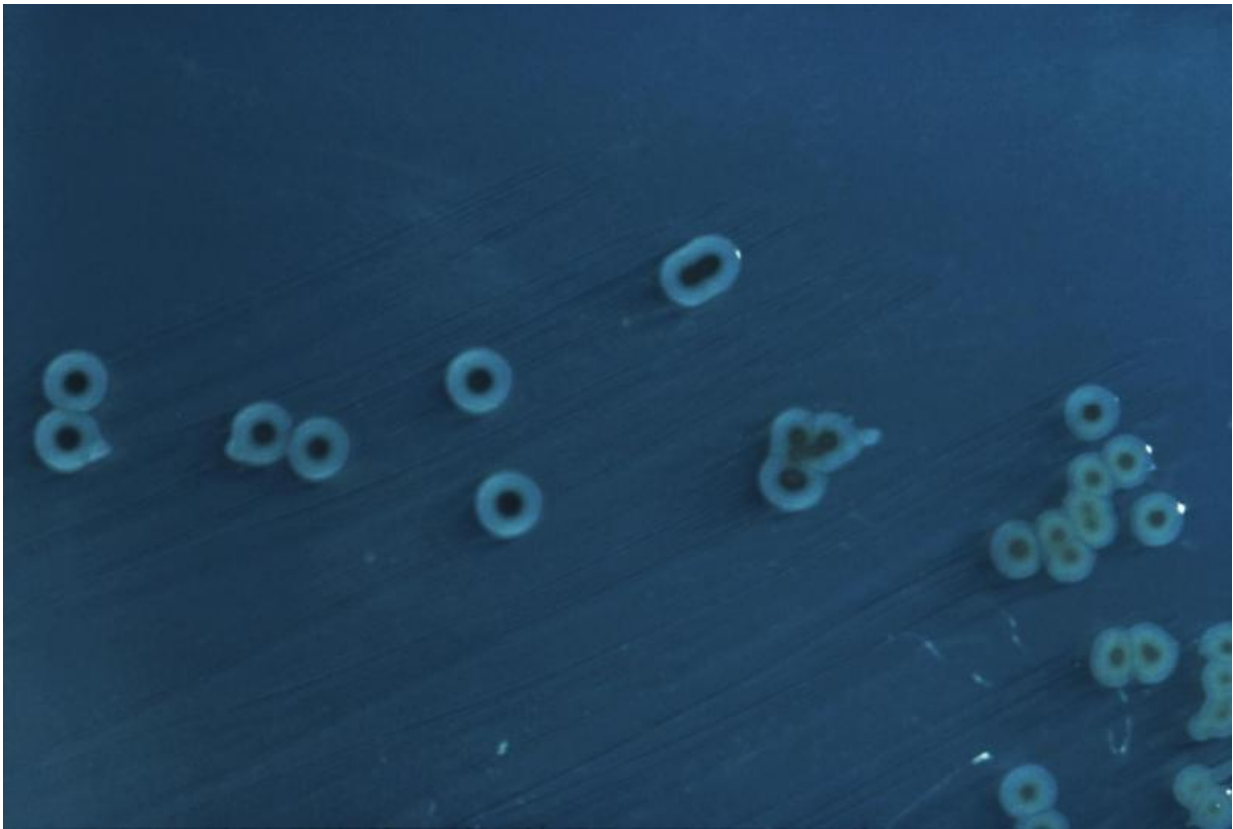


Genomic data reveals emergence in Africa of drug resistant strain of typhoid

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Colonies of pathogenic bacteria growing on an agar culture plate - *Salmonella enterica* (serovar typhimurium). Credit: Centers for Disease Control and Prevention

The team has completed two genomics studies on the tropical disease, a

condition that is estimated to cause up to 30 million illnesses and over a quarter of a million deaths globally each year.

The first study, published in the journal *Nature Genetics*, suggests that the H58-strain, which is likely to have emerged in Asia approximately thirty years ago, is now rapidly spreading across Africa, where it has been introduced on several separate occasions. A key feature of this strain appears to be its ability to acquire resistance to commonly available antibiotics.

Dr Melita Gordon, from the University of Liverpool's Institute of Infection and Global Health, said: "Importantly, the [antibiotic resistance genes](#), which have previously been carried on a separate genetic package, have now been incorporated into the main chromosome of the bacteria itself, which is likely to make it easier for the Typhoid strain to retain these [resistance genes](#)."

Data from the microbiology laboratory at the Malawi-Liverpool-Wellcome Trust Major Overseas Programme, where bloodstream infections have been monitored for 18 years, show that an epidemic of Typhoid fever began in Malawi in 2011.

In a related study, published in the journal *PLoS Neglected Tropical Diseases*, the team has investigated the epidemic and the re-emergence of the disease in Malawi by studying the genomes of the bacteria.

Genomic data from the Malawi strains reveals that up until 2009 no H58 strains were found, and other local strains of *Salmonella* Typhi were fully sensitive to the antibiotics used locally.

After 2010, a large number of different strains, however, appeared in Blantyre, competing for dominance. H58 emerged as the most successful strain, triggering a large epidemic in which up to 800 cases occurred per

year, with a 3% case fatality.

Dr Nick Feasey, from the Liverpool School of Tropical Medicine said: "The rise of [antibiotic resistance](#) among Salmonellae in Africa is a major threat and concern. Not only does it mean that individuals cannot always be effectively treated, but it also appears to make global spread and large epidemics more likely."

Liverpool scientists are now conducting further work at the Malawi-Liverpool-Wellcome Trust Clinical Research Programme, funded by a £4 million Strategic Award from the Wellcome Trust, as part of a team led by the University of Oxford Vaccine Group, to investigate the best ways to use future vaccines to halt the spread of multidrug resistant Typhoid fever in Africa.

More information: Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events, *Nature Genetics* (2015) [DOI: 10.1038/ng.3281](#)

Provided by University of Liverpool

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