung<sup>l</sup>, R. Ford<sup>m</sup>, D. Lehmann<sup>n</sup>, E. Egorova<sup>o</sup>, E. Voropaeva<sup>o</sup>, G. Haraldsson<sup>p</sup>, K.G. Kristinsson<sup>p</sup>, L. McGee<sup>q</sup>, R.F. Breiman<sup>r,s</sup>, S.D. Bentley<sup>b</sup>, C.L. Sheppard<sup>t</sup>, N.K. Fry<sup>t,u</sup>, J. Corander<sup>a,b</sup>, M. Toropainen<sup>c</sup>, A. Steens<sup>d</sup>, The Global Pneumococcal Sequencing Consortium<sup>1</sup>

<sup>a</sup> Department of Biostatistics, Institute of Basic Medical Sciences, University of Oslo, Oslo, Norway

<sup>b</sup> Parasites and Microbes, Wellcome Sanger Institute, Cambridge, UK

<sup>c</sup> Department of Health Security, Finnish Institute for Health and Welfare (THL), Helsinki, Finland

<sup>d</sup> Division of Infection Control and Environmental Health, Norwegian Institute of Public Health, Oslo, Norway

<sup>e</sup> Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK

<sup>f</sup> Cambodia Oxford Medical Research Unit, Angkor Hospital for Children, Siem Reap, Cambodia

<sup>g</sup> Faculty of Medicine and Institute of Life Sciences, University of Southampton, UK

<sup>h</sup> NIHR Southampton Biomedical Research Centre, University Hospital Southampton NHS Trust, Southampton, United Kingdom

<sup>i</sup> Global Health Research Institute, University of Southampton, Southampton, United Kingdom

<sup>j</sup> School of Postgraduate Studies, International Medical University, Kuala Lumpur, Malaysia

<sup>k</sup> Centre for Translational Research, IMU Institute for Research, Development and Innovation (IRDI), Kuala Lumpur, Malaysia

<sup>l</sup> Faculty of Pharmacy, Siam University, Bangkok, Thailand

<sup>m</sup> Papua New Guinea Institute of Medical Research, PO Box 60, Goroka 441, Eastern Highlands Province, Papua New Guinea

<sup>n</sup> Telethon Kids Institute, the University of Western Australia, Perth, WA, Australia

<sup>o</sup> G.N. Gabrichevsky Research Institute for Epidemiology and Microbiology, Moscow, Russia

<sup>p</sup> Department of Clinical Microbiology, Landspítali – The National University Hospital of Iceland, Reykjavik, Iceland and Faculty of Medicine, University of Iceland

<sup>q</sup> Centers for Disease Control and Prevention, Atlanta, USA

<sup>r</sup> Emory Global Health Institute, Atlanta, USA

<sup>s</sup> Rollins School Public Health, Emory University, USA

<sup>t</sup> Vaccine Preventable Bacteria Section, Public Health England - National Infection Service, London, United Kingdom

<sup>u</sup> Immunisation and Countermeasures Division, Public Health England - National Infection Service, London, United Kingdom

### ARTICLE INFO

#### Article history:

Received 22 April 2021

Received in revised form 1 September 2021

Accepted 20 October 2021

Available online 5 January 2022

#### Keywords:

*Streptococcus pneumoniae*

Pneumococcal

Whole genome sequencing

Outbreak

ST801

Molecular epidemiology

Serotype 4

PCVs

PPV23

### ABSTRACT

**Background:** Pneumococcal disease outbreaks of vaccine preventable serotype 4 sequence type (ST)801 in shipyards have been reported in several countries. We aimed to use genomics to establish any international links between them.

**Methods:** Sequence data from ST801-related outbreak isolates from Norway (n = 17), Finland (n = 11) and Northern Ireland (n = 2) were combined with invasive pneumococcal disease surveillance from the respective countries, and ST801-related genomes from an international collection (n = 41 of > 40,000), totalling 106 genomes. Raw data were mapped and recombination excluded before phylogenetic dating.

**Results:** Outbreak isolates were relatively diverse, with up to 100 SNPs (single nucleotide polymorphisms) and a common ancestor estimated around the year 2000. However, 19 Norwegian and Finnish isolates were nearly indistinguishable (0–2 SNPs) with the common ancestor dated around 2017.

**Conclusion:** The total diversity of ST801 within the outbreaks could not be explained by recent transmission alone, suggesting that harsh environmental and associated living conditions reported in the shipyards may facilitate invasion of colonising pneumococci. However, near identical strains in the Norwegian and Finnish outbreaks does suggest that transmission between international shipyards also

\* Corresponding author at: Department of Biostatistics, University of Oslo, P.O. Box 1122, 16 Blindern, 0317 Oslo, Norway.

E-mail address: [r.a.gladstone@medisin.uio.no](mailto:r.a.gladstone@medisin.uio.no) (R.A. Gladstone).

<sup>1</sup> The Global Pneumococcal Sequencing Consortium Collaborators are available in the online version.