

Pathogenicity and virulence of *Listeria monocytogenes* isolates from dairy farms

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Introduction

Listeria monocytogenes serves as foodborne pathogen capable of inducing listeriosis in human and animal hosts. Its remarkable capacity to adapt to a wide range of stress conditions across diverse environments has played a significant role in its widespread distribution.

Objectives

- ✓ Identification of serogroups
- ✓ Distinguishing clonal complexes
- ✓ Genomic characteristics of isolates
- ✓ Virulence and stress adaptation genes

Materials and methods

Isolates collection

DNA extraction

Identification of serogroups

Sequencing by Illumina

Characterization of isolates

Results

8 isolates

IIb
IVb
IVbv1
Emerging risk
Serogroup linked to high number of outbreaks of human listeriosis

Found in sheep and cow (Spain), green bean (Mexico), avocados (Chile) and Human (Chile and Canada)

Identified in food in Italy

Described in compost (Austria) and in meat-half-stuff (Russia)

Found in USA in soil

Previously reported in clinical samples in Mexico

Described as one of the hypervirulent clones

Found in potatoes (Mexico), meat products, seafood (USA and Spain), urban water, farm feed lot, soil, bovine case of listeriosis (USA), snail (Greece), sheep (Spain), human (USA, Canada and Spain)

Pathogenicity islands

LIPI-1
100%

LIPI-3
88%

LIPI-4
50%

SSI-1
25%

Stress survival genes

SigB
100%

Conclusions

This study has characterized isolates of *L. monocytogenes* from dairy farms and discover the main clonal complexes, some were implicated in human cases of listeriosis. Persistence strains in food production environment has been associated to the presence of stress survival islets, that were detected in this study. The prevalence in the agricultural environment highlights the importance of understanding the ecology and the need to increase measures that can reduce its presence through food chain, increasing food safety.

References

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