

Characterisation of *Listeria monocytogenes* serogroup Ib isolated from meat products and meat food production environment

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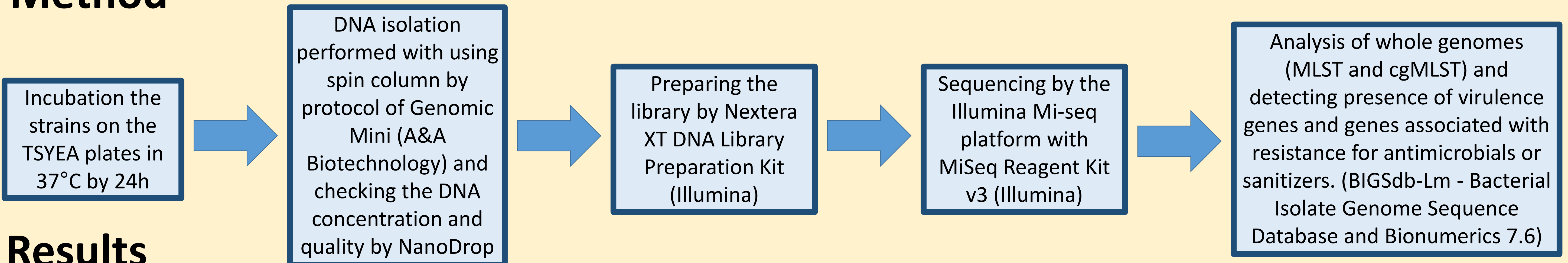
Introduction

Listeria monocytogenes is a Gram positive, foodborne pathogen which can cause wide range of infections including gastroenteritis, meningitis and bacteremia. This ubiquitous organism can be isolated from food (milk, meat and fish products) and food production plants. One of the most common reason of presence *L. monocytogenes* in RTE food is cross-contamination from production environment to final products. Ability to surviving *L. monocytogenes* in meat production environment as well as threat for consumers, depends on presence of virulence genes and genes connected with resistance for sanitizers or antimicrobials.

Material

The material were 16 strains of *Listeria monocytogenes* from collection of Department of Hygiene of Food of Animal Origin, National Veterinary Research Institute in Poland. Strains were collected in years 2015-2016 from meat food and food production environment in area of 4 provinces (Poland).

Method



Results

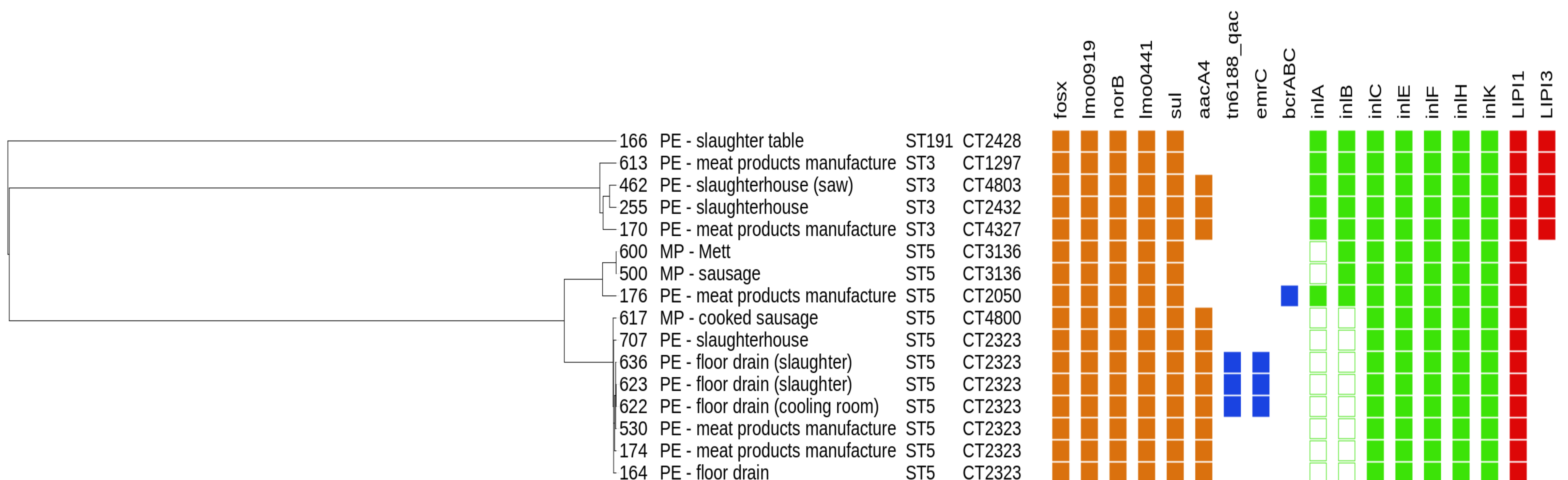


Fig. 1. Phylogenetic tree based on the cgMLST analyses (Bionumerics 7.6) of *Listeria monocytogenes* strains from food and food production environment and prevalence of antibiotic resistant genes (orange), genes connected with resistance to benzalkonium chloride (blue), and virulence genes: internalins (green) and *Listeria* pathogenicity island (LIPI1 and LIPI3) (red).

Benzalkonium chloride resistance and antibiotic resistance genes

MLST and cgMLST

Tested strains were analysed with using two methods: MLST (multilocus sequence typing) and cgMLST (core genome multilocus sequence typing). *L. monocytogenes* were classified to 3 sequence types (ST): ST5, ST3 and ST191 and 9 different cgMLST types (CT): CT2323, CT4800, CT2050, CT3136, CT4327, CT2432, CT4803, CT1297 and CT2428 (Fig. 1.).

Genes related with resistance to fosfomycins (*fosX*), lincosamides (*lmo0919*), quinolones (*norB*), cephalosporins (*lmo0441*) and sulfonamides (*sul*) were found in all of the tested isolates. Gene *aacA4* associated with resistance for aminoglycosides were detected in 11 strains (Fig. 1.).

Benzalkonium chloride resistance genes were found in 4 strains isolated from production environment and floor drains. Genes *tn6188_qac* and *emrC* were in 3 strains (CT2323) and *bcrABC* cassette in 1 strain (CT2050) (Fig. 1.).

Virulence genes

Study showed presence of 8 internalin genes in all of the tested strains (Fig. 1). In none of the isolates *inIG* and *inIJ* were detected. Truncated *inIA* gene (with premature stop codon) was found in 10 isolates. In case strains from CT4800 and CT2323 PMSC (Premature stop codon) mutation type 1 was observed, in isolates CT3136 were detected type of PMSC mutation which has not been described before. It was found that occurrence PMSC in these strains was cause by deletion of adenosine in position 2209 and moving the reading frame. Length of shorter peptide is 753 amino acids. Isolates belongs to CT2323 and CT4800 have additional deletion of 141 nucleotides in the *inIB* gene (Fig.1).

Listeria pathogenicity island 1 (LIPI-1) was detected in all of the isolates and LIPI-3 was present in 5 strains (CT1297, CT4327, CT4803, CT2432 and CT2428). None of the tested isolates have LIPI-4.

Conclusions

- In all of the tested *L. monocytogenes* strains used in study 5 antibiotic resistance genes (*fosX*, *lmo0919*, *norB*, *lmo0441*) were detected. Gene *aacA4*, associated with resistant for aminoglycosides were present only in CT2323 strains.
- From tested strains the most distinctive group were isolates belonged to CT2323. These *L. monocytogenes* have genes associated with resistance for benzalkonium chloride (sanitizers compound) and truncated virulence genes: *inIA* and *inIB*. Probably it may be related with better adaptability to conditions in production environment and make these strains less virulent.

Reference

1. Gelbicová T., Koláčková I., Pantucek R., Karpíšková R. (2015); A novel mutation leading to a premature stop codon in *inIA* of *Listeria monocytogenes* isolated from neonatal listeriosis; *New Microbiologica*, 38, 293-296
2. Letunic I., Bork P. (2016); Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees; *Nucleic Acids Research*, 44 (design & development: biobyte solutions)
3. Moura A., Toudjman M., Leclercq A., Hamelin E., Laurent E., Fredriksen N., Van Cauteren D., Bracq-Dieye H., Thouvenot P., Vales G., Tessaud-Rita N., Maury M. M., Alexandru A., Criscuolo A., Quevillon E., Donguy M.-P., Enouf V., de Valk H., Brisse S., Lecuit Marc (2017); Real-Time Whole-Genome Sequencing for Surveillance of *Listeria monocytogenes*, France; *Emerging Infectious Diseases*, 23, 1462-1470
4. Muhterem-Uyar M., Ciolacu L., Wagner K.-H., Wagner M., Schmitz-Esser S., Stessl B. (2018); New aspects on *Listeria monocytogenes* ST5-ECV1 predominance in a heavily contaminated cheese processing environment; *Frontiers in Microbiology*, 9:64, 1-14