

Study of the transfer of *Listeria monocytogenes* during cattle slaughter by molecular typing

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Introduction

Listeriosis is still considered an important foodborne disease in the EU due to its high hospitalisation and mortality rates. As *Listeria monocytogenes* is an ubiquitous organism, bacterial contamination may occur at every process step in cattle slaughter which makes it hard to characterize and prevent pathogen transfer to carcasses during the slaughter process. There is a need of scientific based knowledge of the complex introduction, persistence and variable contamination sources and routes of this pathogen. The main objective of this study was to assess the occurrence of *L. monocytogenes* and to identify the most important contamination sources by genetically characterisation of *L. monocytogenes* isolates obtained from hides, carcasses and environment during slaughter.

Materials and Methods

On different days in a period of seven months (November 2017–May 2018) the *Listeria monocytogenes* contamination of 110 carcasses from four Belgian slaughterhouses was studied. Prior to evisceration, swab samples (400 cm²) were taken from the hide at both hind legs, the brisket centre line and the inside foreleg. Immediately after slaughter, and also before chilling, these same locations were sampled on the carcasses of the tracked animals. Also environmental samples (knives, air) were taken during slaughtering. *L. monocytogenes* was detected and enumerated according to ISO11290-1 and 2. Positive isolates were submitted to molecular typing by serotype identification and pulsed field gel electrophoresis (PFGE).

Discussion

In almost all animals involved (96%), the skin appeared to be positive for this pathogen for at least one of the sampled locations. Forty-eight percent (95% confidence interval from 39% to 58%) of the carcasses were found *L. monocytogenes* positive at the end of the slaughter line. More specifically the figures were 77%, 50%, 20% and 37% for the four slaughterhouses individually. Molecular typing is still ongoing; the first identified serotypes belong to the groups 1/2a (23%), 1/2b (25%), 1/2c (35%) and 4b (17%). Serotypes 1/2a, 1/2b and 4b are commonly found on the hide of the animals, while 1/2c is predominantly found on the carcasses at the end of the slaughter line. Already 27 PFGE profiles have been identified on the hides of 24 different animals. The study is still in progress, but we can already state that in addition to the hide of the animals other sources of *L. monocytogenes* are possible within the production process. Furthermore, it seems that in some slaughterhouses certain pulsotypes are quite persistent as they are found on several sampling days.