NIHR | Health Protection Research Unit in Gastrointestinal Infections at University of Liverpool

Genomic epidemiology of the first London outbreak of antimicrobial resistant sexually transmitted shigellosis

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BACKGROUND

- Shigellosis is a gastrointestinal illness caused by Shigella bacteria.
- There are four Shigella species: *S. dysenteriae*, *S. flexneri*, *S. sonnei* and *S. boydii*.
- Sexually transmitted shigellosis among men-who-have-sex-with-men (MSM) was first identified in San Francisco, California, 1974.[1]
- In 2004, the first outbreak of MSM associated shigellosis in England was identified. This outbreak was of *S. sonnei*.[2]
- Since then, sexually transmissible shigellosis has become endemic in England.

METHODS

- Public Health England (PHE) provided the SRA Accession numbers for the fourteen London 2004 *S. sonnei* outbreak isolates.
- A phylogenetic tree was created using Enterobase.[3]
- The phylogenetic tree contains the fourteen outbreak isolates, and 'reference' strains with known genotypes from the Hawkey *et al.,* (2020) paper.[4]
- ResFinder 4.0 was used to predict antimicrobial resistance gene data from Illumina paired end read data.[5]
- The tree was visualised using Interactive Tree of Life (ITOL).[6]

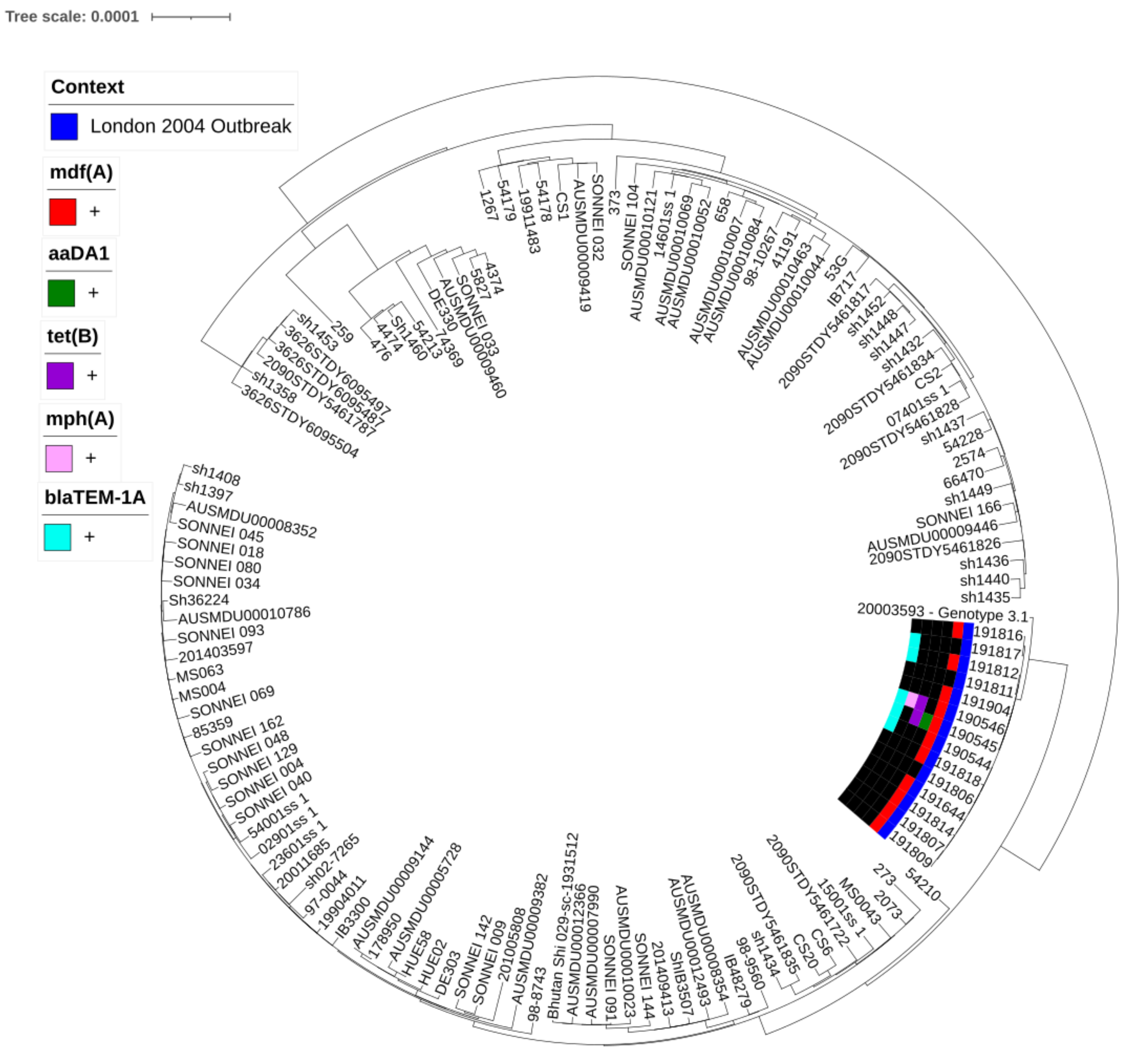

Figure 1. A phylogenetic tree, visualised using ITOL,[6] of the London 2004 *S. sonnei* outbreak isolates (dark blue) with the Hawkey *et al.,* (2020) reference strains with known genotypes.[4] Predicted antimicrobial resistance gene data from ResFinder 4.0 is colour coordinated on the tree for the 2004 isolates.[5]

RESULTS & DISCUSSION

- It is interesting that all fourteen London 2004 outbreak isolates sit at the base of the 3.1 genotype reference isolate.
- Global Lineage III went on to dominate sexually transmitted shigellosis worldwide.[7]
- Future direction includes incorporating other global isolates into the tree from other past outbreaks.
- Another next step includes identifying changes in virulence determinants throughout these outbreak isolates and comparing to reference strains over time.

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