Materials and Methods:

DNA sequencing libraries were prepared using the Nextera XT kit (Illumina, San Diego) and sequenced on an Illumina MiSeq. The sequences were assembled after quality control with SPAdes, and the resulting contigs were ordered with r2cat,[1] using the *L. monocytogenes* F2365 serotype 4b as the a standard reference strain and annotated with by GenDB[2]. The SNPs were identified with the determined by BWA tool and ReadXplorer with the thresholds of a the minimum base quality of 20 and a 90% SNP-frequency with a minimum 10 fold coverage for a particular base.[3] The core-genes, pan-genes and core genome phylogeny were calculated with by 'Efficient Database framework for comparative Genome Analyses using BLAST score Ratios' (EDGAR).[4] The genomes were also analyzed for the analysed for multi-locus sequence types (MLSTs)[5], multi-virulence locus sequence types (MVLSTs)[6] and average nucleotide identities (ANIs)[7].

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