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

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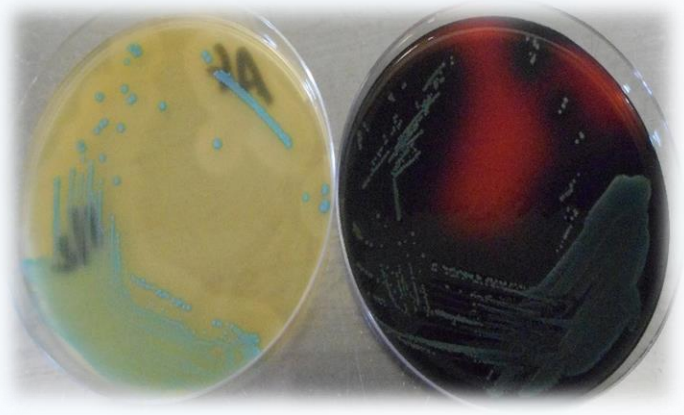
BACKGROUND

Listeria monocytogenes causes invasive Listeriosis, a severe food-borne disease (FBD) in humans or animals. Infection typically takes place through the consumption of contaminated animal or plant-based food. Compared to other FBD, the rate of incidence of listeriosis appears to be low across the UK. However, the mortality rate is high, at around 30%. This study aims to identify the genetic diversity and relatedness of Northern Irish (NI) *Listeria* isolates using Whole-Genome Sequencing (WGS).

METHODS

Data Processing

Raw Reads → (Trim galore) → High-quality reads → (SPADEs) → HQ- Genome Assemblies

Pastuer Institute DB – for *Listeria* (clonal complexes)

WGS Characterisation

MLST/Chewbacca	Prokka/Roary	Resfinder / AbritAMR	Plasmidfinder	Pastuer(online) / Lissero
MLST typing	Genome annotations	AMR profiles	Plasmids	Serotyping

RESULTS

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

● 1/2 c ● 1/2 a ● 1/2 b ● 4b ● L
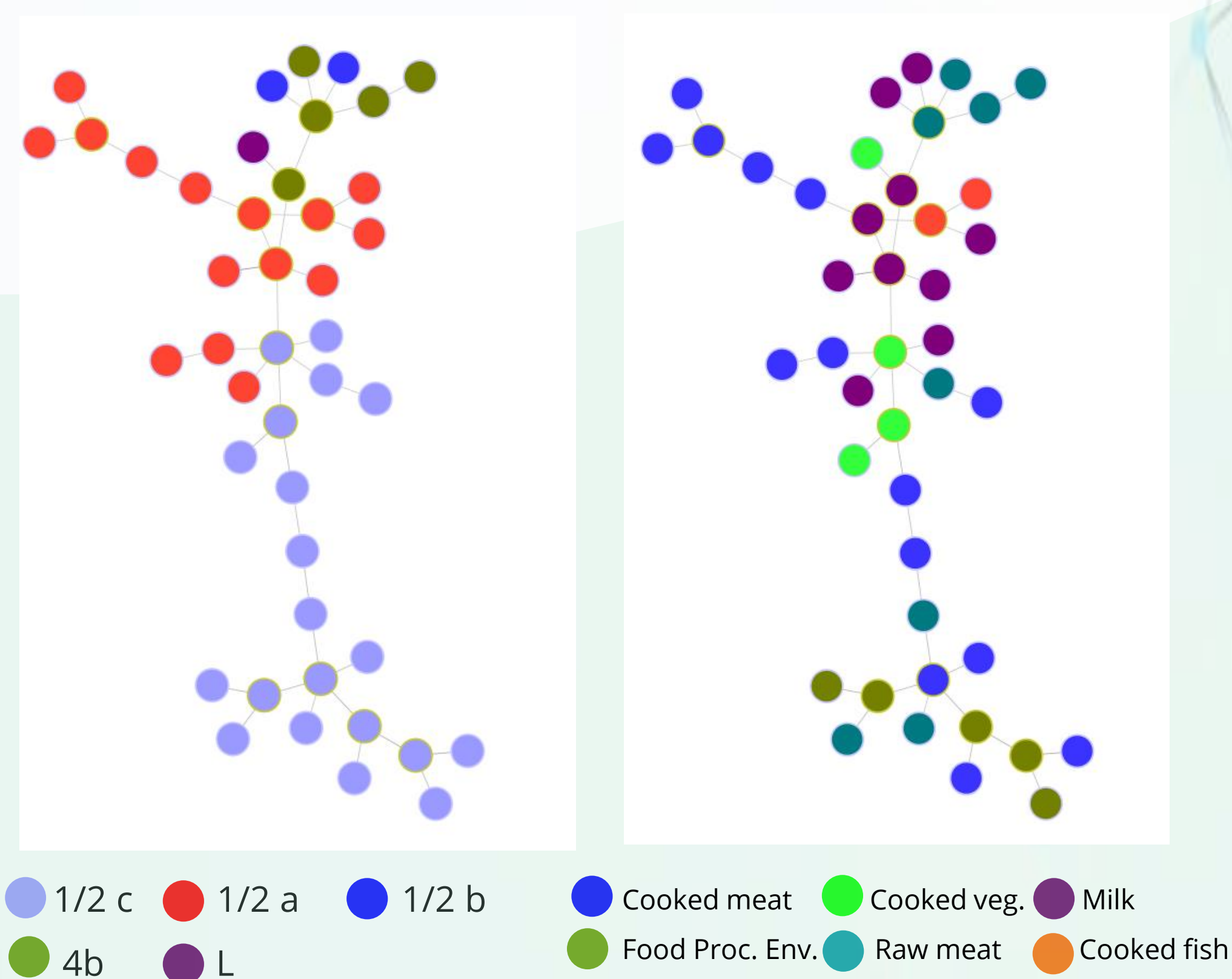■ Cooked meat ■ Cooked veg. ■ Milk ■ Food Proc. Env. ■ Raw meat ■ Cooked fish

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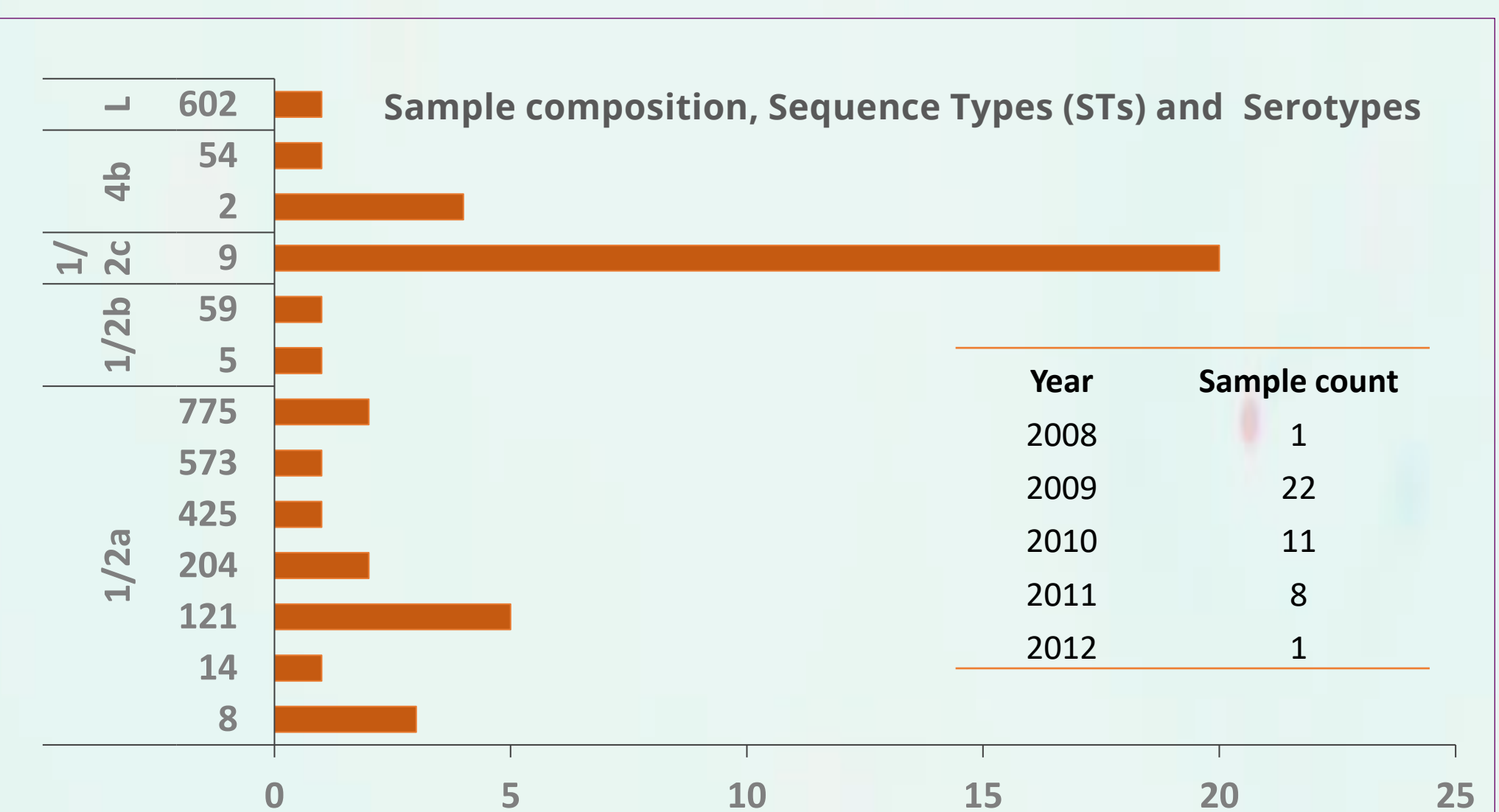

Sample composition, Sequence Types (STs) and Serotypes

Year	Sample count
2008	1
2009	22
2010	11
2011	8
2012	1

Figure 2: An overview of sample composition by serotype, STs and sampling year.

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

Resistance gene	Identity	Alignment Length/Gene Length	Coverage	Position in reference	Phenotype	Accession no.
fosX	100	402/402	100	1..402	Fosfomycin	AL591981

- AMR gene fosX identified in *L. monocytogene* isolates.

[2] Pangenome and Phylogeny

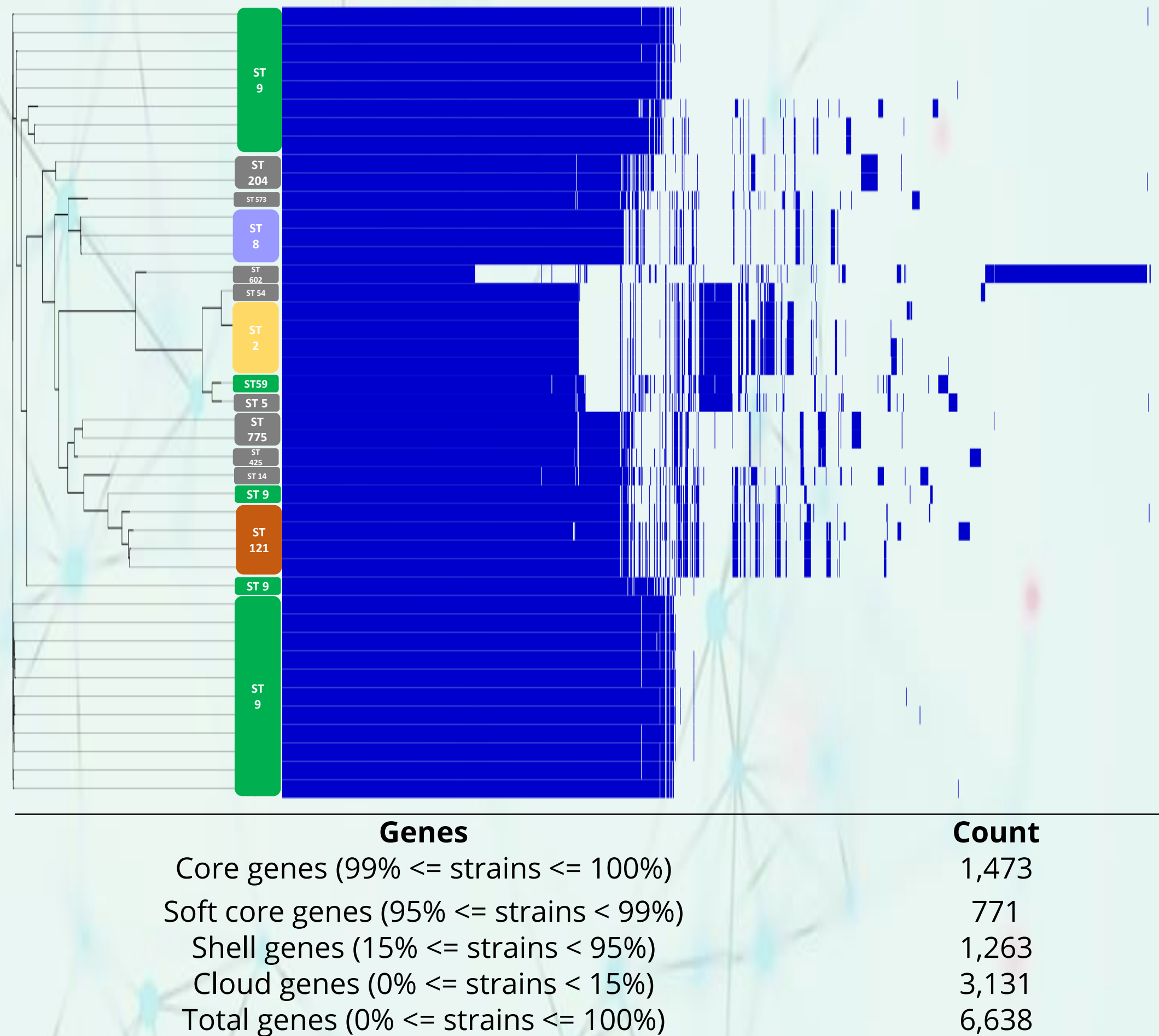| Genes	Count
Core genes (99% <= strains <= 100%)	1,473
Soft core genes (95% <= strains < 99%)	771
Shell genes (15% <= strains < 95%)	1,263
Cloud genes (0% <= strains < 15%)	3,131
Total genes (0% <= strains <= 100%)	6,638

Figure 3: core genome-based phylogeny and pangenome of 43 *L. monocytogenes* isolates.

SUMMARY

- Nearly 50% of the samples (n =22) were collected in 2009, cgMLST analysis classified all 43 isolates into 13 clonal complexes (CCs) and 13 sequence types.

- Serotype 1/2c (2011) and 1/2a (2008-2010) were the most common types where1/2 c isolated from meat (cooked & raw) and food processing environments, 1/2 a from milk and cooked fish, meat & veg. and 4b from raw meat and milk.

- Pangenome shows the high genetic diversity between and within serotypes. ST9 divided into two main sub-clusters with few differences in the pangenome (core & accessory genome). We aim to identify clade-specific regions as predictive markers of groups of bacterial isolates.