



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

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Abstract

Listeria monocytogenes (*L. mono*) cause rare but critical diseases, particularly for at risk population that include pregnant women. Food-borne origin of listerioses is clearly recognised only since 1984. Since then, a great number of grouped cases occurred and milk or meat products, and 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 provide 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 shows 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.