Listeria monocytogenes (Lm) is an ubiquitous bacterium that causes a foodborne illness, the Listeriosis. PFGE-based studies revealed low genetic diversity among 126 strains isolated from pork products from 2000 to 2001, in France. 78% of these strains displayed two AsCl PFGE profiles “a1” and “a2”, which were pork specific, in comparison to clinical strains during the same period1.

The French National Reference Laboratory (NRL) has constituted a large collection of strains isolated from the main food production sectors, in France, over the past twenty years. It has developed a database centralizing epidemiological, genotypic and phenotypic data for about 2000 food strains. The food matrices listed within the database were divided according to the classification of EFSA2.

A close collaboration between the NRL and the French Institute for Pig and Pork Industry made possible to access a collection of 284 strains isolated from pigs, pork cuts and the environment plants, in France, between 2003 and 2013. The objective of our study was to structure this population. We compared the diversity of these strains to the one observed for strains isolated from other food sources, using PFGE and MLST. A similarity limit of 80% was chosen to distinguish the PFGE groups.

The 284 strains were divided into 28 PFGE groups, 20 Sequence types (STs) and 11 clonal complexes (CCs). 24 % of these strains clustered within a same sub-type, corresponding to ST121. This ST includes “a1” and “a2” AsCl profiles previously described1. The ST121 is the most frequently observed in the French NRL database. It included strains isolated from a large diversity of food sources.

In opposite to literature, these results revealed (1) a large genetic diversity of strains isolated from the pig chain and (2) the absence of genetic group specific to strains of the pork sector.

References

1Anses, Maisons-Alfort Laboratory for Food Safety, Maisons-Alfort, France.; 2Ifip, French Institute for Pig and Pork Industry, Maisons-Alfort, France.