



Listeria monocytogenes: a One Health pathogen

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WOAH CC FH, IZS-Teramo National Reference Laboratory for Listeria monocytogenes ERFAN Laboratory training course 17-21 October 2022





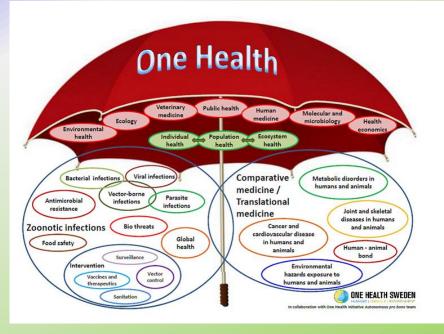
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The One Health concept is a worldwide strategy for expanding interdisciplinary collaborations and communications in all aspects of health care for humans, animals and the environment.

The One Health concept recognizes a unity of purposes irrespective of barriers and the impedance they impose. Close collaboration and communication between the various disciplines of human and veterinary medicine represents a powerful strategy for today's and tomorrow's world.



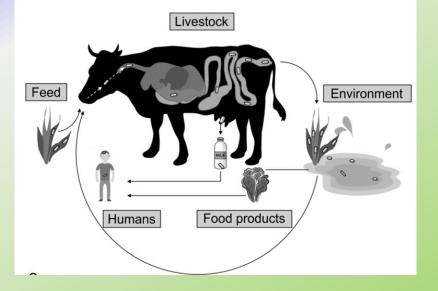
www.onehealthinitiative.com





The complex links between human, animal and environmental health require coordinated multidisciplinary and close collaboration to address the threats from zoonotic diseases.

This can be done through One Health an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems.



Review

Listeria monocytogenes at the interface between ruminants and humans: A comparative pathology and pathogenesis review

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Stefano Bagatella¹, Leticia Tavares-Gomes¹, and Anna Oevermann¹©





One Health is not new, but it has become more important in recent years. This is because many factors have changed interactions between people, animals, plants, and our environment.

Why now?

- Human populations are growing and expanding into new geographic areas. As a result, more people live in close contact with wild and domestic animals, both livestock and pets.
- The earth has experienced changes in climate and land use, such as deforestation and intensive farming practices. Disruptions in environmental conditions and habitats can provide new opportunities for diseases to pass to animals.
- The movement of people, animals, and animal products has increased from international travel and trade. As a result, diseases can spread quickly across borders and around the globe.



Why now?



Today, zoonoses with a wildlife reservoir constitute a major public health problem, affecting all continents.

- The total number of zoonoses is unknown; 1415 known human pathogens have been catalogued, and 62% are of zoonotic origin. Over time, more and more human pathogens are found to be of animal origin. Moreover, most emerging infectious diseases in humans are zoonoses.
- Wild animals seem to be involved in the epidemiology of most zoonoses, and serve as major reservoirs for the transmission of zoonotic agents to domestic animals and humans
- The concept of the 'One Health' approach—involving collaboration between veterinary and medical scientists, policymakers, and public health officials—is necessary in order to promote joint cooperation and control of emerging zoonotic diseases.

Animals (Basel). 2022 Feb; 12(4): 480.				
Published online 2022 Feb 15. doi: 10.3390/ani12040480				

PMCID: PMC8868120 PMID: 35203188

Zoonoses and Wildlife: One Health Approach David González-Barrio



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The European Union (EU) system for the monitoring and collection of information on zoonoses is based on Zoonoses Directive 2003/99/EC1, which obliges EU Member States (MS) to collect relevant and, when applicable, comparable data on zoonoses, zoonotic agents, antimicrobial resistance and foodborne outbreaks.

Since 2019, the annual EU Summary Reports on zoonoses, zoonotic agents and foodborne outbreaks have been renamed the 'EU One Health Zoonoses Summary Report' (EUOHZ), which is co-authored by EFSA and ECDC. The production of the EUOHZ 2020 report was supported by the Consortium ZOE (Zoonoses under a One health perspective in the EU) Work-package 1 composed by the Istituto Superiore di Sanità (Rome, Italy), the Istituto Zooprofilattico Sperimentale delle Venezie (Padova, Italy), the French Agency for Food, Environmental and Occupational Health & Safety (Maisons-Alfort, France), the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise (Teramo, Italy), the Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (Brescia, Italy) <u>under the</u> coordination of the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise (Teramo, Italy).

Listeria is among Zoonoses and zoonotic agents included in compulsory annual monitoring (Directive 2003/99/EC List A)



Listeriosis had the highest proportion of hospitalised cases of all zoonoses under EU surveillance: although there was a reduction in cases and a decrease in notification rates for listeriosis, this change is less marked than for other foodborne zoonoses.

L. monocytogenes was identified as the causative agent in nine strong-evidence and seven weak-evidence foodborne outbreaks in 2020 that together affected 120 people in the EU. Foodborne outbreaks caused 83 hospitalisations (Germany, 34; the Netherlands, 24; Finland, 14; Italy, 7; France, 2; and Austria, 2) and 17 deaths in the EU, the highest number of deaths related to foodborne outbreaks.

SCIENTIFIC REPORT



doi: 10.2903/j.efsa.2021.6971

The European Union One Health 2020 Zoonoses Report

European Food Safety Authority European Centre for Disease Prevention and Control

Abstract

This report of the EFSA and the European Centre for Disease Prevention and Control presents the results of zoonoses monitoring activities carried out in 2020 in 27 EU Member States (MS) and nine non-MS. Key statistics on zoonoses and zoonotic agents in humans, food, animals and feed are provided and interpreted historically. Two events impacted 2020 MS data collection and related statistics: the Coronavirus Disease 2019 (COVID-19) pandemic and the withdrawal of the United Kingdom from the EU. In 2020, the first and second most reported zoonoses in humans were campylobacteriosis and salmonellosis, respectively. The EU trend for confirmed human cases of these two diseases was stable (flat) from 2016 to 2020. Fourteen of the 26 MS reporting data on Salmonella control programmes in poultry met the reduction targets for all poultry categories. Salmonella results for carcases of various species performed by competent authorities were more frequently positive than own-checks conducted by food business operators. This was also the case for Campylobacter quantification results from broiler carcases for the MS group that submitted data from both samplers, whereas overall at EU level, those percentages were comparable. Yersiniosis was the third most reported zoonosis in humans, with 10-fold less cases reported than salmonellosis, followed by Shiga toxin-producing Escherichia coli (STEC) and Listeria monocytogenes infections. Illnesses caused by L. monocytogenes and West Nile virus infections were the most severe zoonotic diseases with the highest case fatality. In 2020, 27 MS reported 3,086 foodborne outbreaks (a 47.0% decrease from 2019) and 20,017 human cases (a 61.3% decrease). Salmonella remained the most frequently reported causative agent for foodborne outbreaks. Salmonella in 'eggs and egg products', norovirus in 'crustaceans, shellfish, molluscs and products containing them' and L. monocytogenes in 'fish and fish products' were the agent/food pairs of most concern. This report also provides updates on tuberculosis due to Mycobacterium bovis or Mycobacterium caprae, Brucella, Trichinella, Echinococcus, Toxoplasma, rabies, Coxiella burnetii (Q fever) and tularaemia.

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Keywords: Campylobacter, foodborne outbreaks, Listeria, monitoring, parasites, Salmonella, zoonoses

Requestor: European Commission Question number: EFSA-Q-2020-00787 Correspondence: zoonoses@efsa.europa.eu IZS

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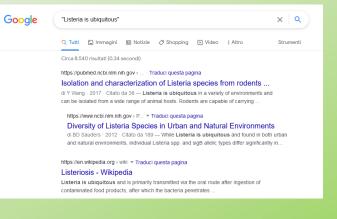
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Listeria monocytogenes (Lm) is a ubiquitous bacterium that causes foodborne illness, listeriosis. The capacity of some strains to adapt to the environmental conditions found in the food industry makes production of high quality, safe food a major challenge. Lm can be found in outdoor environments, farm environments, vegetation, animals, water, sewage and food-processing environments.

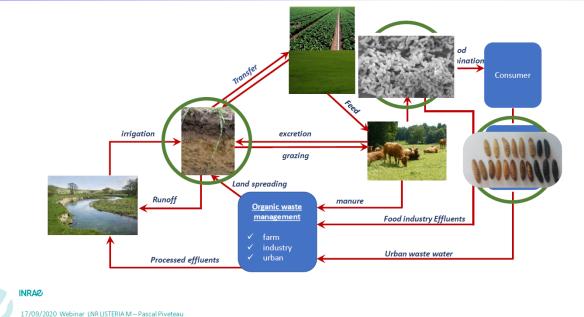
In contrast to most other foodborne pathogens, *Lm* can grow at a wide pH range, at high salt concentrations and at refrigeration temperature.

This capacity to persist and multiply in the food environment makes it especially difficult to control.

The wide growth range and the biofilm-forming capacity allows this pathogen to subsist in the food processing plant environment, survive various food processing hurdles and proliferate in food products.







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Listeria is a paradigm for studying environmental adaptation of pathogenic bacteria.



ListAdapt project

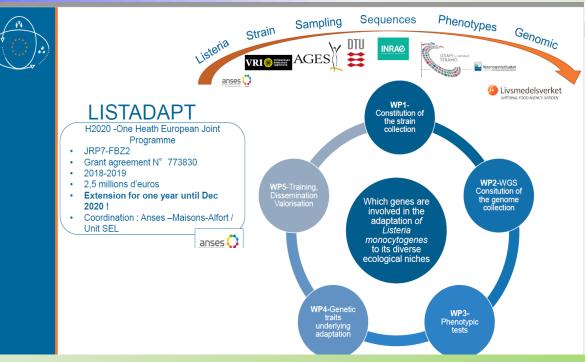
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The primary outcome was to detect the overall prevalence of *L. monocytogenes* in humans, animals, food, and the environment (one health concept).



ListAdapt project



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As part of the H2020 "One Health" European Joint Program, the 3 years research project "LISTADAPT" (Adaptive traits of *Listeria monocytogenes* to its diverse ecological niches) aims to identify genomic mutations and mobile genetic elements underlying adaptation of *Lm* to different environments.

During the project 1484 genomes from strains isolated in 20 European partners including food, environment, veterinary and public health laboratories were typed.

This dataset encompasses a very wide genetic diversity of *Lm* as it covers ~80 different CCs/STs including the most prevalent CCs in Europe and worldwide.

The dataset contributed to improve understanding of *Lm* ecology and will aid in the surveillance of *Lm*.



ListAdapt: Adaptive traits of Listeria monocytogenes to its diverse ecological niches







Strains isolated from:

- soil and farm environment
- Wild and farm Animals
- Health Animals and with clinical symptoms
- Food (RTE fish, meat, dairy and vegetables & fruits) and food production environment

ListAdapt project











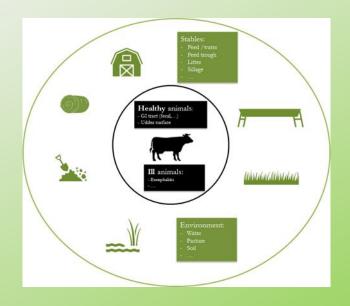


ListAdapt project



Working Packages of LISTADAPT

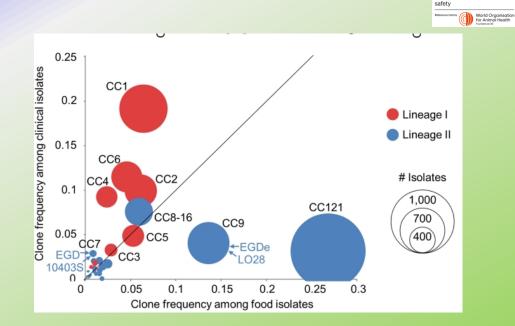
- WP1: Strain collections (existing strains + new sampling)
- WP2 : Sequencing (2000 strains)
- WP3: Phenotypic characterization on 200 selected strains (antibiotics and biocides resistance, biofilm formation, survival in stress conditions)
- WP4: Identification of genetic traits in *Listeria* monocytogenes underlying adaptation to the ecological niches (GWAS)





Listeria Clonal Complex

Many investigations have focused on food and clinical strains by comparing the prevalence of clonal complexes and their preferential association to food and human sectors. ST1, ST2, ST4, ST6 are demonstrated as being strongly associated with a clinical origin and are those most likely to cause disease, in particular human central nervous system or maternal-neonatal listeriosis. Others, such as ST9 and ST121, are more often isolated in highly immuno-compromised patients and are food-associated clones.



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Maury MM, Tsai YH, Charlier C, Touchon M, Chenal-Francisque V, Leclercq A, Criscuolo A, Gaultier C, Roussel S, Brisabois A, Disson O, Rocha EPC, Brisse S, Lecuit M. Uncovering Listeria monocytogenes hypervirulence by harnessing its biodiversity. Nat Genet. 2016 Mar;48(3):308-313. doi: 10.1038/ng.3501. Epub 2016 Feb 1. Erratum in: Nat Genet. 2017 Mar 30;49(4):651. Erratum in: Nat Genet. 2017 May 26;49(6):970. PMID: 26829754; PMCID: PMC4768348.



Listeria Clonal Complex

Bagatella et al., 2022:

Major Lm CCs have also been shown to spread globally over time. Within a given geographic region, predominant lineages might shift over time. Clones are emerging in the 21st century in various continents. This is speculated to occur due to genetic diversification, possibly as a result of fitness adaptation or global dispersion through human travel, animal, or food trade.

CC1 CC412 CC20 CC220 CC54	Environmenta	
CC7 ST184 CC18 CC415 CC26	CC21 CC4-CC217 CC37 CC6 CC59	
CC77	CC8 CC2 CC11	CC14 CC451
		CC29 CC9 ST36
Clinical		CC31 CC379



Bagatella S, Tavares-Gomes L, Oevermann A. *Listeria monocytogenes* at the interface between ruminants and humans: A comparative pathology and pathogenesis review. Veterinary Pathology. 2022;59(2):186-210. doi:10.1177/03009858211052659.



ListAdapt project: results

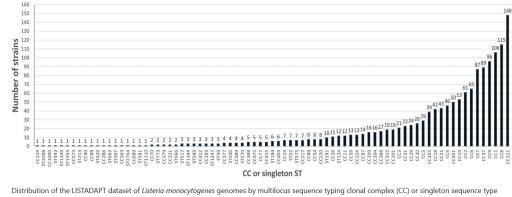


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Overall, the 1484 strains clustered into 137 MLST STs, which belonged to 54 CCs, 25 singleton STs and 22 unknown (novel ST)

Fig. 3

From: A European-wide dataset to uncover adaptive traits of Listeria monocytogenes to diverse ecological niches



(ST).



ListAdapt project: results



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Difference ENV- FOOD		1.4 1.4 1.7 1.8 2.2 2.3 3.0 4.6 4.9 12.2
Food strain	144 5.5 7.1 4.8 2.8 2.4 1.9 2.2 0.5 1.0 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	1,1 0,3 0,3 1,5 0,8 1,3 0,0 2,6 2,6 6,1
Animal and environmental strains	26 21 40 22 0.8 0.4 0.5 0.9 0.0 0.6 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	25 1,7 20 3,3 3,0 3,7 3,0 7,2 7,5 18,3
MLST clonal complex	CC3 CC3	CC20 CC412 CC28 CC28 CC28 CC21 CC7 CC37 CC37 CC37 CC37 CC37 CC451 CC37 CC451 CC37 CC451 CC37 CC451 CC37 CC37 CC18 CC18 CC18 CC18 CC18 CC18 CC18 CC1



ListAdapt project: results

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WP3-WP4 results: Phenotypic tests were performed to investigate the ability of these strains to survive in the soil.

Genome Wide Association Studies (GWAS) analysis did not evidence any link between the origin, the lineage or CC and the fitness in soil.

This data suggest that the ability to survive in the soil is linked to multiple genetic factors. However, GWAS applied on smaller and more genetically homogeneous subset (strains from the same CC or from the same origin) successfully identified phage-related- genes associated with soil survival rate.

We also tested the antimicrobial susceptibility toward 11 antibiotics and 4 biocides.

Results revealed that strains isolated from food exhibited overall higher minimal inhibitory concentrations (MIC) for ammonium quaternary compounds (QACs) and peracetic acid (PAC) than strains isolated from animals and natural environments.

Conversely, no significant difference was observed among MIC of antibiotics for strains depending on their origins.



ListAdapt project: conclusion



- The constructed dataset provides a better understanding of the Listeria monocytogenes transmission routes from the farm/natural environment to food and FPE and improves our understanding of its ecology.
- The dataset may also help to assess the importance of animal and food strains for human infection.
- It can be used by the scientific community to improve our understanding of the Lm population structure and the Lm evolutionary history, to facilitate the detection of the emerging Lm clones and to identify genetic traits related to the adaptation of Lm to particular ecological niches (ecophysiology).





THANK YOU!

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