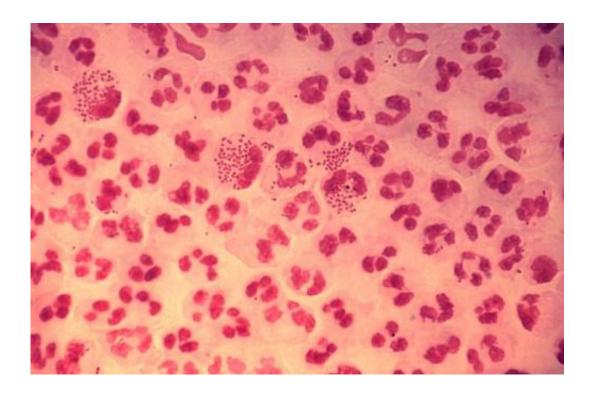


Gene sequencing offers way to beat global spread of gonorrhea

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Credit: CDC

With drug-resistant strains of sexually-transmitted infection gonorrhoeae increasing, scientists from Brighton, Oxford University and Public Health England have found that genetic sequencing can track the spread of infection. They show coordinated national and international strategies are required to stop drug-resistance spreading further.



Their study, funded by the National Institute for Health Research (NIHR) Oxford Biomedical Research Centre (BRC) and the NIHR Healthcare-Associated Infections and Antimicrobial Resistance Health Protection Research Unit (HPRU), is published in *The Lancet Infectious Diseases* today.

Using samples collected in Britain and the USA they aimed to find out if they could identify genetic evidence that individual cases were linked to each other.

Dr John Paul from Public Health England said: "There are 78 million cases of gonorrhoeae across the world each year, with almost 35,000 in England in 2014, an increase of 19% on the previous year. However, not all cases lead to obvious symptoms, meaning that some people may go untreated and unaware, spreading the disease. The usual way to understand how a disease is spreading is by partner-tracing but this relies on people knowing and being willing to report who they have had sex with."

The team used just under 1300 samples of gonorrhoea collected in Brighton between 2011 and 2015. They compared these samples to each other and to samples from London, Wales, northern England and the USA using a new genetic sequencing-based tool they developed for tracking gonorrhoea spread. Unsurprisingly most infections were acquired from someone in the same city. Three-quarters of infections in Brighton could be linked to earlier Brighton cases.

They also found evidence of gonorrhoea spreading to and from Brighton from the rest of the UK and the US. Despite including fewer samples from outside Brighton, 18% of Brighton infections were connected to cases elsewhere in the UK and 9% to cases in the USA, including drugresistant infections found in Brighton and across the USA.



Dr David Eyre, who co-led the study, from Oxford University said:
"There are several potential applications of this study. It clearly shows that action to tackle antibiotic-resistant gonorrhoea needs to be coordinated across national boundaries. However, using whole genome sequencing to track transmission of these infections is feasible.

Sequencing can overcome some of the weaknesses in traditional partner notification tracing, while at the same time enabling us to spot risk factors and better target health interventions. It could even be used to notify contacts by using the same apps used to set up sexual encounters."

More information: Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae: an observational study, *The Lancet Infectious Diseases*, DOI: 10.1016/S1473-3099(16)30157-8

Provided by University of Oxford

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