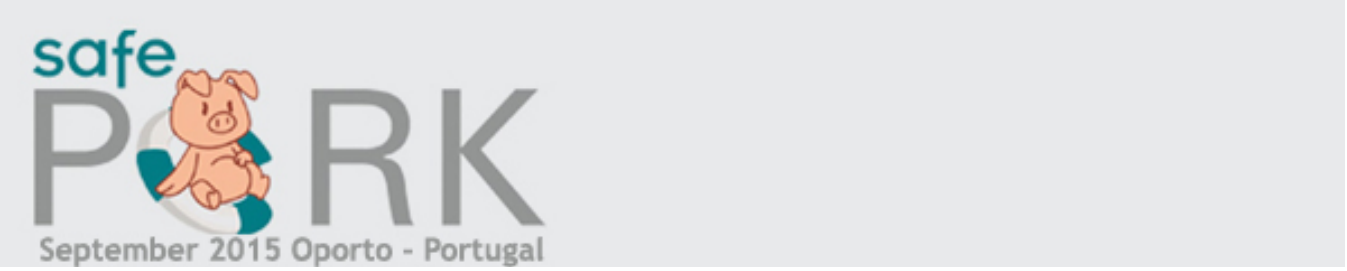

Detection and serovars distribution of *Listeria monocytogenes* isolates in pork slaughterhouse and cutting facilities after cleaning and disinfecting procedures in Quebec

Neira Kersti, Cherifi Tamazight, Letellier Ann, Quessy Sylvain, Fravalo Philippe
Research Chair in Meat Safety, Veterinary Medicine Faculty, Université de Montréal, Quebec, Canada.

Abstract

L. monocytogenes (L. mono) is recognised as a zoonotic foodborne pathogen, its control is focused to the "Ready-to Eat" food production level, including meat related. Recently, Health Canada reinforced its "Policy on *L. mono* in Ready-to-Eat Foods", highlighting environmental verification and control of meat processing facilities as important risk reduction tools. The industrial sector aims at evolve their management of *L. mono* risk, taking into account previous steps of meat production. Nowadays, there is little information concerning this pathogen in pork slaughterhouse and cutting facilities in Canada. A better knowledge of detection rate and identification of the *L. mono* isolates after sanitation procedures is a pre-requisite to achieve the optimization of the management measures by the industrials.

The objectives of the present study were to detect residual *L. mono* contamination and to analyse of their serovars distribution in and between slaughterhouse and cutting facilities in Quebec during one year. Four main slaughterhouses were included, representing above 60% of annual pork slaughter rate in Quebec. A total of 16 exhaustive sampling were carried out in four different seasons in one year. Each sampling represented a total of 156 samples that were distributed to characterize the different step of the slaughter/cutting process: 53, 18, 23, 08 and 54 samples in lairage, slaughtering, carcass dressing, refrigeration and cutting room respectively. All samples were performed after cleaning and disinfection process, analysed following a sensitive bacteriological procedure. Strains (2 per positive samples) were characterized to serovars by a new combination of PCR and agglutination steps.

9.7% (242/2,496) of all samples allowed detection of *L. mono* on one year of study. Detection rate significantly differ between plant, and depending of the step of the process, defining specific plant types. Analyses provided 477 isolates, available characterisation shows that genoserogroup IIA is strongly represented (47%), serovars determinations are currently in course.