

## SUMMARY

*Yersinia enterocolitica* One Health approach: an investigation into the sources of transmission to man from isolated samples from the national territory.

Keywords: *Yersinia enterocolitica*, molecular characterisation, source attribution

Zoonoses are pathologies that can be naturally transmitted from animals to man through the consumption of contaminated foods. Their severity is extremely variable.

EFSA's data related to the prevalence of zoonotic agents, which in 2020 identified *Y. enterocolitica* (Ye) as the third etiological agent in Europe for food-transmitted diseases, represent the basis upon which to build monitoring programmes along the supply chains of animal and plant-based products.

The trouble in deploying monitoring programmes for better understanding the epidemiology of such an enteropathogen, which is highly invasive, comes from the limited knowledge of its multifactorial pathogenicity mechanisms, of its infection pathways in animals, and of its interaction with the food supply chain.

Such challenges, due mostly to the exclusive use of a long, laborious and hardly sensitive standard microbiological method, have been partly overcome by the publication of an opinion by EFSA (2007), suggesting the development of

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molecular methods for a rapid search of Ye in food and environmental samples. This led in 2015 to the adoption of a standard method based on Real Time PCR (ISO/TS 18867).

Following EFSA's guidelines, a previous joint research programme by IZSLT, ISS, IZSME and IZSLER developed innovative molecular methods to evaluate the presence of Pathogenic Ye in the swine supply chain.

Furthermore, as the different strains of Ye are characterised by highly variable virulence and as only some bio-serotypes are pathogenic to man and animals, the investigation focused on the molecular analysis of different virulence genes.

The new molecular panels have been used to evaluate strains from clinical, food and environmental samples, and from samples that have been collected in the swine supply chain, thus allowing a rapid evaluation of the true prevalence of the microorganism in such contexts.

This project allowed the investigation of the prevalence of the pathogen in further food contexts and the implementation of innovative molecular methodologies for the identification and characterisation of Ye strains that are present in Italy.