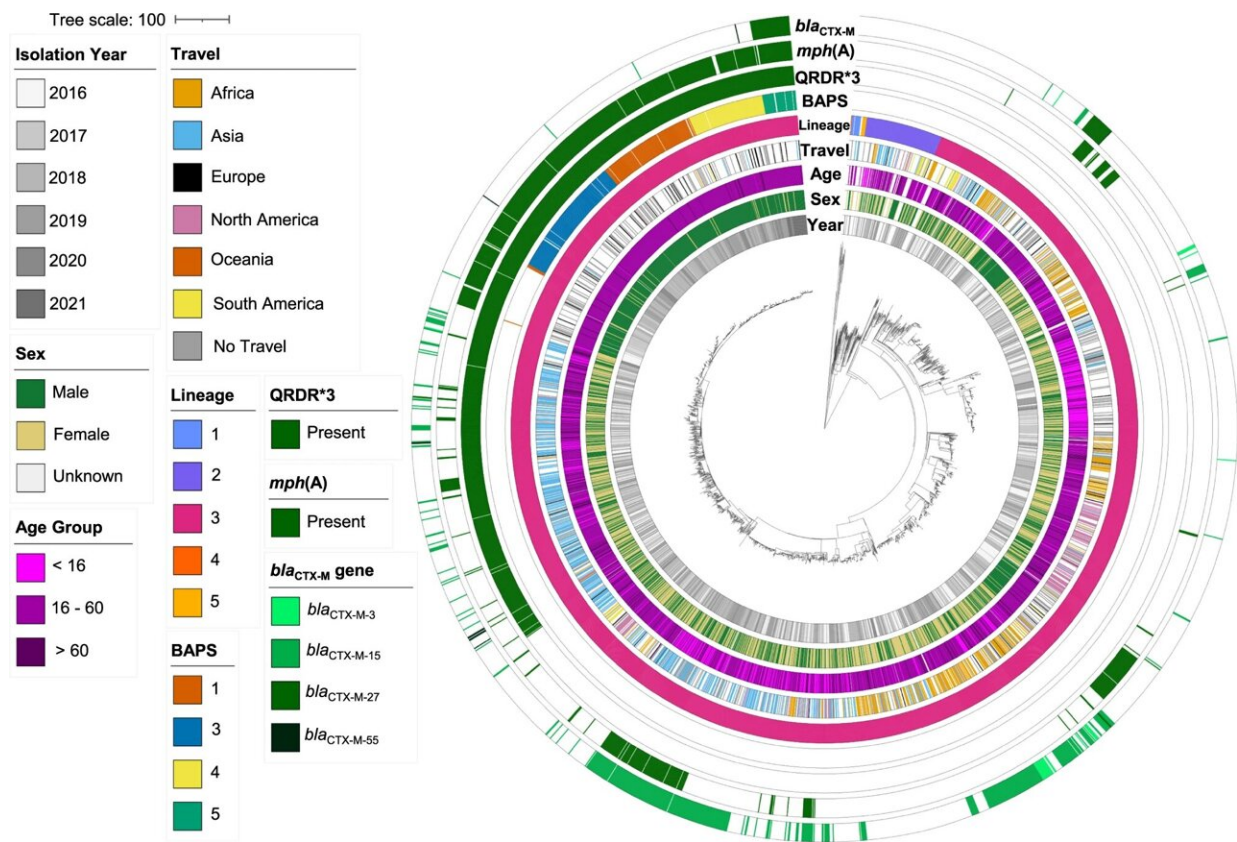


Working to tackle antibiotic resistant bacteria

May 2 2023



The emergence of an XDR *S. sonnei* outbreak in the United Kingdom. A cgMLST dendrogram (midpoint rooted) of clinical isolates from the UK ($n = 2,820$) and genomic subtype references ($n = 120$) with the scale bar indicating distance in cgMLST alleles. Metadata tracks show patient and genomic features for isolates colored according to the inlaid keys. Specifically, from inner to outer, the patient data comprises: year of isolation, patient sex, age group, and travel history (for UK isolates only), with missing/unavailable/not determined data shown as white. Genomic features then show: isolate lineage, BAPS clusters

(for isolates belonging to the t10.377 cluster only), and the presence of mutations in the Quinolone Resistance Determining Region (QRDR*3 denotes all three canonical mutations; *gyrA*_D87G, *gyrA*_S83L and *parC*_S80I) and *mph*(A), and *bla*_{CTX-M} genes, where white indicates absence of the gene. Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-37672-w

Researchers at the University of Liverpool are working to tackle an increasingly antibiotic resistant bacterium.

The UK Health Security Agency has reported a UK increase in this sexually transmissible bacterium, which has also been identified in countries across Europe. The bacterium, called *Shigella sonnei*, can cause severe diarrhea and the strain of interest is resistant to the majority of antibiotics recommended for its treatment.

Experts at the University's National Institute for Health and Social Care Research's Health Protection Unit in Gastrointestinal Infections led an [international collaboration](#) between scientists and [public health workers](#) from the UK, France, Belgium, Australia, and the United States of America. Together they investigated the [genetic makeup](#) and international spread of the bacterium in order to better understand the drivers behind the epidemic and predict and prevent future outbreaks.

By analyzing samples of the bacteria found in all the collaborative countries, the team developed greater insight into this antimicrobial resistant outbreak, which disproportionality affects gay, bisexual, and other men who have sex with men (MSM).

Lewis Mason, a Medical Microbiology Ph.D. Student, University of Liverpool said, "Antimicrobial resistance (AMR) is an urgent global public health crisis and our work studying this sexually transmissible

intestinal infection played a key role in understanding and addressing the issue of AMR. Through this work we have learnt of the power of collaboration and the progress we've made shows how by cooperating and sharing genomic data we can better detect emerging disease threats around the globe."

Kate Baker, Professor of Applied Microbial Genomics, University of Liverpool says, "Combining pathogen [genomic data](#) from across international surveillance systems allows us to pick up the spread of new strains much earlier than previously possible. We saw this with COVID as well and now we need to build on that to make the most of pathogen genomics for tackling [antimicrobial resistance](#)."

The paper is published in the journal *Nature Communications*.

More information: Lewis C. E. Mason et al, The evolution and international spread of extensively drug resistant *Shigella sonnei*, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-37672-w](https://doi.org/10.1038/s41467-023-37672-w)

Provided by University of Liverpool

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