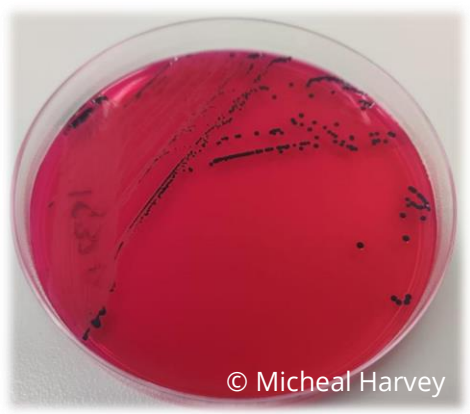


Whole-Genome Sequencing of archived Northern Ireland *Salmonella* spp. isolates

Purnika Ranasinghe¹, Pam Scates², Ryan Devaney¹, Adrian Allen¹

¹ TB Genomics, Bacteriology Branch, Veterinary Science Division, AFBI, Belfast, UK

² Food Microbiology Unit, Bacteriology Branch, Veterinary Science Division, AFBI, Belfast, UK



BACKGROUND

Salmonella is a multi-host zoonotic and food-borne pathogen that causes salmonellosis (food poisoning). To date, over 2,500 *Salmonella* serovars have been identified and invasive serotypes with multi-drug resistance have been reported. Surveillance of food-borne pathogens in food and livestock is therefore required to enable the rapid detection of FBD, antimicrobial resistance (AMR), and transmission in food-borne pathogens. This study aims to identify the genetic diversity and relatedness of Northern Irish (NI) *Salmonella* isolates using Whole-Genome Sequencing (WGS).

RESULTS

[1] In silico Multi-Locus Sequence Typing (MLST) & Serotyping

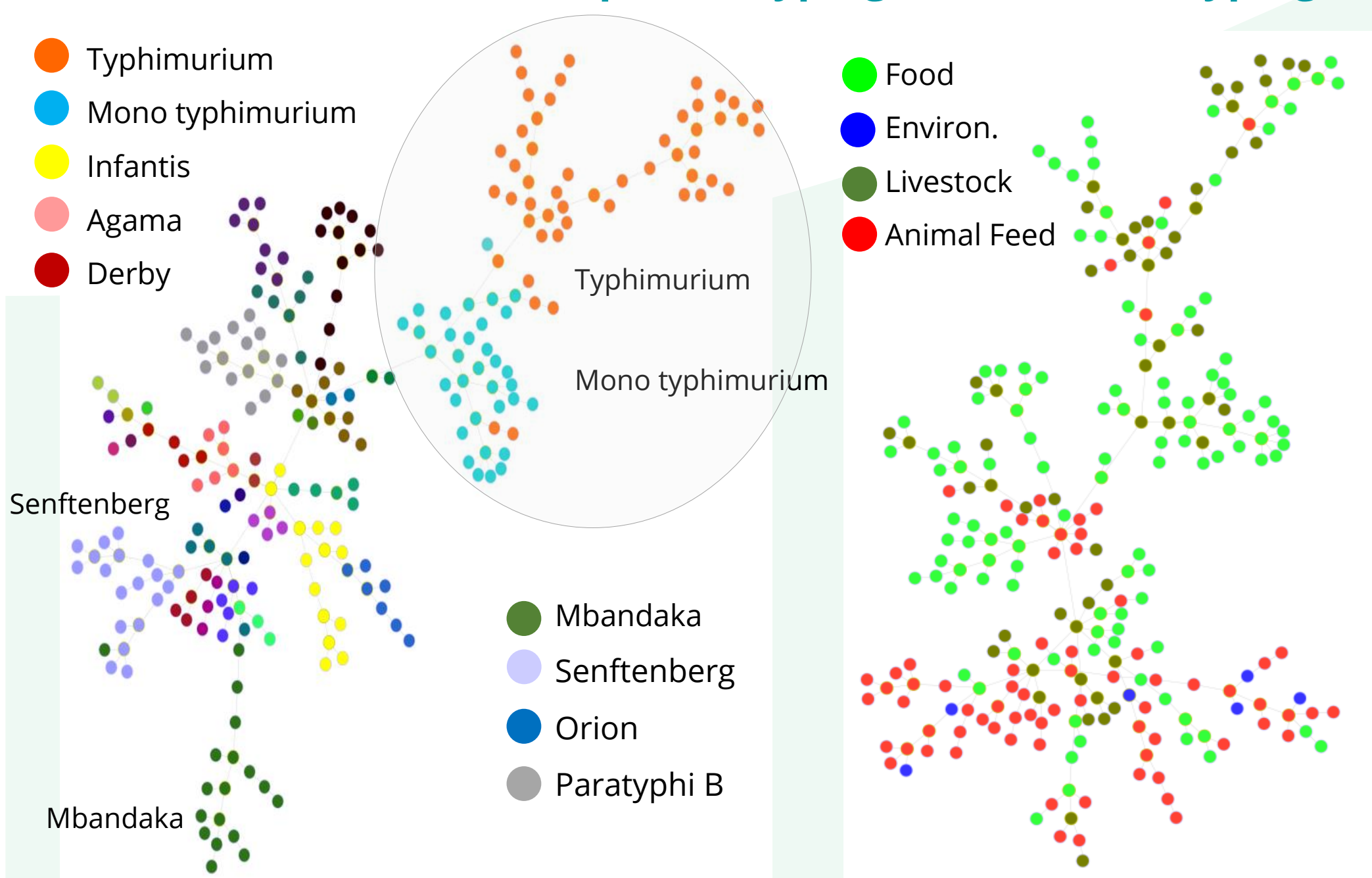


Figure 1: Minimum spanning tree (MST) analysis based on cgMLST allelic profiles of 43 *S. enterica* isolates. The circles represent cgMLST types (CTs) coloured by (A) serotype and (B) source.

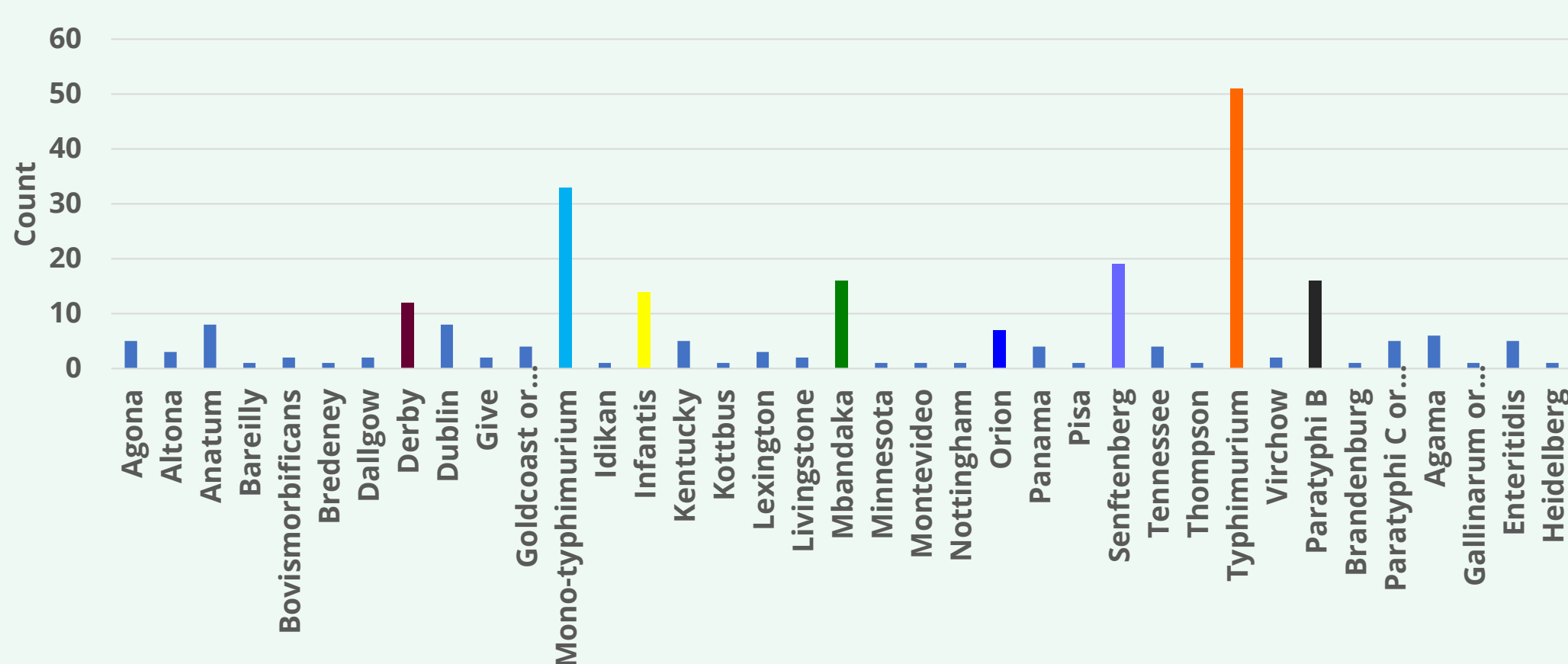


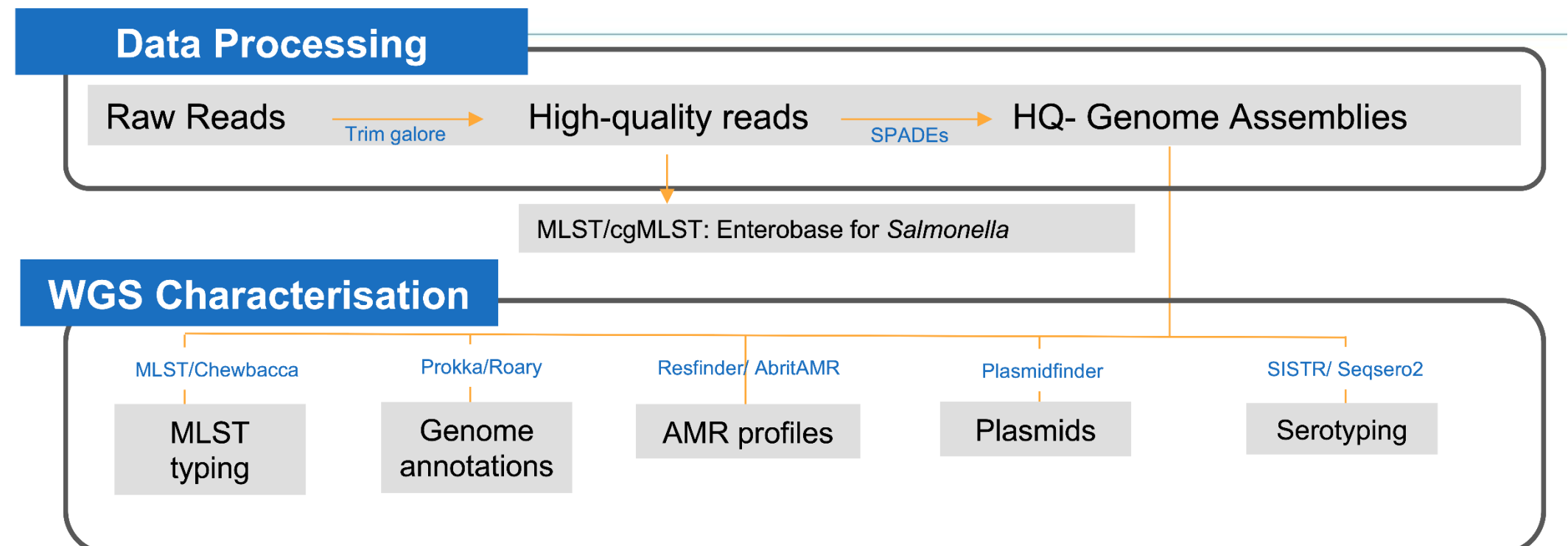
Figure 2: An overview of sample composition by serotype

[3] Antimicrobial Resistance (AMR) in *Salmonella* isolates

AMR_gene	Count of serotypes	Dominant_serotypes
aac(6)-Iaa	35	Typhimurium, Mono Typhi., Senftenberg, Mbandaka, Paratyphi, Derby, Infantis
aph(3'')-1b	8	Anatum, Cholerausuis, Derby, Give, Mbandaka, Mono typhi., Tennessee, Typhimurium
sul2	11	Anatum, Cholerausuis, Derby, Give, Heidelberg, Mbandaka, Mono typhi., Paratyphi, Tennessee, Typhimurium, Virchow
aph(6)-Ia	8	Anatum, Cholerausuis, Derby, Give, Mbandaka, Mono typhi., Tennessee, Typhimurium
sul1	5	Infantis, Mbandaka, Mono typhi., Paratyphi, Typhimurium
aadA1 -46	5	Typhimurium, Mono Typhi., Mbandaka, Paratyphi, Infantis
tet-B	4	Derby, Mbandaka, Mono typhi., Typhimurium

- In total, 39 AMR genes (ARGs) were identified.
- In silico phenotyping: majority of ARGs showed multi-drug resistance.

METHODS



[2] Pangenome and Phylogeny

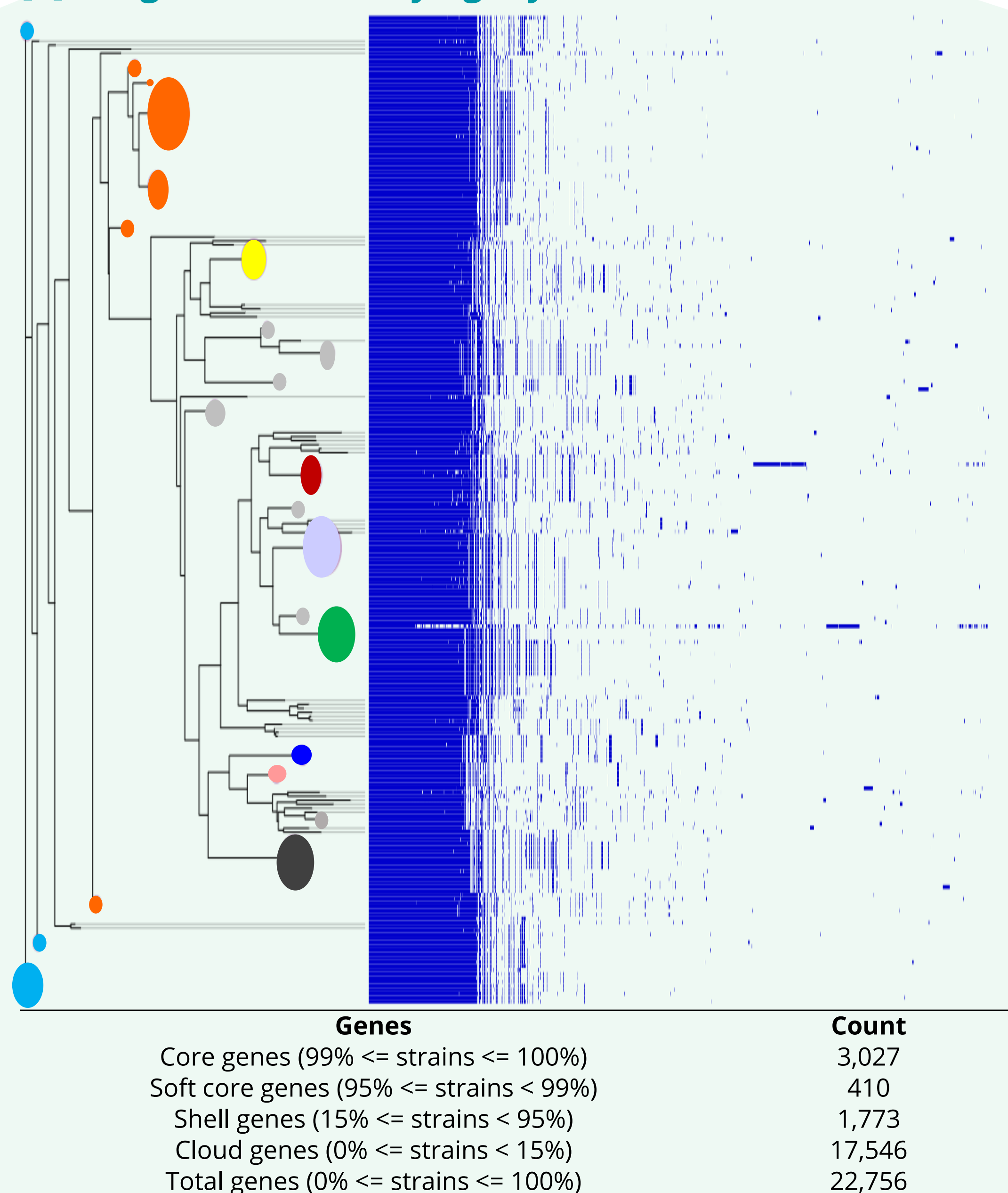


Figure 3: Core-genome phylogeny and pangenome of 250 *S. enterica* isolates.

SUMMARY

- 37 different serovars were identified from all NI isolates.
- Serovars: Typhimurium (n=51), Mono. typhimurium (n=33) isolated from food and livestock – Poultry, Bovine, Porcine samples, serovar Senftenberg (n=19), Mbandaka (n=18) and Derby (n=12) isolated from animal feed.
- Pangenome shows the genetic diversity of the *Salmonella* isolates. Phylogeny enabled the clustering of serovars by the distribution of their clade-specific regions. We aim to continue analyses serovar-specific predictive regions to target function of *Salmonella* isolates.