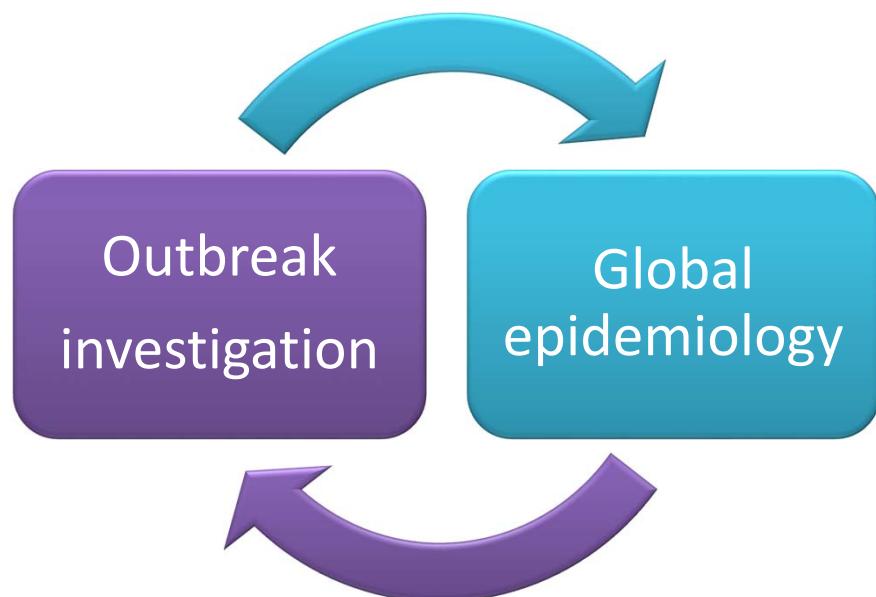

Epidemiologia molecolare della listeriosi: dal fingerprinting al WGS

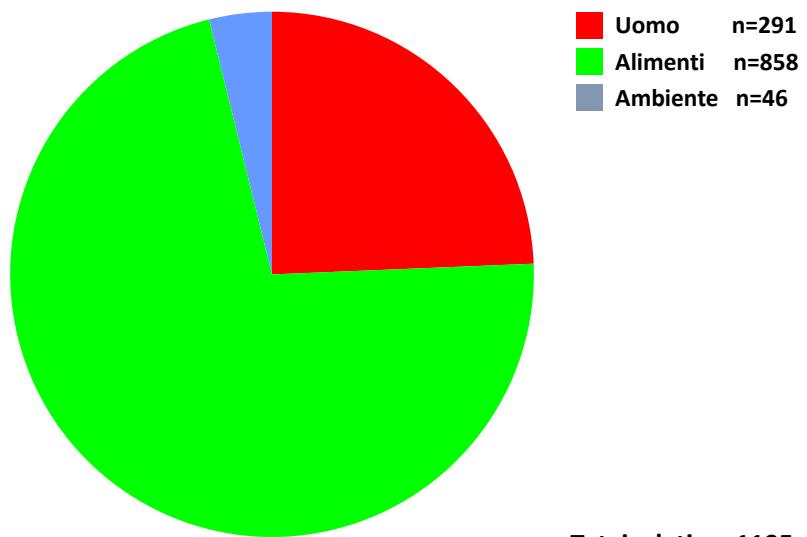


Dr. Antonio Parisi

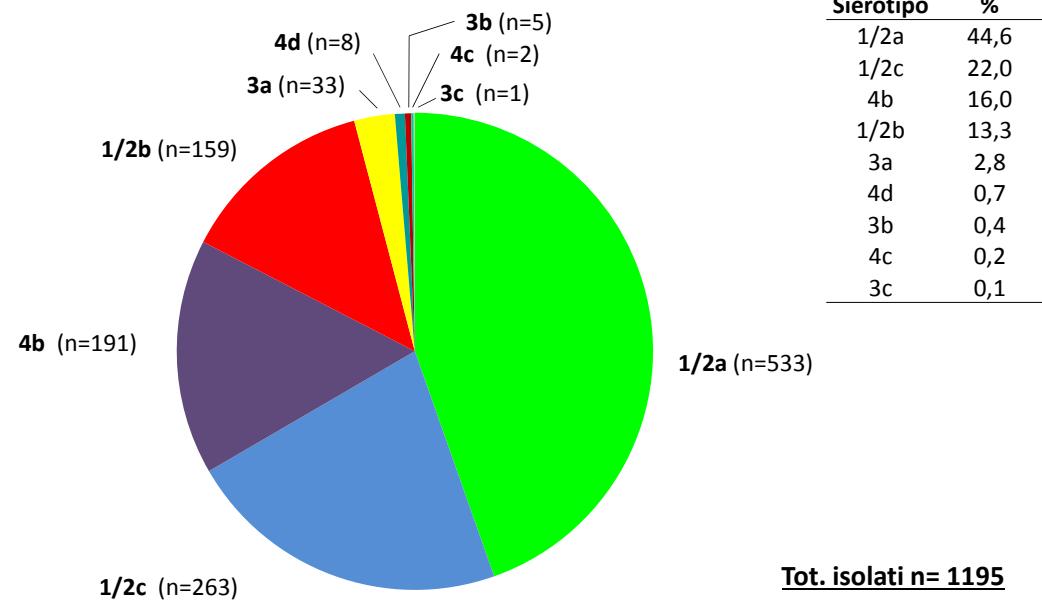
Epidemiologia molecolare

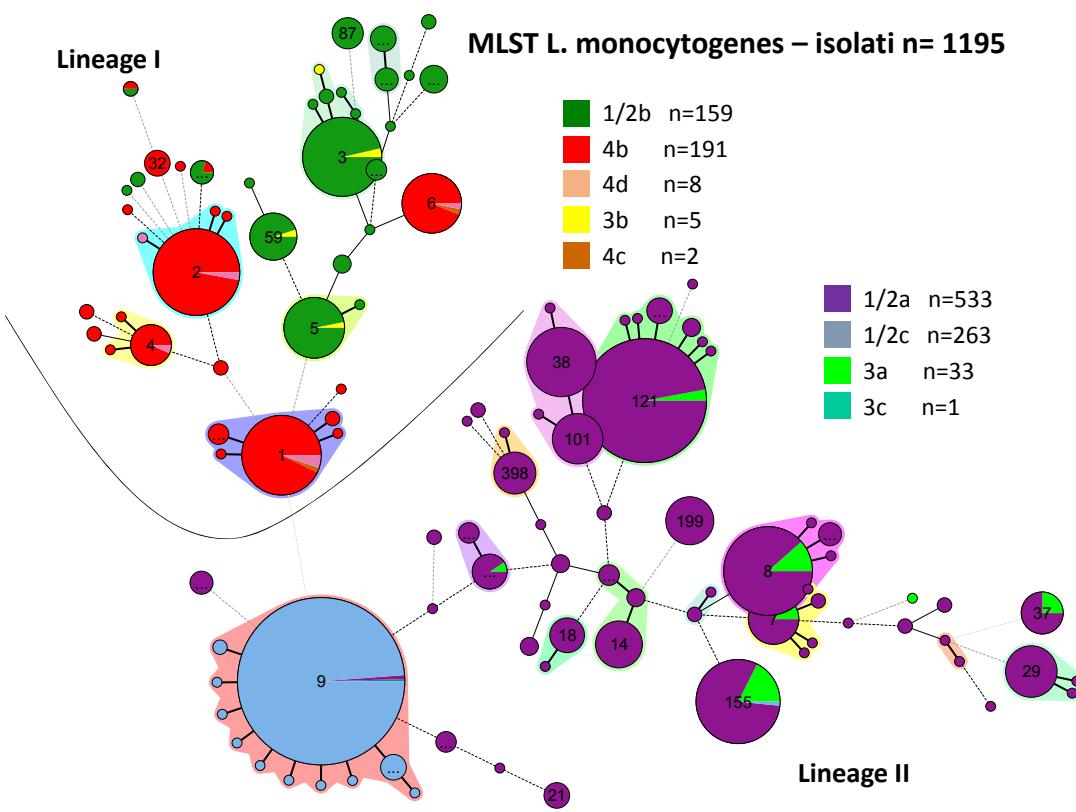


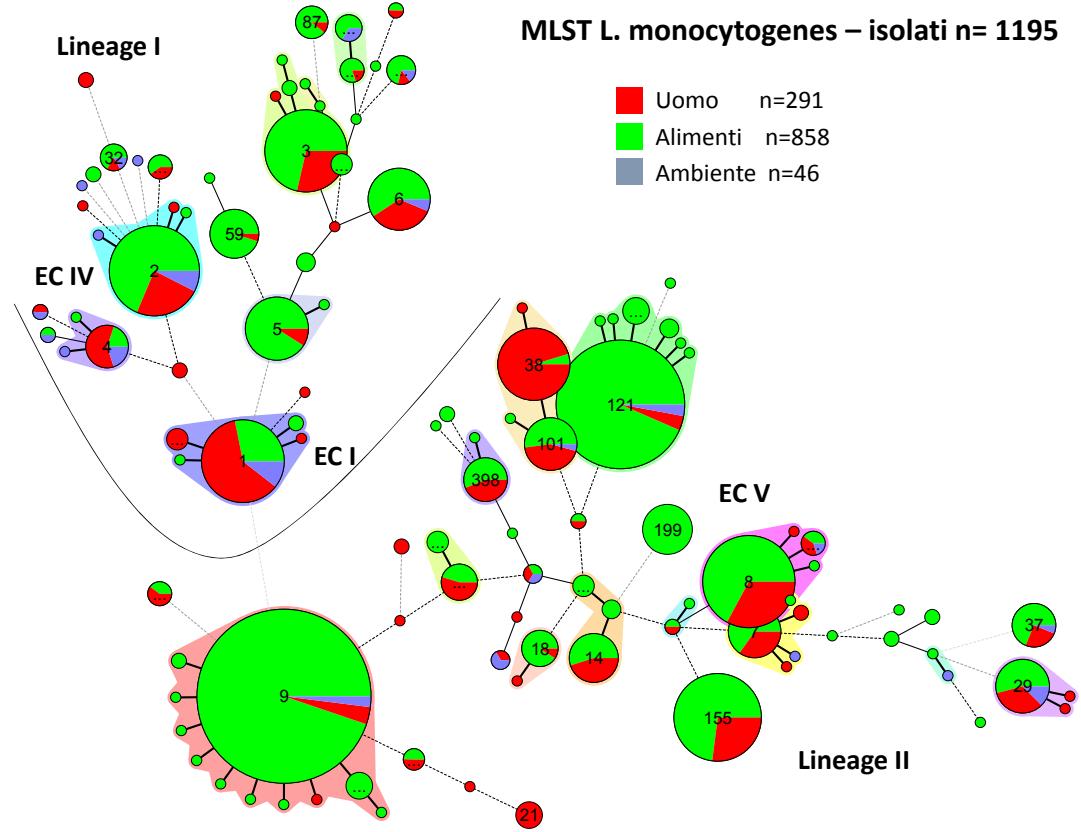
L. monocytogenes – isolati



L. monocytogenes - sierotipi



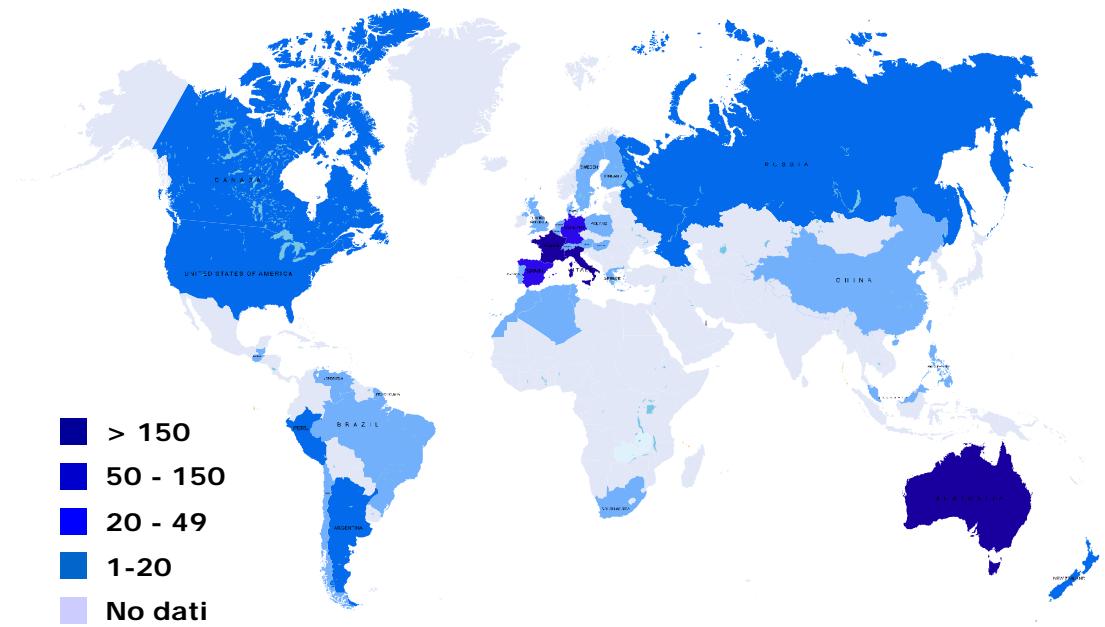




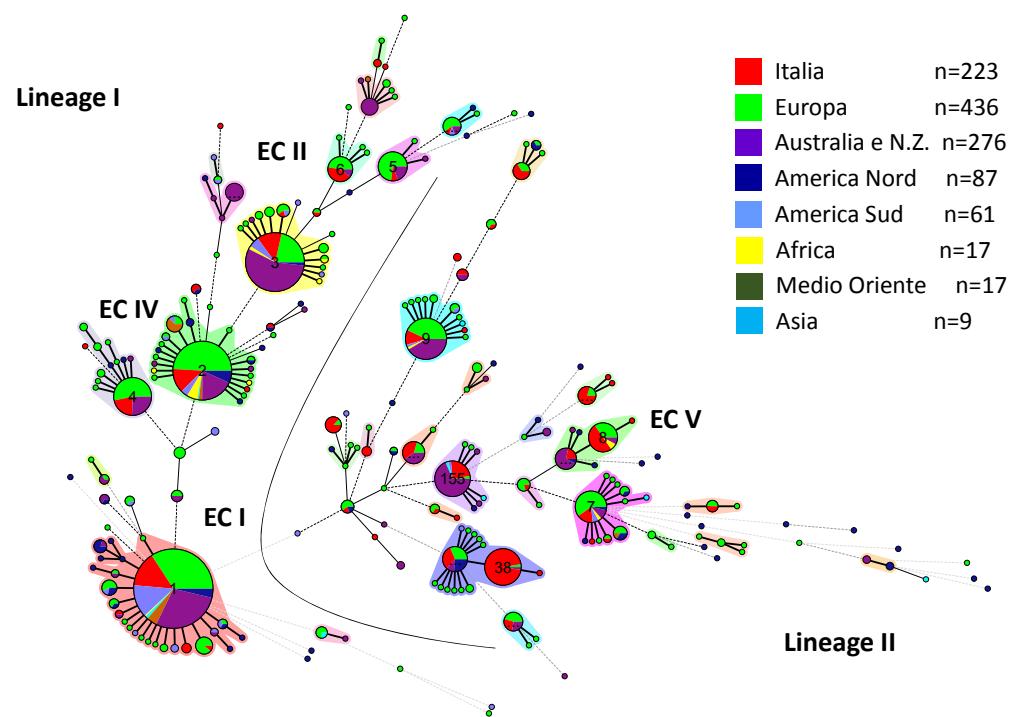
L. monocytogenes Cloni Epidemici (EC)

- **ECI (Lineage I, 4b, *comK* prophage -)**
 - Canada coleslaw, 1981
 - LA soft cheese, 1985
 - Switzerland soft cheese, 1989
- **ECII (Lineage I, 4b, *comk* prophage +)**
 - U.S. hot dog, 1998-1999
 - U.S. turkey deli, 2002
 - Belgium time-linked cluster of cases, 2006-2007
- **ECIII (Lineage II, 1/2a, *comK* prophage +)**
 - U.S. hot dog, 1989
 - U.S. turkey deli, 2000
- **ECIV (Lineage I, 4b, *comK* prophage +)**
 - Boston vegetable, 1979
 - UK pate, 1989
 - Northern Italy corn, 1997
- **ECV (Lineage II, 1/2a, *comK* prophage +)**
 - 2008 Canadian RTE meat outbreak
 - 2010 Canadian prosciutto ham outbreak

MLST database – Uomo (n=1126)



L. monocytogenes – Uomo (n=1126)

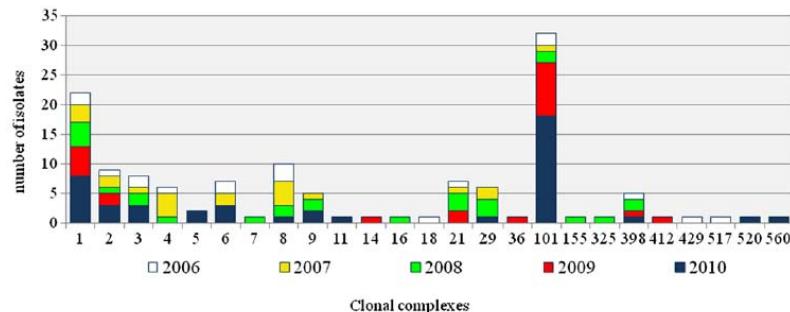


RESEARCH ARTICLE

Open Access

Enhanced surveillance of invasive listeriosis in the Lombardy region, Italy, in the years 2006-2010 reveals major clones and an increase in serotype 1/2a

Caterina Mammina^{1*}, Antonio Parisi², Anna Guaita³, Aurora Aleo¹, Celestino Bonura¹, Antonino Nastasi⁴ and Mirella Pontello³



Whole Genome Sequencing

Nextera XT
Library prep
Miseq

Assembly
pipeline
Galaxy
SPAdes 3.12

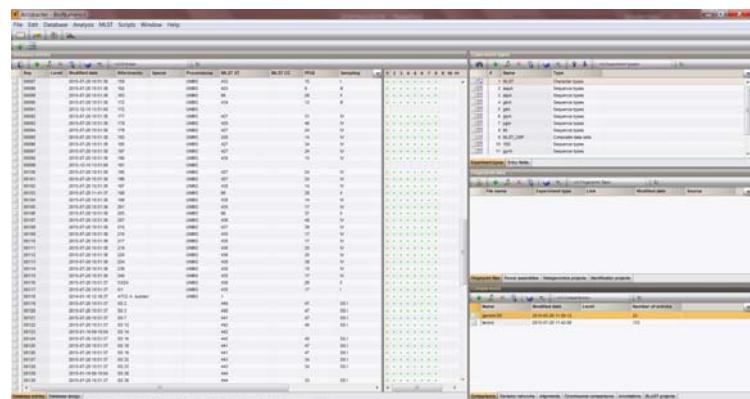
MLST
database

VFDB
NCBI blast

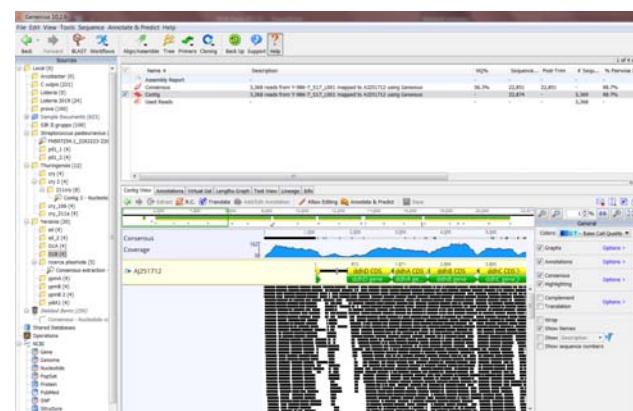
CARD
ARGannot
RESfinder
NCBI

Conclusioni

Bionumerics



Geneious



Galaxy

Tools

- Get Data
- Send Data
- Collection Operations
- Lift-Over
- Text Manipulation
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association
- BITPER-NEW
- ABRicate Mass screening of configts for antimicrobial and virulence genes
- ABRicate List all of abricate's available databases.
- Trimmomatic flexible read trimming tool for Illumina NGS data
- SPAdes genome assembler for regular and single-cell projects
- Filter SPAdes repeats Remove short and repeat configts/scaffolds

SPAdes genome assembler for regular and single-cell projects (Galaxy Version 3.12.0+galaxy1)

Single-cell? Yes No

This option is required for MDA (single-cell) data. (--sc)

Run only assembly? (without read error correction) Yes No

(--only-assembler)

Careful correction Yes No

Tries to reduce number of mismatches and short indels. Also runs MismatchCorrector – a post processing tool, which uses BWA tool (comes with SPAdes). (-careful)

Automatically choose k-mer values Yes No

k-mer choices can be chosen by SPAdes instead of being entered manually

K-mers to use, separated by commas

Comma-separated list of k-mer sizes to be used (all values must be odd, less than 128, listed in ascending order, and smaller than the read length). The default value is 21,33,55.

Coverage Cutoff

Libraries are IonTorrent reads? Yes No

Libraries

1: Libraries

Library type

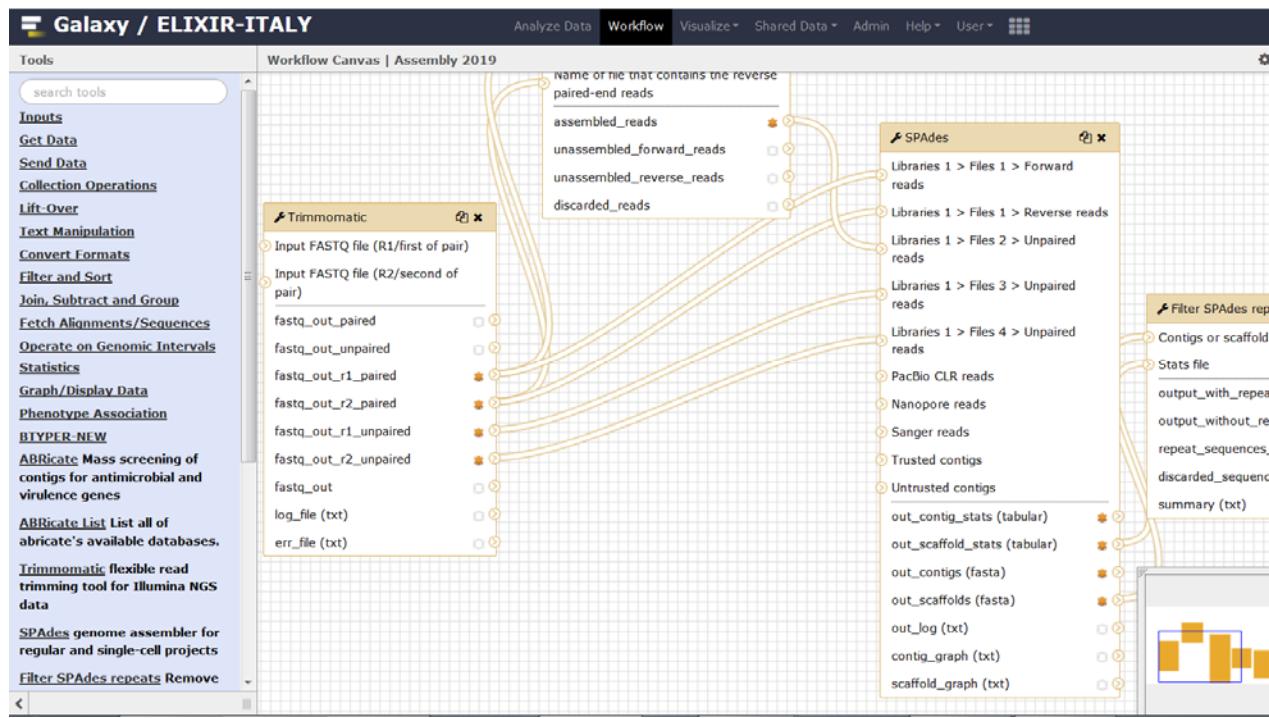
Orientation

History

BC106 Assembly 2019
18 shown 1.33 GB

- 18: ABRicate on data 13 report file
- 17: Results summary
- 16: Discarded sequences
- 15: Repeat sequences
- 14: Filtered sequences (no repeats)
- 13: Filtered sequences (with repeats)
- 12: SPAdes on data 4_data_3_and_others: assembly graph with scaffolds
- 11: SPAdes on data 4_data_3_and_others: assembly graph
- 10: SPAdes on data

Galaxy



Whole Genome Sequencing

Nextera XT
Library prep
Miseq

Assembly
pipeline
Galaxy
SPAdes 3.12

MLST
database

VFDB
NCBI blast

CARD
ARGannot
RESfinder
NCBI

<https://bigsdb.pasteur.fr>

Query: Search | Browse | List
PasteurMLST Options: General | Schemes | Loci | Scheme fields
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Curate

Log in Toggle: ⓘ

Listeria locus/sequence definitions database

The Listeria PasteurMLST sequence definition database contains allele and profile data representing the total known diversity of Listeria species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence or genome.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching criteria (all loci together).
- Locus-specific sequence attribute search - select, analyse and download specific alleles.
- Search, browse or enter list of profiles.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.

Downloads

- Allele sequences
- MLST
- Profiles

Option settings

- Set general options
- Scheme options

Submissions

- Manage submissions

General information

- Number of sequences: 316,347
- Number of profiles: Show
- Last updated: 2019-06-27
- Profile update history
- About BIGSdb

Export

- Profiles
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

https://bigsdb.pasteur.fr

Query: Search | Browse | List
Options: General | Schemes | Loci | Scheme fields
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Curate

Log in Help Toggle

Sequence query - Listeria locus/sequence definitions

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

Please select locus/scheme Order results by

All loci All loci (multiple contigs up to whole genome in size)

MLST
cgMLST1748
PCR-serogroup
Virulence
Antibiotic Resistance
Metal & Detergent Resistance
Listeria Stress Islands
Stress Islands
sigB operon
Rhamnose operon

locus

Alternatively upload FASTA file or enter Genbank accession

Select FASTA file: Nessun file selezionato.

Action

IRIDA ARIES

IRIDA Progetti ▾ Analisi ▾

Cerca Help ▾ 🔍

Dettagli dell'Analisi

ID	1184
Tipo	PHANTAsTIC Pipeline
Versione	0.3
Stato	Completata
Creato	27 Jun 2019

File di Output

- H566-phantastic_vir.tab
- H566-phantastic_contigs.fasta
- H566-phantastic_amr.tab
- H566-phantastic_dm.tsv
- H566-phantastic_tree.newick
- H566-phantastic_out.json

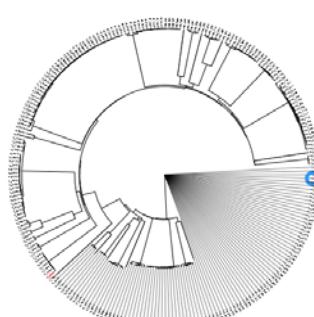
Scarica File

Azioni

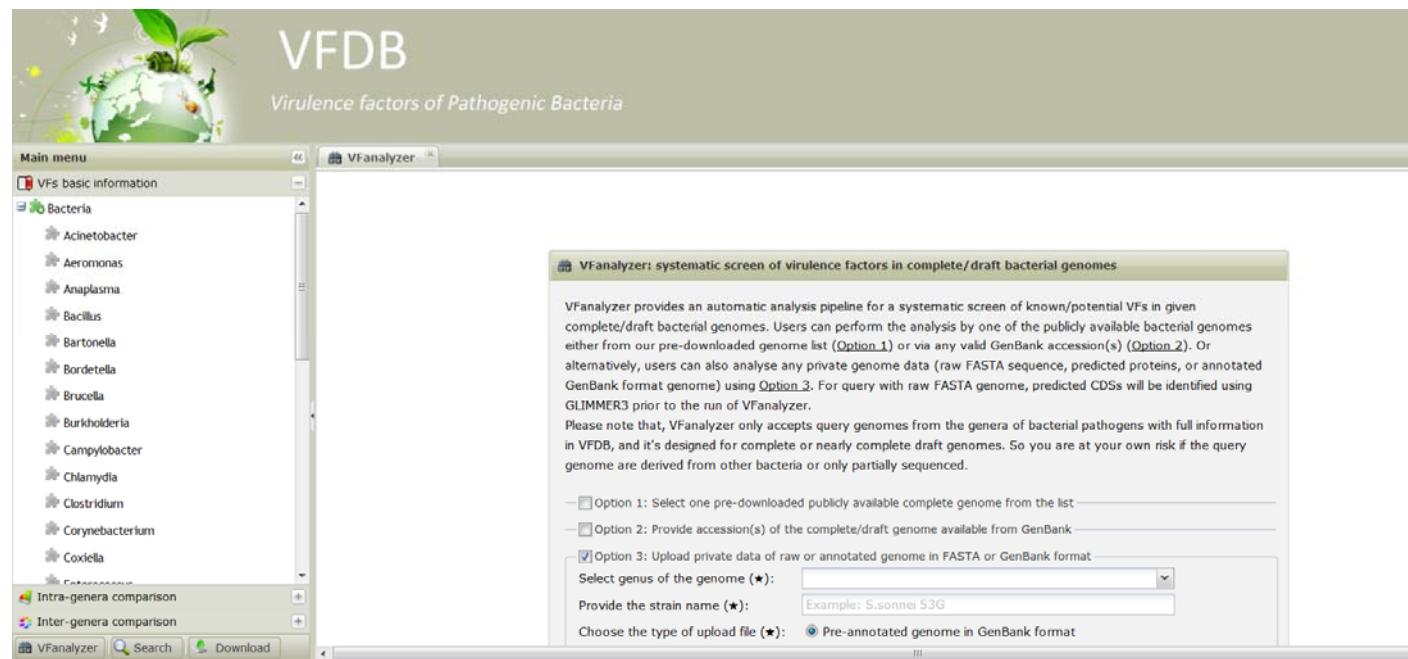
Anteprima File di Input Provenienza

Rettangolare Circolare Radiale Diagonale Gerarchico

His



Virulenza



The screenshot shows the VFDB (Virulence factors of Pathogenic Bacteria) web interface. The top banner features a green globe with a sprout and the text "VFDB" and "Virulence factors of Pathogenic Bacteria". The main menu includes "Main menu", "VFs basic information", "Bacteria" (selected), "Intra-genera comparison", and "Inter-genera comparison". A sub-menu under "Bacteria" lists genera: Acinetobacter, Aeromonas, Anaplasma, Bacillus, Bartonella, Bordetella, Brucella, Burkholderia, Campylobacter, Chlamydia, Clostridium, Corynebacterium, Coxella, and Pasteurellales. The central panel displays the "VFAnalyzer: systematic screen of virulence factors in complete/draft bacterial genomes" dialog. It explains the analysis pipeline, noting that VFAnalyzer only accepts query genomes from bacterial pathogens with full information in VFDB. It provides three options: 1) Select one pre-downloaded publicly available complete genome from a dropdown menu; 2) Provide accession(s) of the complete/draft genome from GenBank; or 3) Upload private data of raw or annotated genome in FASTA or GenBank format. A dropdown menu for "Select genus of the genome" is open, showing "Corynebacterium". A text input field for "Provide the strain name" contains "Example: S.sonnei 53G". A radio button for "Choose the type of upload file" is set to "Pre-annotated genome in GenBank format".

Antibiotico-resistenza

Center for Genomic Epidemiology

Username:
Password:

Home Services Instructions Output Overview of genes Article abstract

ResFinder 3.0

CARD
Use or Download Copyright & Disclaimer

Browse Analyze Download About

Search

Home > Microbiology & Humanities Sciences > Database > ARO-ANNOT

MICROBIOLOGY & HUMANITIES SCIENCES

ARG-ANNOT

Antibiotic Resistance Gene-ANNOtation

NCBI Resources How To

BioProject BioProject Advanced Browse by Project attributes

Display Settings: Send to:

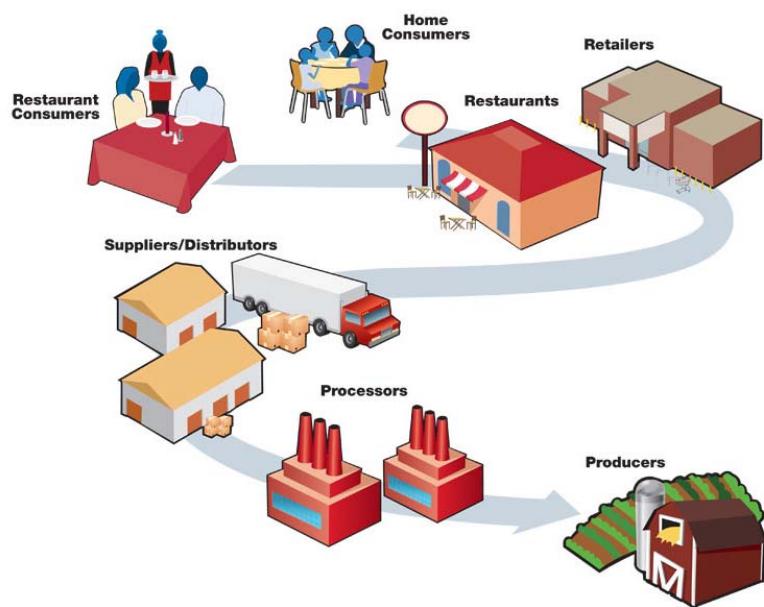
Sign in to NCBI

Bacterial Antimicrobial Resistance Reference Gene Database

Accession: PRJNA313047 ID: 313047 Full text in PMC

Outbreak investigation

Tracing the Food Back to the Source



AFLP > PFGE

International Journal of Food Microbiology 149 (2011) 177–182



Contents lists available at ScienceDirect
International Journal of Food Microbiology

journal homepage: www.elsevier.com/locate/ijfoodmicro



Short communication

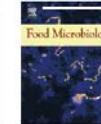
Comparison of two AFLP methods and PFGE using strains of *Listeria monocytogenes* isolated from environmental and food samples obtained from Piedmont, Italy

Food Microbiology 27 (2010) 101–108



Contents lists available at ScienceDirect
Food Microbiology

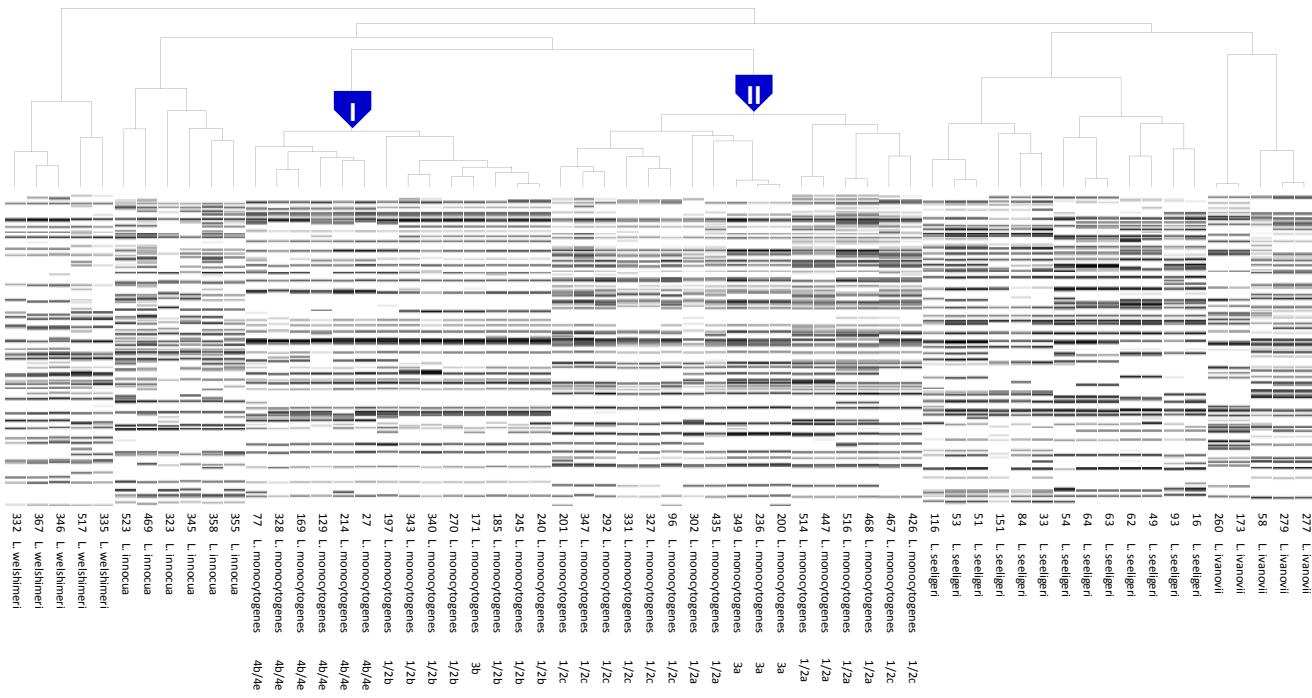
journal homepage: www.elsevier.com/locate/fm



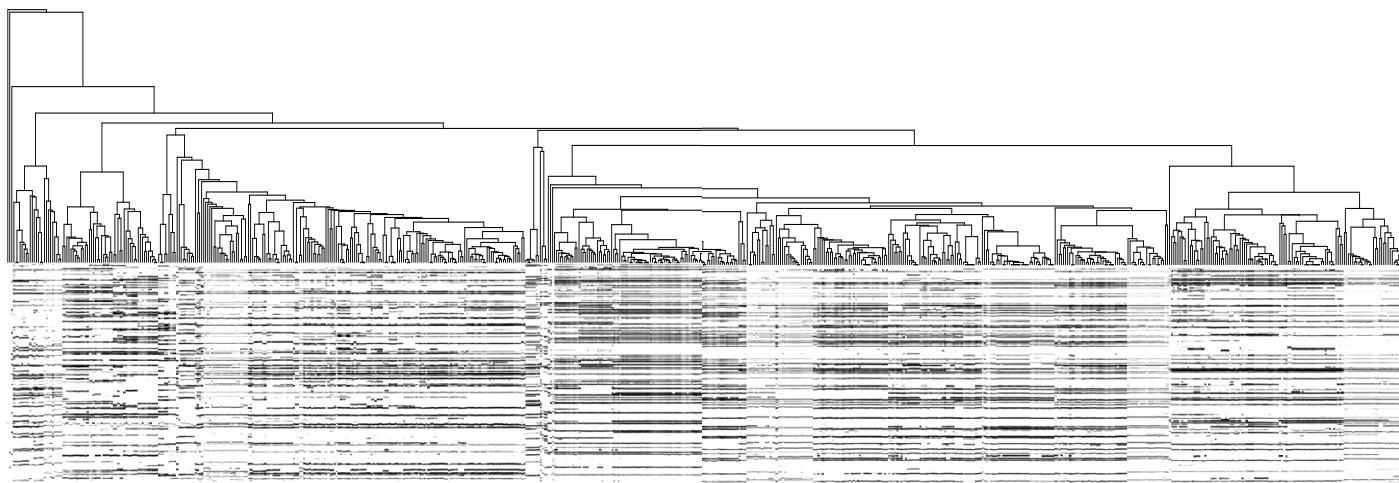
Amplified Fragment Length Polymorphism and Multi-Locus Sequence
Typing for high-resolution genotyping of *Listeria monocytogenes*
from foods and the environment

Antonio Parisi^{a,*}, Laura Latorre^a, Giovanni Normanno^b, Angela Miccolupo^a,
Rosa Fraccalvieri^a, Vanessa Lorusso^b, Gianfranco Santagada^a

Fingerprinting



AFLP



N=670

Listeria e alimenti

Journal of Food Protection, Vol. 70, No. 6, 2007, Pages 1507–1512
Copyright ©, International Association for Food Protection

Low Prevalence of *Listeria monocytogenes* in Foods from Italy

L. LATORRE,^{1,*} A. PARISI,² R. FRACCALVIERI,¹ G. NORMANNO,³ M. C. NARDELLA LA PORTA,⁴ E. GOFFREDO,⁴
L. PALAZZO,⁵ G. CICCARESE,⁶ N. ADDANTE,² AND G. SANTAGADA¹

Listeria e alimenti



Food Control
Available online 23 May 2012
In Press, Accepted Manuscript — Note to users

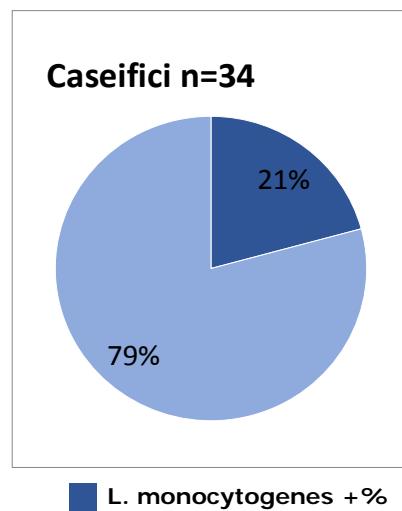
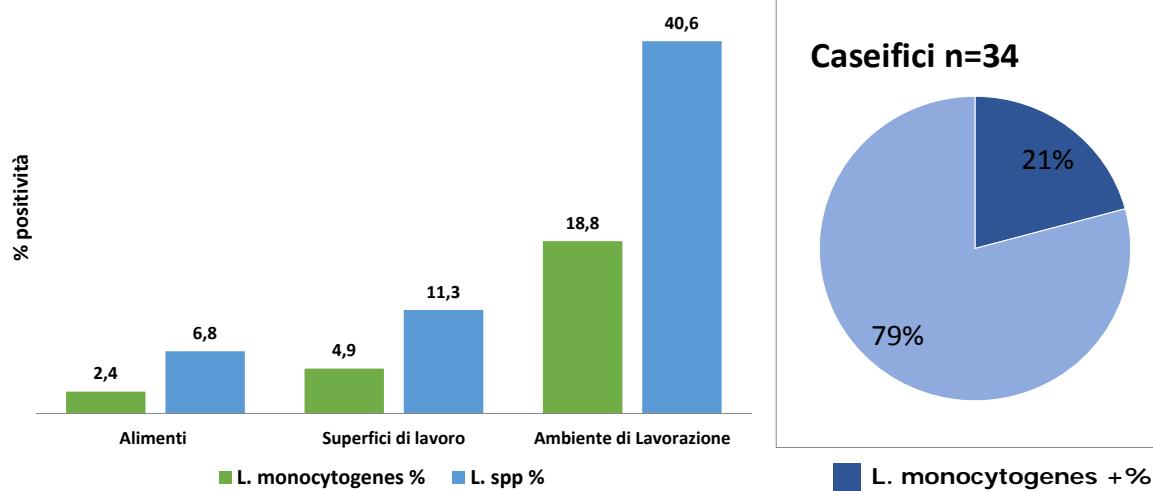


Occurrence of *Listeria* spp. in Dairy plants in southern Italy and Molecular subtyping of isolates using AFLP

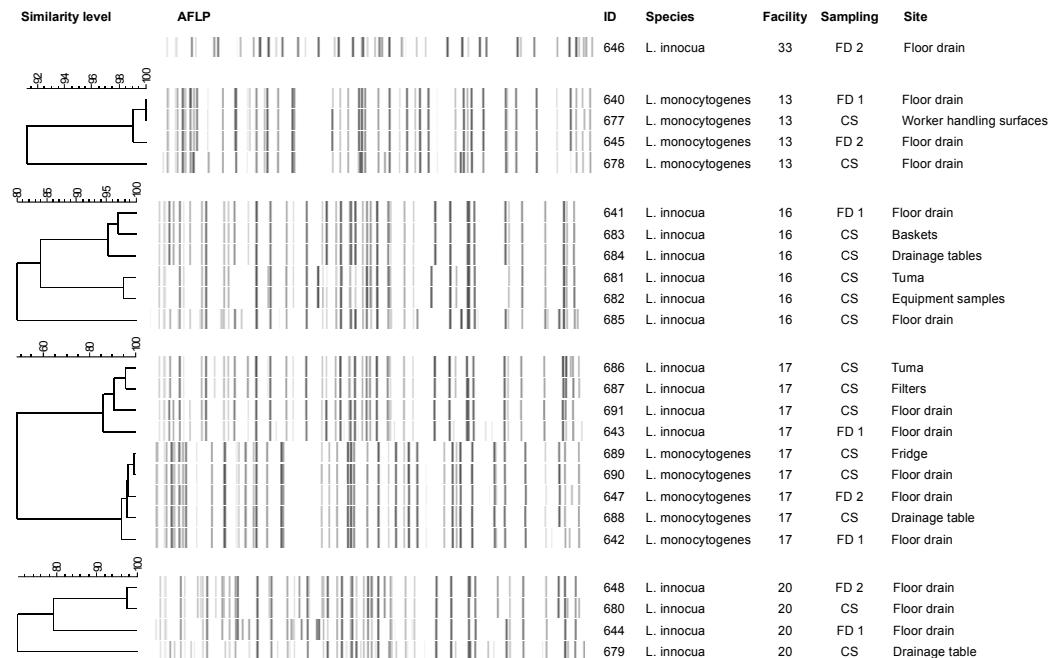
A. Parisi^a , L. Latorre^a, R. Fraccalvieri^a, A. Miccolupo^a, G. Normanno^b, M. Caruso^a, G. Santagada^a



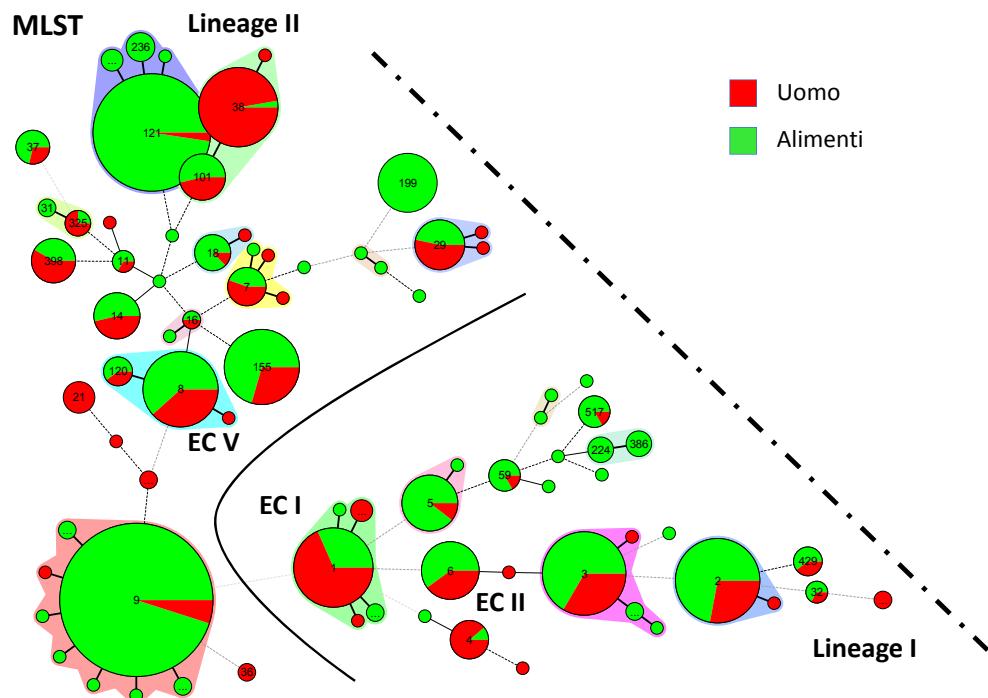
Listeria e alimenti



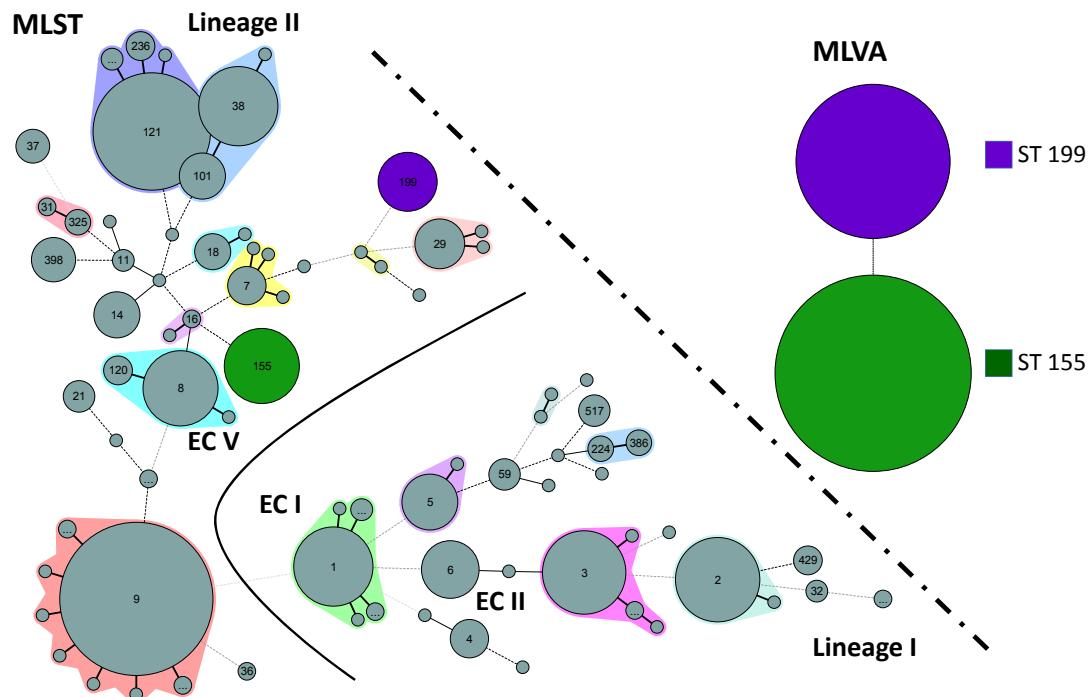
Listeria e alimenti



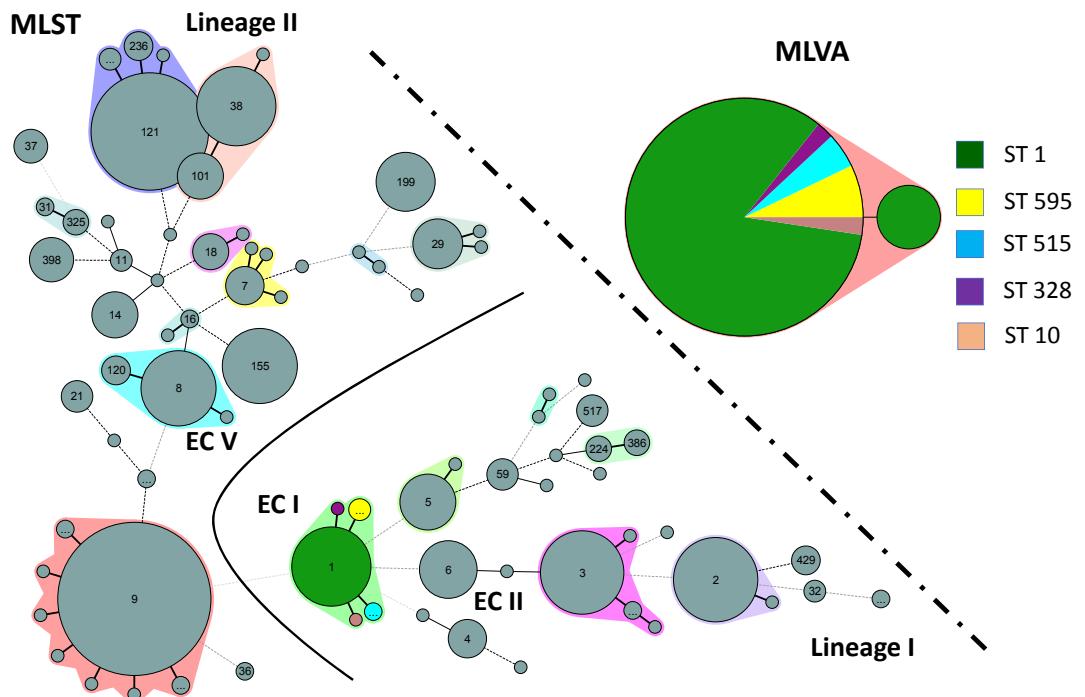
MLVA>MLST



MLVA>MLST



MLVA>MLST



MLVA>MLST

 **MLVAbank** for Microbes Genotyping

Home Users Databases

Public Databases

Listeria

Owned by aparis

Query Views ▾ Panel selection ▾

Columns (click to hide) : Key - MLST_ST - Serotype - data - origine - matrice - Nazione - Provincia - abcZ - bgIA - cat - dapE - dat - Idh - IhkA

Strains per page 100 ▾ 1 2 3 > Go to page 1 ▾

Key	MLST_ST	Serotype	data	origine	matrice	Nazione	Regione	Provincia	abcZ	bgIA	cat	dapE	dat	Idh	IhkA	LMV1	LMV3	LMV9	LM32	LMV6	LM15
338	224	1/2b	2005	ALIMENTI	Salsiccia stagionata	Italia	Basilicata		11	3	12	38	3	94	2	20	3	11	17	5	5
1231	3	1/2b	2010	ALIMENTI	salame	Italia	Lazio	Roma	4	4	4	3	2	1	5	20	8	10	17	5	8
1232	9	1/2c	2010	ALIMENTI	carne macinata	Italia	Lazio	Roma	6	5	6	4	1	4	1	24	7	7	13	4	3
1233	8	1/2a	2010	ALIMENTI	salmone	Italia	Lazio	Roma	5	6	2	9	5	3	1	21	6	7	13	4	3
1234	386	1/2b	2010	ALIMENTI	Latte da Sezione	Italia	Toscana	Arezzo	11	3	12	38	3	94	42	20	3	11	17	5	5
1235	155	3a	2010	ALIMENTI	muscolo bovino	Italia	Basilicata		7	10	16	7	5	2	1	20	2	7	13	3	3
1242	6	4b/4e	2010	ALIMENTI	Mozzarella	Italia	Puglia		3	9	9	3	3	1	5	16	2	10	17	9	4
1243	6	4b/4e	2010	ALIMENTI	Mozzarella	Italia	Puglia		3	9	9	3	3	1	5	16	2	10	17	8	4
1244	1	4b/4e	2010	ALIMENTI	Salsiccia piccante fresca	Italia	Puglia		3	1	1	1	3	1	3	19	2	10	18	4	4
1245	9	1/2c	2010	ALIMENTI	Salsiccia fresca di suino	Italia	Basilicata		6	5	6	4	1	4	1	23	7	7	13	5	3

Multistate Outbreak of Listeriosis



Dati CDC

N. casi	22
Decessi	4
Stati	14



Multistate Outbreak of Listeriosis



Ministero della Salute

Ti trovi in: [Home](#) > [Temi](#) > [Alimenti](#) > [Sicurezza alimentare](#) > [Archivio in evidenza](#) > Dettaglio In evidenza

Sicurezza alimentare

Listeriosi umana negli USA dovuta a consumo di ricotta italiana

Si comunica che a seguito dell'attività condotta dal Ministero della salute con la collaborazione dell'Istituto superiore di sanità e del Comando carabinieri per la tutela della salute-Nas, per determinare le cause di listeriosi umana verificatesi negli Stati Uniti, a seguito di consumo di ricotta della ditta "Fattorie Chiarrappa" con stabilimento in Conversano (BA), il procuratore della repubblica di Bari ha disposto il sequestro su tutto il territorio nazionale dei seguenti prodotti:

- Ricotta frescolina marite tipo toscanella
- Ricotta Torretta Marte
- Ricotta frescolina Marte arrostita
- Ricotta marzotica Marte tipo greca
- Ricotta marzotica Marte.

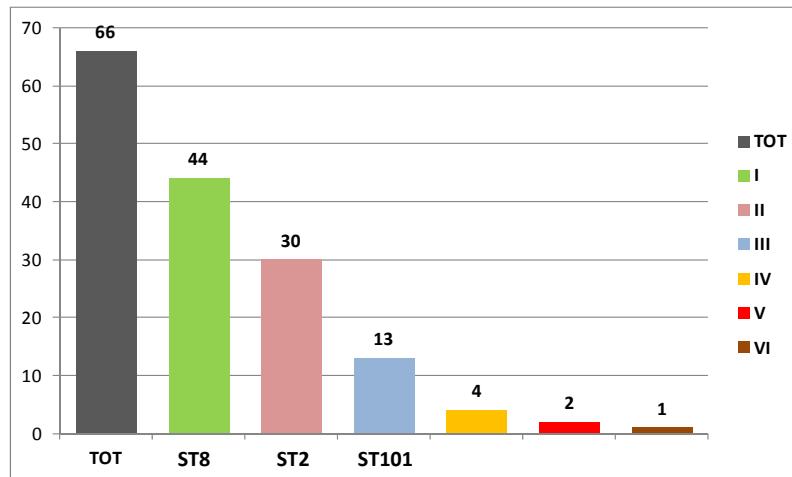
A cura di:
**Direzione generale per
l'igiene e la sicurezza degli
alimenti e la nutrizione**

Il sequestro, sempre su disposizione della procura, sarà effettuato dal Nas e dal Corpo forestale dello stato.
Il ritiro dal mercato dei prodotti indicati, si è reso necessario a scopo precauzionale in quanto, non sono state riscontrate le garanzie sanitarie richieste dalle disposizioni normative in materia di igiene della produzione.
Si ricorda al consumatore che la listeriosi fa parte del gruppo di malattie definibili come tossinfezioni alimentari, e prende il nome dall'agente patogeno che la causa, il batterio Listeria monocytogenes.
La listeriosi è particolarmente pericolosa per le persone immunodepresse, malati di cancro, diabete, Aids, le persone anziane, i neonati e le donne in gravidanza.

Multistate Outbreak of Listeriosis



Multistate Outbreak of Listeriosis



Multistate Outbreak of Listeriosis

TOTALE	392	270	74	33	10	4	1
--------	-----	-----	----	----	----	---	---

Profili genetici isolati	Profilo MLVA	Prob. MLST	MLST
I	21 7 7 13 4 3	ST8	ST8
II	19 2 11 17 5 6	ST2	ST2
III	21 2 7 14 4 7	ST38	ST101
IV	19 2 7 14 4 5	ST121	ST121
V	20 4 10 15 4 5	ST5	ST5
VI	21 6 7 13 4 3	ST8	ST8



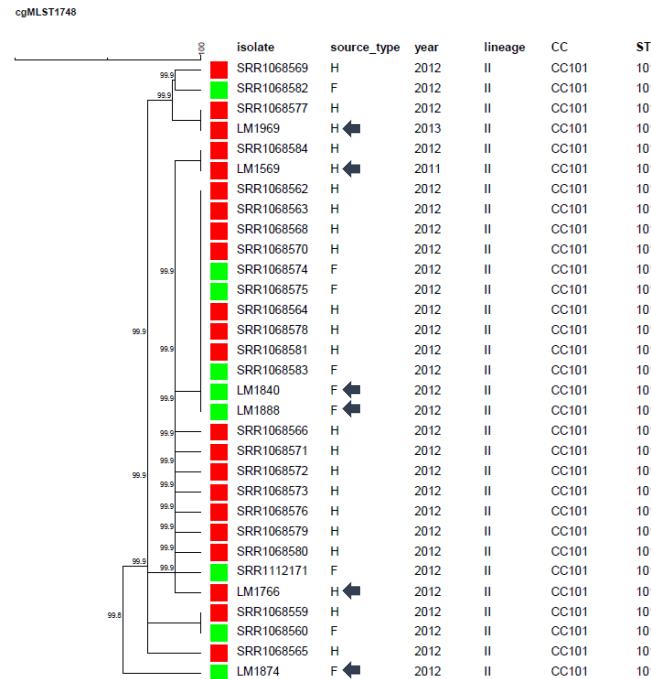
Multistate Outbreak of Listeriosis



Draft Genome Sequences of Six *Listeria monocytogenes* Strains Isolated from Dairy Products from a Processing Plant in Southern Italy

Matteo Chiara,^a Anna Maria D'Erchia,^b Caterina Manzari,^b Alice Minotto,^a Cosimo Montagna,^c Nicoletta Addante,^c Gianfranco Santagada,^d Laura Latorre,^d Graziano Pesole,^{b,e} David S. Horner,^a Antonio Parisi^c

cgMLST: 1748 genes



Conclusioni

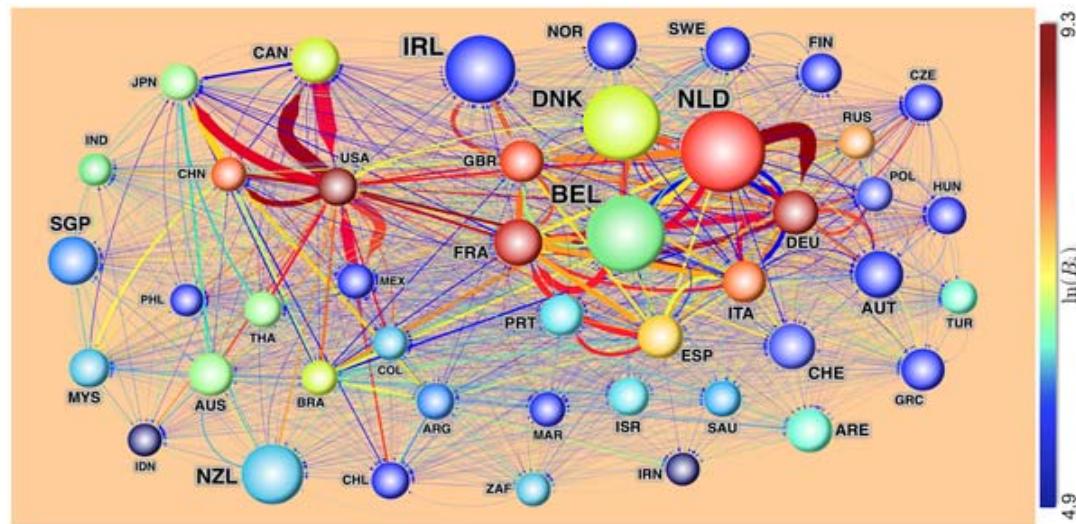


Conclusioni



The ability to recognise,
investigate and identify the likely
source of an outbreak remains
critically important for food and
waterborne diseases.

The backbone of the IFTN based on the 2007 dataset.



Ercsey-Ravasz M, Toroczkai Z, Lakner Z, Baranyi J (2012) Complexity of the International Agro-Food Trade Network and Its Impact on Food Safety. PLoS ONE 7(5): e37810. doi:10.1371/journal.pone.0037810
<http://www.plosone.org/article/info:doi/10.1371/journal.pone.0037810>

Conclusioni

Globalisation of Food Trade *"The World on your Plate"*



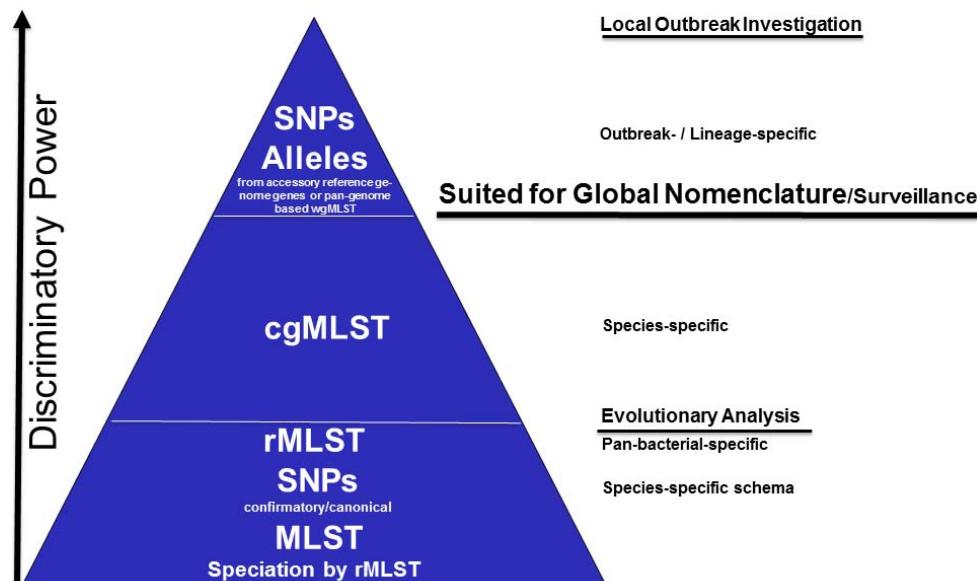
Chicken Kiev

Herb Butter:	Salted butter - Ireland garlic puree - China, USA, Spain garlic salt - China, USA, Spain lemon - USA parsley - France, UK pepper - India water - Ireland
Chicken Breast:	Chicken - Ireland, Belgium UK, Thailand etc. - Belgium, France - Ireland
Batter:	Flour Water
Bread Crumb:	Bread crumb - Ireland, UK Rape-seed oil - EU, Australia Eastern Europe

Conclusioni



Conclusioni



XIX



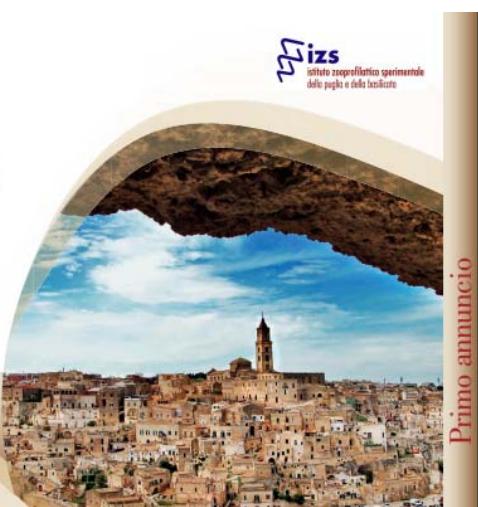
SOCIETÀ ITALIANA DI DIAGNOSTICA
DI LABORATORIO VETERINARIA

Congresso Nazionale S.I.Di.L.V.

Matera 23-25 Ottobre 2019
Hotel MH Matera

INFORMAZIONI GENERALI

- Accreditamento ECM per Medici Veterinari, Biologi, Chimici e Tecnici di Laboratorio
- Il programma preliminare sarà inviato ai Soci nel mese di **Maggio 2019**
- Scadenza per l'invio delle comunicazioni scientifiche **21 Luglio 2019**



Primo annuncio

**Grazie per la cortese
attenzione**