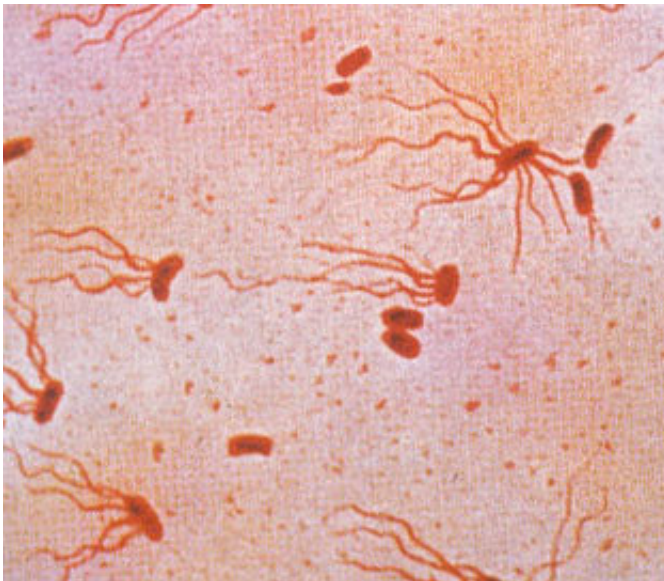


Tracing travelers' typhoid to get an early warning of emerging threats

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Salmonella typhi. Credit: Wikipedia

Salmonella enterica serovar *Typhi* causes more than 20 million cases of typhoid fever each year, and disproportionately infects children in low and middle income countries. Now, in a paper published in *PLOS Neglected Tropical Diseases*, researchers demonstrate how routine data collected by Public Health England (PHE) can be used to gain insight into the genomics of *S. Typhi* in countries around the world, providing an early warning system for emerging threats such as antibiotic resistance and disease outbreaks abroad.

Typhoid fever is a bacterial infection that can spread throughout the body. Without prompt treatment, it can cause serious complications and can be fatal. There are growing concerns about multi-drug resistant *S. Typhi*, with different forms of the bacteria showing resistance to different classes of drugs. Using Whole Genome Sequencing (WGS), it is possible to predict susceptibility to antibiotics, highlighting the opportunity to use genomic technologies to inform treatment strategies. However, in areas where typhoid fever is endemic, isolation of the bacteria and blood culture confirmation of infection are not routinely performed

PHE carries out surveillance of Salmonella using Whole Genome Sequencing, among many other bacteria, in order to provide accurate diagnoses, rapidly detect outbreaks and pinpoint the emergence of new threats. As the majority of cases of *S. Typhi* in England are acquired abroad, the data provides a rich source of information to paint a global picture of *S. Typhi* infections. In the new work, Danielle Ingle of The Australian National University, and colleagues analyzed whole genome sequencing data from all *S. Typhi* isolates sent to PHE between April 2014 and March 2017, primarily in travelers returning from high risk regions.

The 533 isolates collected by PHE during the study period included 449 cases in which patients reported recent foreign travel to 26 countries. The majority of cases reported travel to South Asia, particularly India, Pakistan and Bangladesh. WGS revealed 31 unique *S. Typhi* genotypes, although the majority of isolates (73.4%) belonged to one subtype of the bacteria, which was identified in cases with travel to 15 countries. Overall, 24% of isolates were multidrug resistant *S. Typhi*, and those were associated with travel to 10 countries in South Asia, East Africa and West Africa. The researchers were able to identify a number of trends in which genotypes and drug resistance patterns were present in which countries around the world, including the first case of ESBL *S.*

Typhi in England, from a patient with travel to Pakistan described in 2018.

"The [whole genome sequencing](#) data presented here provide insight into changing antimicrobial resistance dynamics within *S. Typhi*," the researchers say.

"Public Health England is a world leader in using [whole genome](#) sequencing technologies for routine Salmonella surveillance. Excitingly, this study shows the data now being generated routinely by PHE and other public health laboratories could serve as sentinel genomic surveillance for typhoid-endemic countries that currently lack formal local surveillance programs, providing valuable information on the strains and antimicrobial resistance that could help local disease management," says Professor Kathryn Holt.

"Routine genomic surveillance of pathogens from travelers who have acquired their infection abroad allows us to gain insight into what strains are circulating in different parts of the world. This provides an early warning system against emerging threats including those posed by antimicrobial resistant organisms. Our technology can also play an important role for source tracking future outbreaks in foreign countries, helping to guide public health advice for travelers," added Dr. Tim Dallman.

More information: Danielle J. Ingle et al. Informal genomic surveillance of regional distribution of Salmonella Typhi genotypes and antimicrobial resistance via returning travellers, *PLOS Neglected Tropical Diseases* (2019). [DOI: 10.1371/journal.pntd.0007620](https://doi.org/10.1371/journal.pntd.0007620)

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