Molecular serotyping and virulence potential of Listeria monocytogenes isolated from bovine, swine and human in the province of Quebec.


Listeria monocytogenes (L mono) cause rare but critical diseases, particularly for at risk population that include pregnant women. Food-borne origin of listeriosis is clearly recognised only since 1984. Since then, a great number of grouped cases occurred and milk or meat products, particularly pork meat, were implicated. Management of this zoonotic pathogen considers all strains as at equal risk. Recently a new perspective for characterisation of strain virulence was allowed since unaltered sequence of InlA was recognised as a key for strain virulence. Such complete InlA were reported as infrequent in so called environmental strains. Analyses of InlA sequences in strains involved in clinical cases will contribute to establish a risk based surveillance of L mono in food production. The aim of the project was, based on serovar and InlA sequencing characterisations of the strains, to compare L mono involved in animal from human cases, and clinical strains from environmental ones. In Quebec in 2013/2014 the surveillance of L mono clinical isolates provided a total of 20 strains from animal origin, and 16 PFGE-type isolated from human cases. The strain collection was completed by 32 L mono strains from holding pens of 3 main pork slaughter facilities in Quebec in 2011/2014. A PCR multiplex PCR protocol for serogrouping was used, and we propose a complement to easily reach the serovar identification (flaA PCR and agglutination against limited number of serum). InlA gene sequencing allows analysing the presence of SNP that conduct to truncated or modified InlA (PMSC-SNP). Serovar analyses show that proportions of IVB IIB vs. IIA serogroups differ according to the origin of the strain (Fisher p<0.05). Detection of low proportion of PMSC-SNP in inlA gene from clinical origin will be discussed in perspective of industrial management of the L mono risk.

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