

# Characterising Genomic Variation within *Salmonella* Paratyphi A Isolates Associated with the Bacterial Carrier State

## Objective

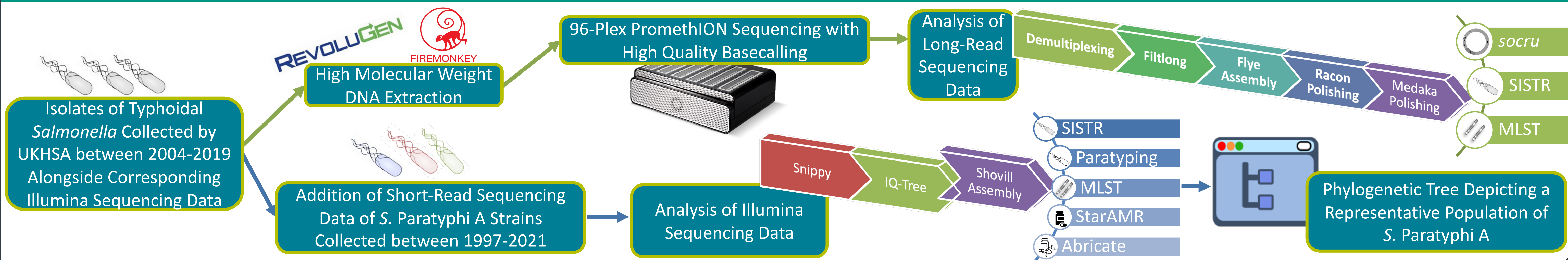
To explore the genomics and genealogy of *S. Paratyphi* A isolates, primarily those associated with bacterial carriage in UK patients, utilising both short and long read sequencing technologies, in comparison to *S. Typhi*.

## Background

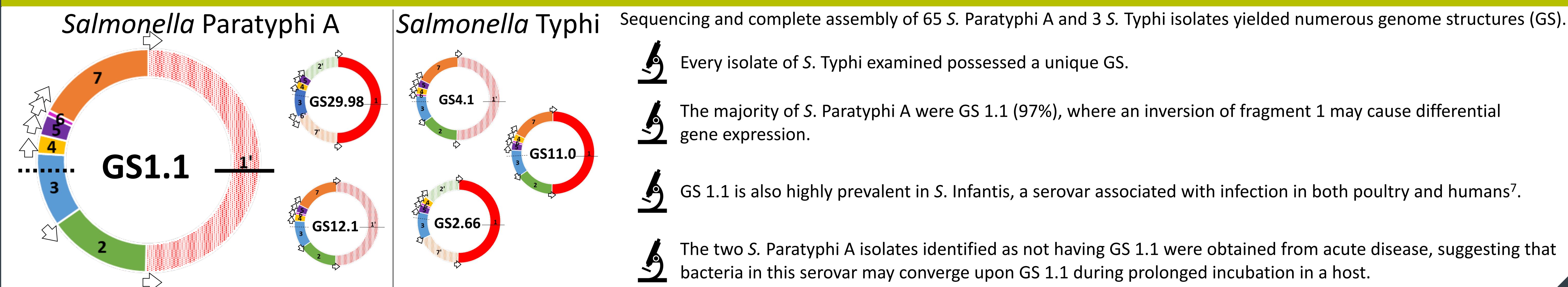
- Enteric fever is the inclusive term for infections caused by *Salmonella enterica* serovar Typhi and serovars Paratyphi A, B and C.
- 14.3 million cases of enteric fever are recorded per annum, causing 135,900 deaths<sup>3</sup>.
- S. Paratyphi* A is responsible for 36-50% of cases<sup>4,5</sup>.

- Humans can harbour typhoidal *Salmonella* asymptomatically and sporadically excrete the bacteria. This is known as the carrier state.
- This form of bacterial persistence can be detrimental to both the carrier and their direct contacts<sup>6</sup>.
- Chromosomal rearrangements and small genetic variations may affect gene expression in *S. Paratyphi* A carrier isolates.

## Methodology



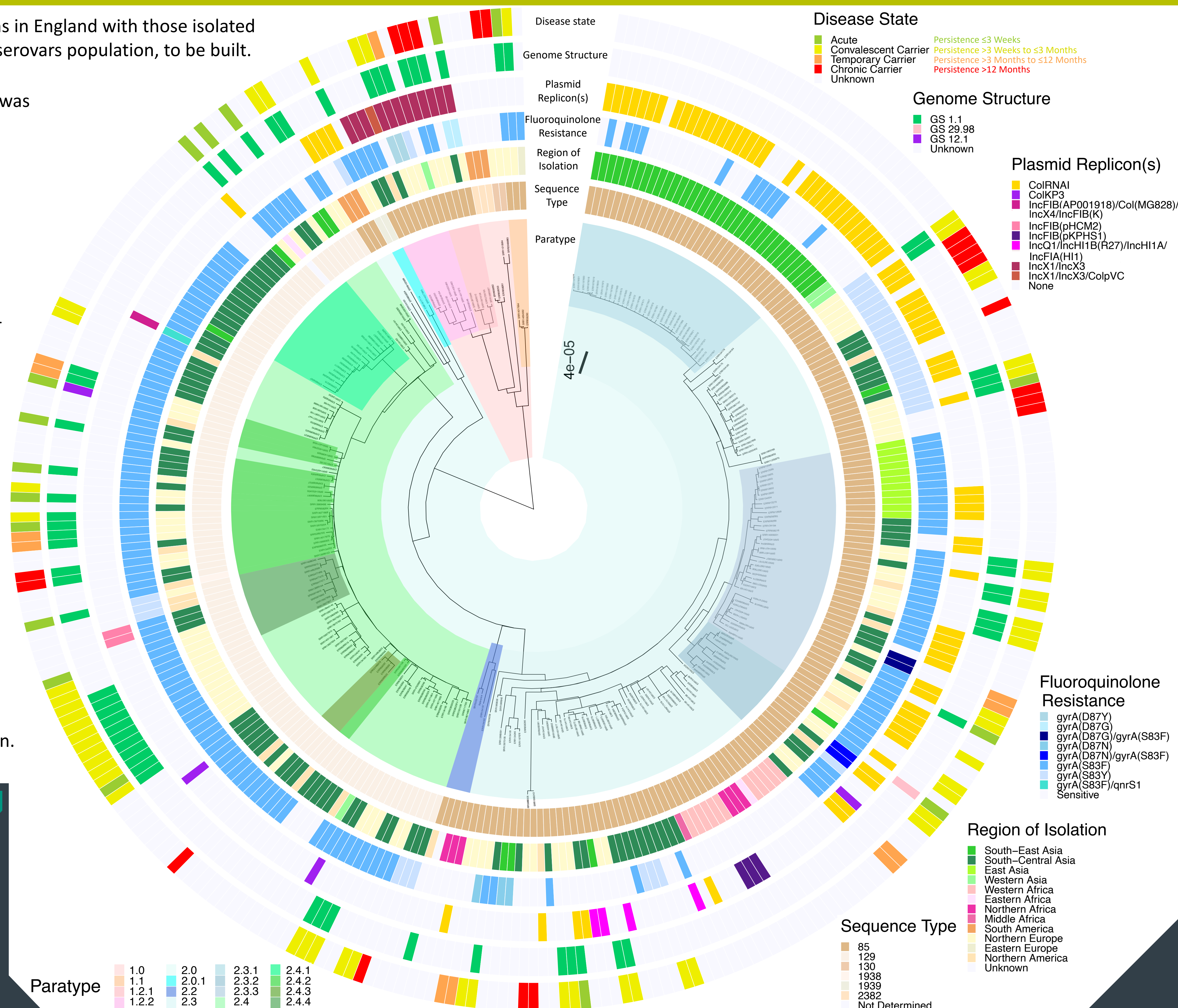
## Genome Level Variation



## Nucleotide Level Variation

Combining short-read data from *S. Paratyphi* A infections in England with those isolated around the world allowed a tree, representative of the serovars population, to be built.

- No specific SNP profile or epidemiological cluster was associated with carriage.
- UK isolates with confirmed GS were distributed throughout the tree.
- The ColRNAI and IncX1/IncX3 plasmid replicons were observed almost exclusively in paratypes 2.4 and 1.2 respectively but were not associated with a specific antibiotic resistance profile.
- Fluoroquinolone resistance, via point mutations in *gyrA*, was present in ~70% of *S. Paratyphi* A isolates.
- <2% of isolates exhibited multi-drug resistance (MDR), and no extensive drug resistance (XDR) was observed.
- The Paratype scheme was used to type isolates. Results aligned with known epidemiological data regarding geographical location of sample isolation.



## Conclusions

- Variability of GS possession between *S. Typhi* and *S. Paratyphi* A, may highlight differences in their lifestyle and persistence mechanisms.
- No specific SNP profile is associated with carriage, suggesting persistence capacity may depend on host and environmental factors.