Table S1. Brief characteristics of the *L. monocytogenes* strain 4/52-1953 after the automatic contig annotation that was generated based on the NCBI Prokaryotic Genome Annotation Pipeline (PGAP).

			Number of Genes				Number of Pseudo Genes					GC, %
Totally	CDSs	Coding proteins	tRNAs/complete tRNAs	ncRNA	CDSs (without proteins)	Total	Ambiguous residues	With frameshift	Incomplete	With internal stop	Multiple problems	
3.027	2.950	2.925	5, 5, 5 (5S, 16S, 23S)	4	25	25	0 of 25	11 of 25	14 of 25	3 of 25	3 of 25	38.17

Table S2. The number of SNPs in the *L. monocytogenes* housekeeping genes of ST 201 versus ST157.

abcZ	*bglA*	*cat*	*dapE*	*dat*	*ldh*	*lhkA*
10	7	5	2	3	3	70

[1] BIGSdb-Lm provides access to genotypic data for *L. monocytogenes* isolates based on multi-locus sequence typing (MLST) (https://bigsdb.pasteur.fr/listeria/, accessed on 01 June 2022).

Table S3. Antibiotic resistance genes identified using the CARD RGI tool in the whole genome sequence of *L. monocytogenes* strain 4/52-1953.

RGI Criteria	ARO Term	Detection Criteria	AMR Gene Family	Drug Class	Resistance Mechanism	% Identity of Matching Region	% Length of Reference Sequence
Strict	*lin*	protein homolog model	lincosamide nucleotidyltransferase (LNU)	lincosamides	antibiotic inactivation	98.28	100.00
Strict	*L. monocytogenes mprF*	protein homolog model	defensin resistant mprF	peptide antibiotics	antibiotic target alteration	98.73	100.00
Strict	*fosX*	protein homolog model	fosfomycin thiol transferase	fosfomycins	antibiotic inactivation	93.98	100.00