

Three deadly bacteria families responsible for nearly 60 percent of meningococcal cases

October 28 2015

Scientists at Oxford University have identified the key groups of bacteria responsible for the majority of meningococcal disease cases in England and Wales over the past 20 years.

Genome analysis of 899 individual bacterial isolates revealed the presence of 20 families, or [lineages](#), of the bacterium *Neisseria meningitidis* in England and Wales over the two-year period between 2010 and 2012. But only three of these lineages caused 59% of cases. Researchers were able to compare this with previous data to shed light on [disease](#) fluctuations over more than 20 years.

The researchers found strong associations between bacterial lineages and particular age groups, meaning these results - and those from similar studies carried out in the future - will play an important role in making sure meningitis vaccines are as effective as possible.

Meningococcal disease, caused by *Neisseria meningitidis*, or meningococcus, is one of the major causes of meningitis and septicaemia worldwide. At least 10% of those who develop the disease will die (the rates are higher with some strains of the disease), and many more will be left with serious disabilities such as amputations or brain damage.

The Oxford research, which generated and analysed the genetic blueprints and stored them in the Meningitis Research Foundation Meningococcus Genome Library (MRF-MGL), is published in the

journal *The Lancet Infectious Diseases*.

Professor Martin Maiden, Professor of Molecular Epidemiology at Oxford University, leads the Oxford research into *Neisseria meningitidis*. He said: 'It is hugely important to have high-quality, high-resolution information on bacterial lineages.'

'Meningococcal disease has been around for a long time and has undergone wide fluctuations in incidence. Having access to a coherent set of genomic sequence data for *Neisseria meningitidis* will enable clinicians and [scientists](#) to recognise patterns in disease trends, predict outbreaks, develop targeted interventions and evaluate how well vaccines are working.'

'This will be particularly important for monitoring the success of the new MenB vaccine (Bexsero), which was introduced to the UK childhood immunisation programme in September.'

Meningococci taken from patients with the disease in England and Wales are routinely submitted to the Public Health England Meningococcal Reference Unit (PHE-MRU), where the strain of the disease-causing bacterium is identified. In 2010, a collaboration was formed comprising PHE-MRU, the Wellcome Trust Sanger Institute, and the University of Oxford.

Through this partnership, the complete genetic blueprints of all disease-causing meningococci isolated in England, Wales and Northern Ireland have been assembled, annotated and published online in the MRF-MGL.

The Oxford study, 'Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study', is published in *The Lancet Infectious Diseases*.

More information: Dorothea M C Hill et al. Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study, *The Lancet Infectious Diseases* (2015). [DOI: 10.1016/S1473-3099\(15\)00267-4](https://doi.org/10.1016/S1473-3099(15)00267-4)

Provided by Oxford University

Citation: Three deadly bacteria families responsible for nearly 60 percent of meningococcal cases (2015, October 28) retrieved 27 April 2024 from <https://medicalxpress.com/news/2015-10-deadly-bacteria-families-responsible-percent.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.