Attribution of *Listeria monocytogenes* human cases to food and animal sources in Northern Italy

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Abstract

Human listeriosis is a rare but serious foodborne disease, with high hospitalization (up to 90%) and fatality rates (20-30%) in at-risk population i.e. [icons].

Source attribution of foodborne diseases based on microbial subtyping is widely used to ascertain the main sources of infection by quantifying the relative contributions of different foods to human disease.

Our objective was to assess the contribution of different animal and food sources of human listeriosis in Piedmont and Lombardy regions (Northern Italy) from 2005 to 2016.

A representative collection of 670 *L. monocytogenes* isolates were typed with multi-locus sequence typing (MLST) and multi-virulence locus sequence typing (MVLST).
The Dutch and STRUCTURE source attribution modeling approaches were applied in a comparative fashion.

In both models, the primary source of listeriosis cases was estimated to be dairy (up to 48% of human cases), followed by poultry (3-18%) and game meat (3-16%). Pork (2-3%) and beef (2-4%) seemed to play a minor role. Differences in attributions were observed based on the modeling approach and typing method. Combining MLST and MVLST data did not significantly influence the results of attribution modeling.

Source attribution based on microbial subtyping is a valuable tool for quantifying the contribution of different food-animal sources of human listeriosis to guide public health interventions.

Our results strongly suggest dairy products to be the most important source of human listeriosis in Northern Italy, underlining the lasting need of specific control measures to reduce *L. monocytogenes* contamination in such products.

Introduction

Source attribution:
Quantification of contributions of food and animal reservoirs to human cases of food-borne illness
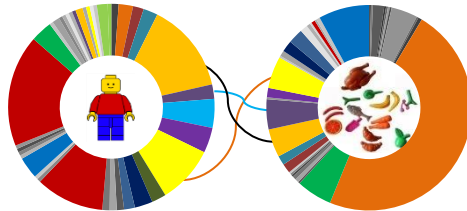
Microbial strain subtyping:
Comparison of the distribution of subtypes *and* Identification of associations between subtypes and sources
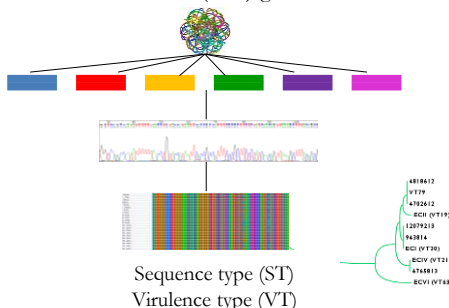
Materials and methods
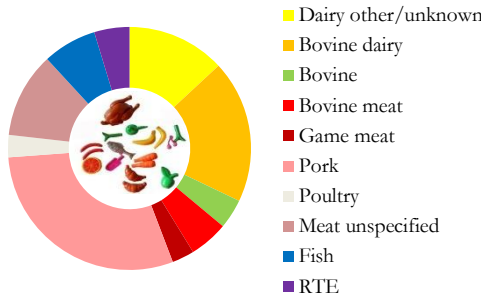
Samples
670 isolates

Clinical   Food/animal
n=230   n=440

Strain typing:
MLST and MVLST
Sequencing of housekeeping (n=7) or virulence (n=8) genes

Sequence type (ST)
Virulence type (VT)

Modeling approach

Dutch	vs.	STRUCTURE
Frequentist		Bayesian
Number of isolates within a given subtype		Frequency of alleles within a source
ST, VT		ST, VT, ST+VT

Discussion arena

Food/animal isolates by source

- Dairy other/unknown
- Bovine dairy
- Bovine
- Bovine meat
- Game meat
- Pork
- Poultry
- Meat unspecified
- Fish
- RTE

Primary source ➔ **dairy products** (bovine + mixed = up to 48% of human cases)

STRUCTURE model ➔ game meat and poultry as possible secondary causes.

Like humans, ruminants and poultry are susceptible to *L. monocytogenes* and thus **virulence genes** responsible for infection may be common in both species. Samples were collected from lymph nodes in ruminants, and from both raw meat and Ready to Eat (RTE) food in poultry.

Combining MLST and MVLST in the STRUCTURE model did not influence the results.

Differences in attributions due to:
- modeling approach and typing method,
- overrepresentation of pork may influence the results of Dutch model.

Dairy products are the most important source of human listeriosis in the studied area ➔ need of **specific control measures** to reduce *L. monocytogenes* contamination in these products.

Usually only RTE are included in listeriosis source attribution but also **raw meat** (game and poultry) may be at risk for **cross-contamination at household level** and must not be under evaluated.

Source attribution based on microbial subtyping is a risk assessment tool to guide and prioritize public health interventions on an evidence based approach.

This is the first study applied to listeriosis in Italy, and its **systematic** use may help to reduce the impact of such a severe disease.