



LABORATORIO
NAZIONALE
DI RIFERIMENTO PER
CAMPYLOBACTER

Poultry Supply Chain Impact on Campylobacteriosis Surveillance in Italy Over One Year

Giuliano Garofolo

The 19th EURL-Campylobacter workshop 21-23 October 2024



Human cases

Notification rate
(per 100,000 population)

41.1

Trend
(2017-2021)



127,840 Cases of illness

81,311 Infections acquired in the EU

10,469 Hospitalisations

704 Infections acquired outside the EU

26 Deaths

45,825 Unknown travel status or unknown country of infection

Human cases in foodborne outbreaks

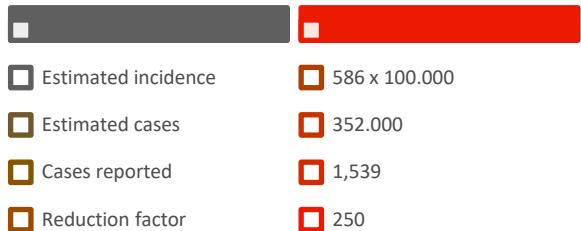
249 Foodborne outbreaks

20 Strong-evidence outbreaks
229 Weak-evidence outbreaks

1,051 Cases of illness

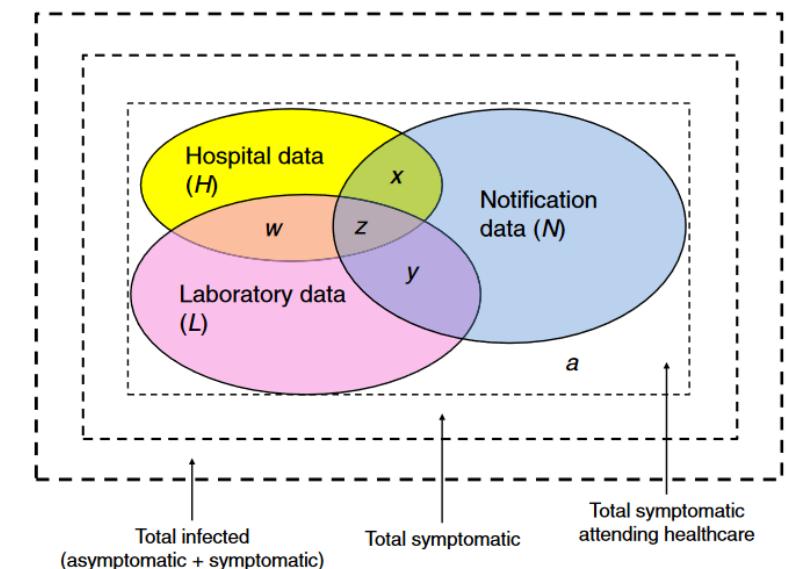
134 Hospitalisations
6 Deaths

Campylobacter Italy



ICEBERG effect

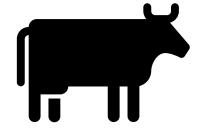
Asyntomatic
Self-limiting



under-ascertainment (UA) Underreporting



Campylobacter - Animals



Animal reservoirs/Amplifying hosts



Healthy animals

Campylobacter is often found in warm-blooded animals, which are normally considered natural hosts

Prevalence*

- 71% *C. jejuni/C. coli* in broilers
- 45% *C. jejuni* in dogs
- 36% *C. jejuni* in cattle
- 42% *C. jejuni/C. coli* sheep
- 42% *C. coli* in pigs





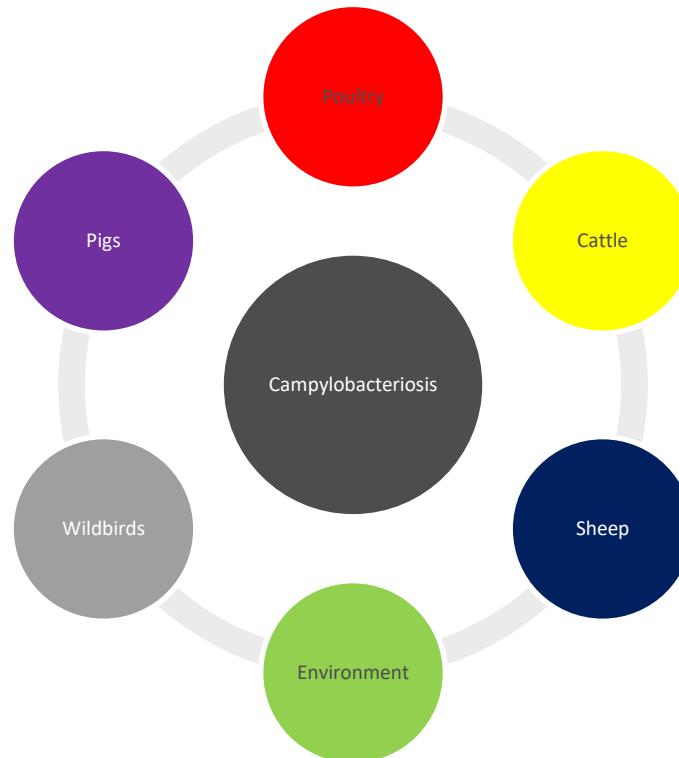
Tracing Back Clinical *Campylobacter jejuni* in the Northwest of Italy and Assessing Their Potential Source

Elisabetta Di Giannatale¹, Giuliano Garofolo¹, Alessandra Alessiani^{1*}, Guido Di Donato¹, Luca Candeloro², Walter Vencà³, Lucia Decastelli⁴ and Francesca Marotta^{1*}

Input model

- Italy_No.687 *C. jejuni* strains
- PubMLST Nu. 6911 ù
DA 6 RESERVOIR

CROSS-VALIDATION
97% Pollame,
98% Ruminanti
77% uccelli selvatici,
62% ambiente

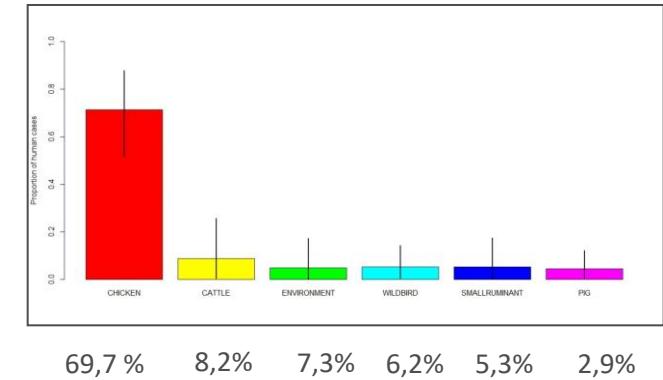


Source attribution of 44 human *Campylobacter jejuni* isolates Piedmont, August 2012.

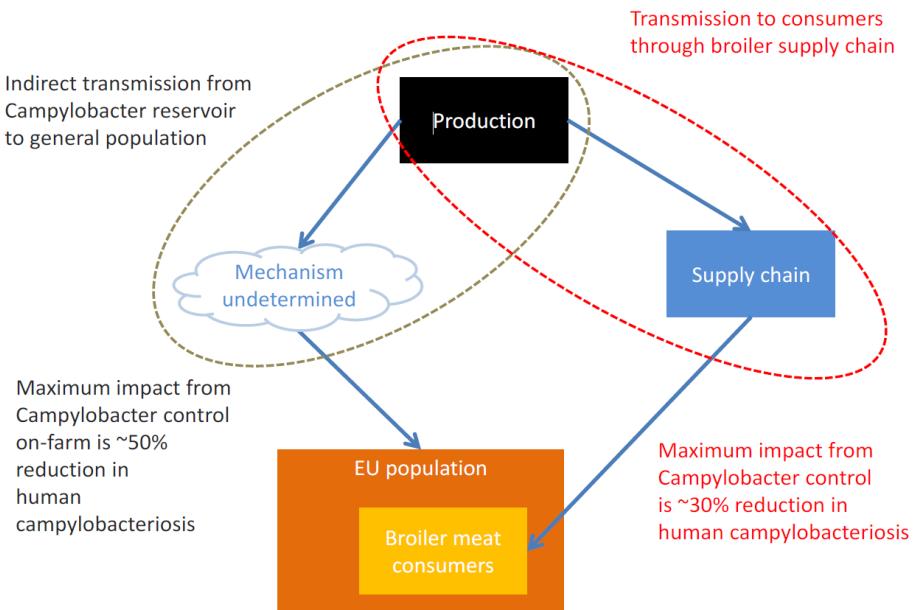
MLST

Asymmetric island assignment model

Phylogenetic approach with probabilistic assignment of cases to the considered sources of infection.



Source



- Poultry as source 50-80%

Wilson, Daniel J., et al. "Tracing the source of campylobacteriosis." *PLoS genetics* 4.9 (2008): e1000203.

Mullner, Petra, et al. "Assigning the source of human campylobacteriosis in New Zealand: a comparative genetic and epidemiological approach." *Infection, Genetics and Evolution* 9.6 (2009): 1311-1319.

Gras, Lapo Mughini, et al. "Risk factors for campylobacteriosis of chicken, ruminant, and environmental origin: a combined case-control and source attribution analysis." *PLoS one* 7.8 (2012): e42599.

Sheppard, Samuel K., et al. "Campylobacter genotyping to determine the source of human infection." *Clinical Infectious Diseases* 48.8 (2009): 1072-1078.



- 2015-2016
- 450 batches

	Italy		
	Conv.	f. r.	Org.
Broiler farms	6.088		
	5.812	100	176
percentage	95,5%	1,6%	2,9%
Broilers/farm	40.000	14.000	12.000
Breeding farms	208		
Broiler slaughterhouses	177		

*Positive carcasses 69.2% (64.9-73.9%)

Slaughterhouse in Italy



Campylobacter at retail in Italy

Chicken	Neg	Pos	P %
Breast and Tight	1032	216	17,37



Bovine	Neg	Pos	P %
Hamburger Italian traditional preparations	1196	7	0.58



17.37%

>

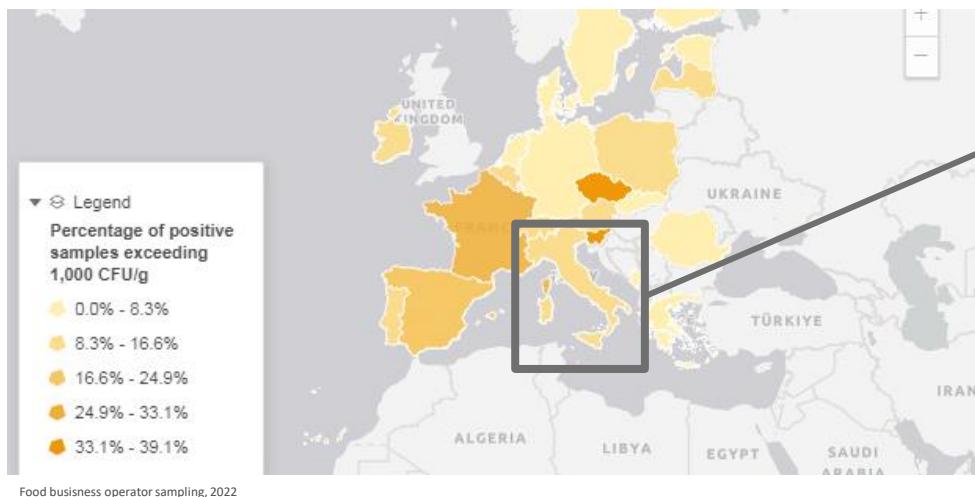
0,58%

p<0,0001; X²TEST



CAMPYLOBACTER IN THE CONTEXT OF REGULATION (EC) NO 2073/2005

It establishes a regulatory limit (process microbiological hygiene criterion - PHC) of 1,000 CFU/g of *Campylobacter* on the neck skins of chilled chicken carcasses. Compliance with the PHC indicates that the production process is functioning correctly



Italy 2022	
N samples tested	1611
N (%) samples positive	719 (44,6%)
N (%) samples above PHC limit	296 (18.4%)

Competent authorities sampling

Corrective measures required!



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Campylobacter

SCOPE

- Studies for the identification of the origin of *Campylobacter* infection in humans are poorly undertaken in Italy and other international settings
- Surveillance of other foodborne pathogens using high-resolution typing methods has proven effective in detecting outbreaks and monitoring trends in epidemic strains
- A similar system for *Campylobacter* has not been widely adopted or made significant contributions



This study aims to understand the dynamics of *Campylobacter* strains circulating in poultry meat and their correlation with human case clusters occurred in Italy in 2023, using whole genome sequencing (WGS)

150 HUMAN ISOLATES

127 - *C. jejuni*

23 – *C. coli*

109 POULTRY ISOLATES

66 - *C. jejuni*

43 - *C. coli*

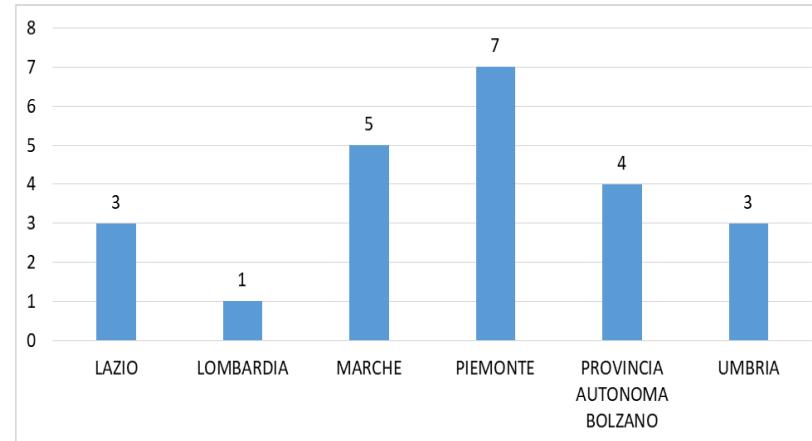
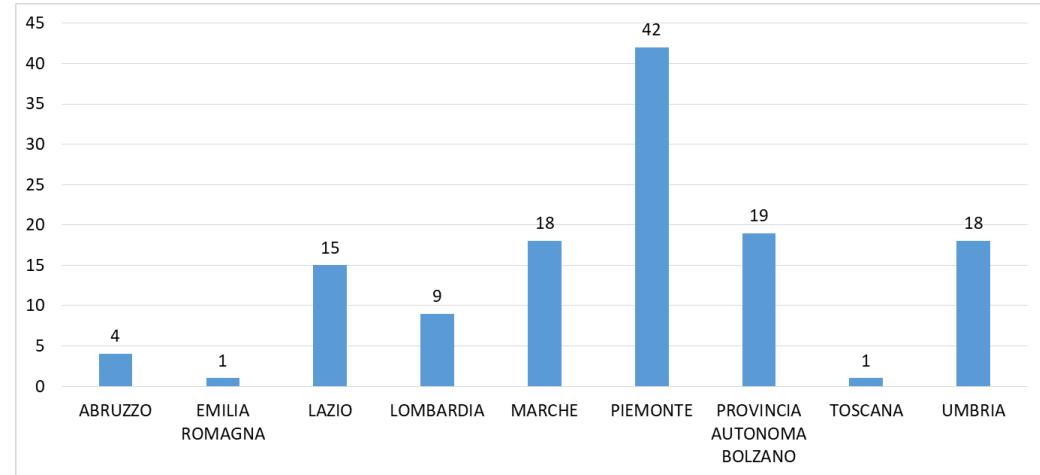
127 - *C. jejuni*

Isolated from stools

23 - *C. coli*

22 *isolated from stools*
1 *isolated from blood*

Humans - Enternet 150 - *Campylobacter*



109 - *Campylobacter*

66 - *C. jejuni*

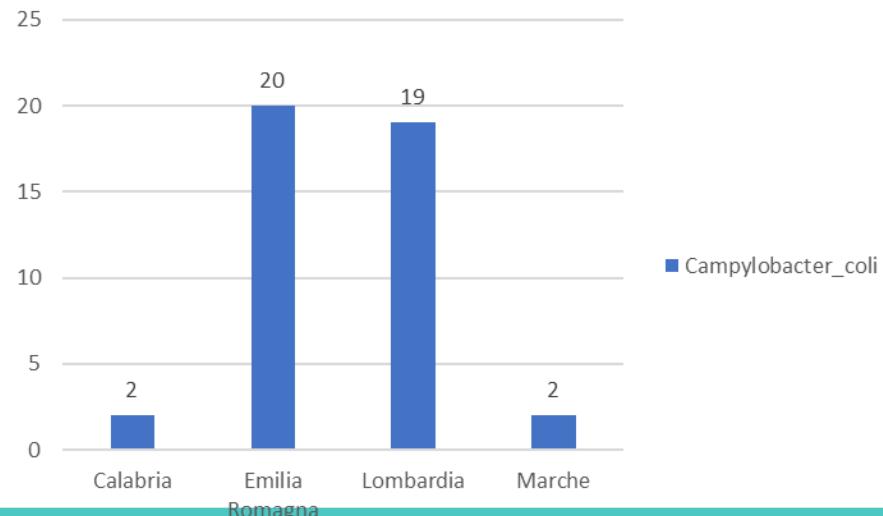
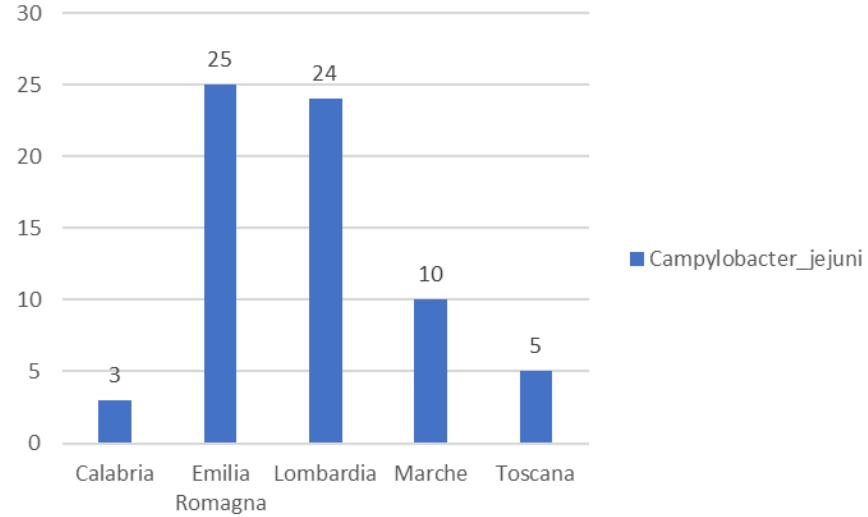
Isolati – Alimenti

17 - Aziende

43 - *C. coli*

Isolati – Alimenti

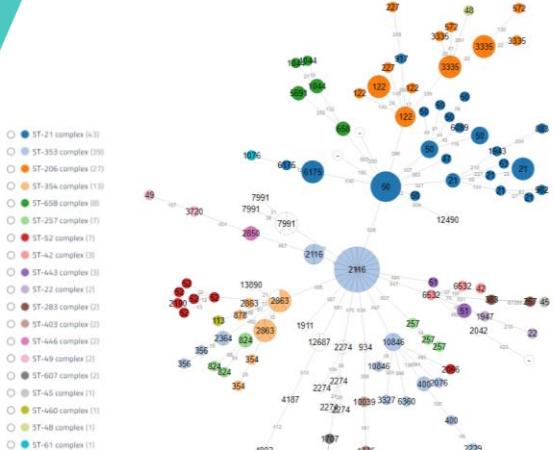
10 - Aziende



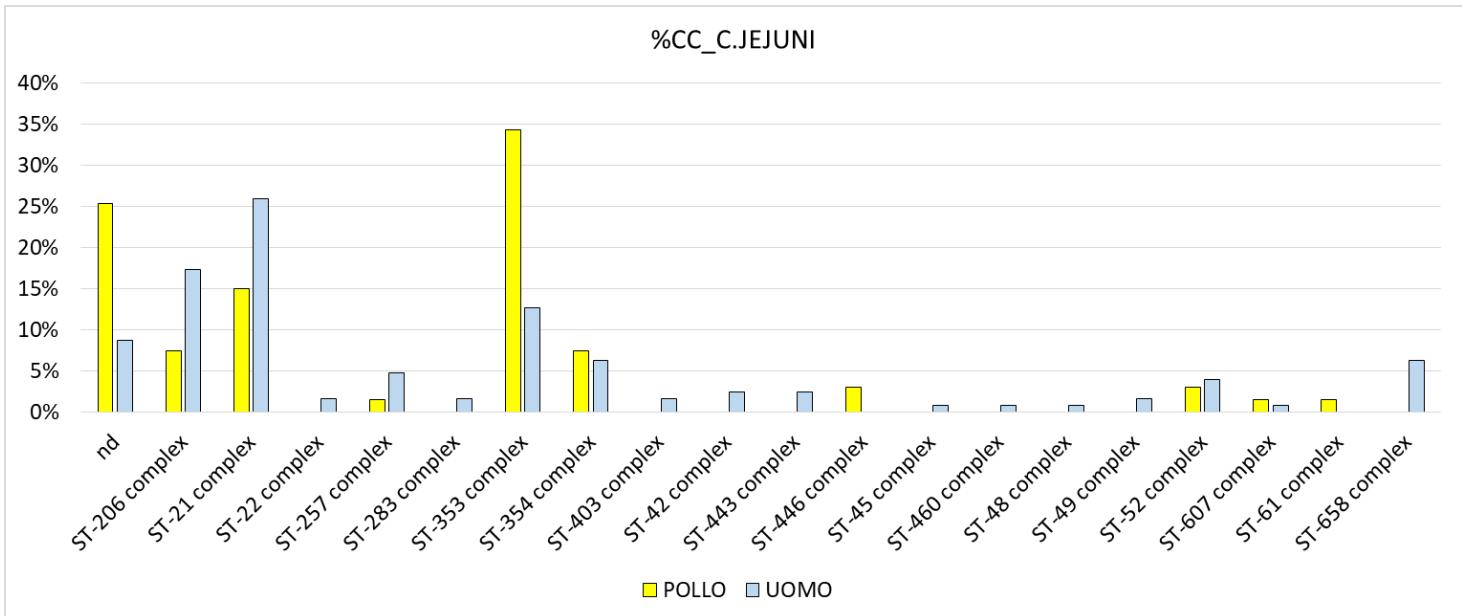
Year 2023
Surveillance
C. jejuni

Poultry= 66
Humans= 127

19 CCs
9 CC - SHARED



MLST C.JEJUNI





23% →

C. jejuni isolates

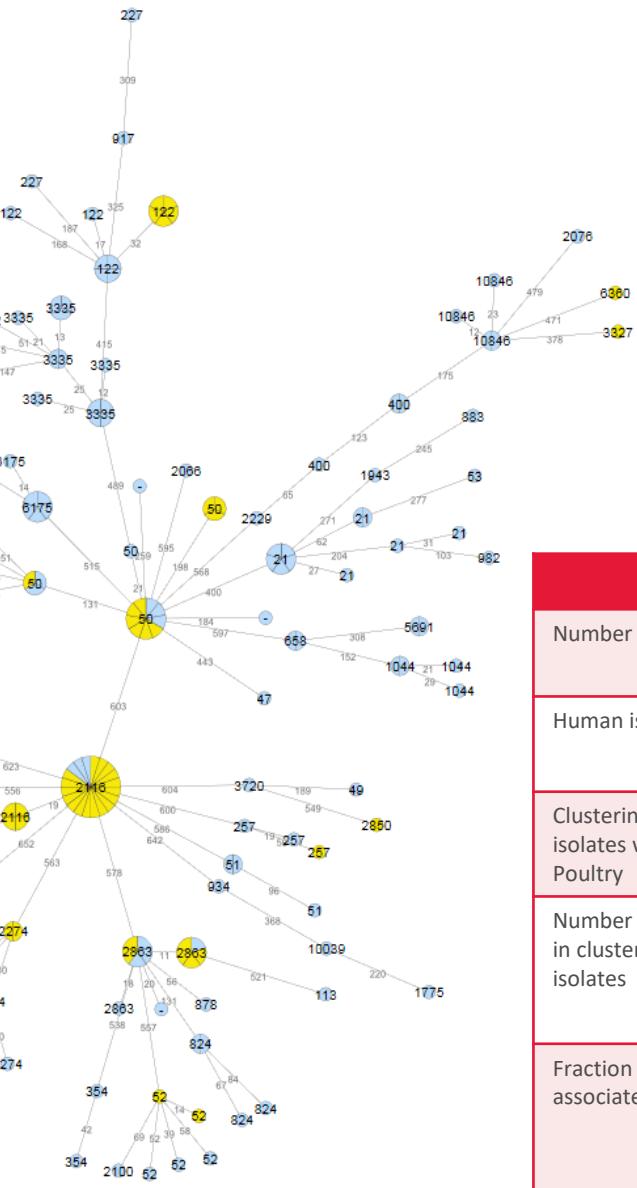
127 - Human

66 - Poultry

- ST2116
- ST2863
- ST50

RESULTS

cgMLST _*C. jejuni*_678



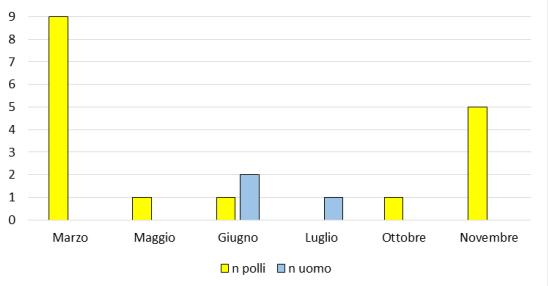
Host origine
POULTRY
HUMAN

C. jejuni **10 alleles cut-off ***

Number of clusters	25
Human isolates in clusters	53
Clustering index of human isolates with Human or Poultry	42%
Number of human isolates in clusters with poultry isolates	12
Fraction of human isolates associated with poultry	23%

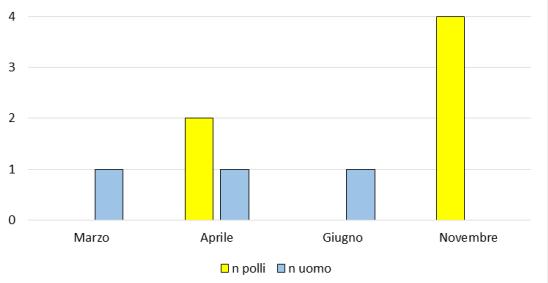
*Reference: Joseph, Lavin A., et al. "Evaluation of core genome and whole genome multilocus sequence typing schemes for *Campylobacter jejuni* and *Campylobacter coli* outbreak detection in the USA." *Microbial Genomics* 9.5 (2023): 001012.

Num. C.jejuni con ST2116 isolati da pollo e uomo



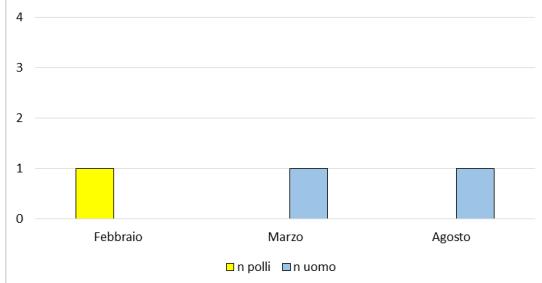
✓ 6 slaughterhouses – Emilia Romagna/Lombardia;
Cases – Piemonte.

Num. C.coli con ST50 isolati da pollo e uomo



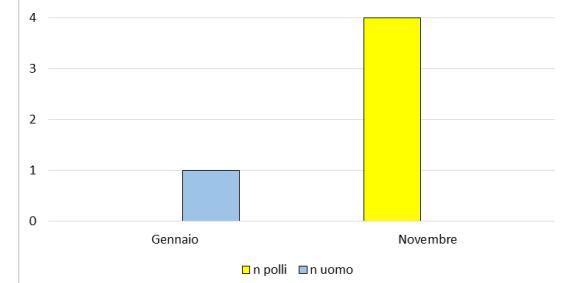
✓ 2 slaughterhouses – Emilia Romagna/Marche;
cases - Piemonte-Umbria-Marche.

Num. C.jejuni con ST50 isolati da pollo e uomo



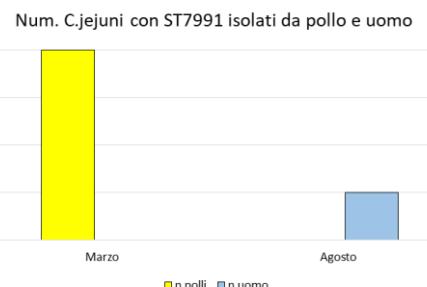
✓ 1 Slaughterhouse – Lombardia;
Casi – Bolzano-Lombardia.

Num. C.jejuni con ST2863 isolati da pollo e uomo



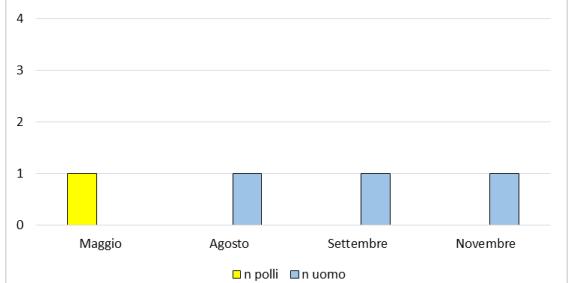
✓ 1 slaughterhouse –
Lombardia;
Casi – Bolzano.

22 cluster - Humans



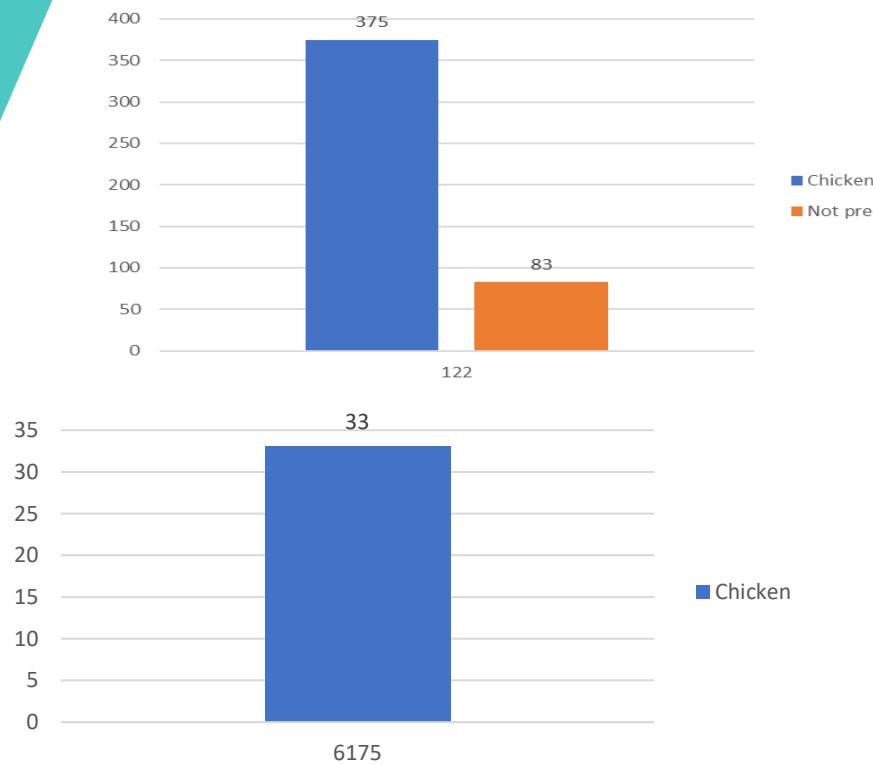
✓ 1 slaughterhouses –
Marche;
Cases – Umbria.

Num. C.jejuni con ST2863 isolati da pollo e uomo



✓ 1 slaughterhouse – Lombardia;
Casi – Marche-Bolzano.

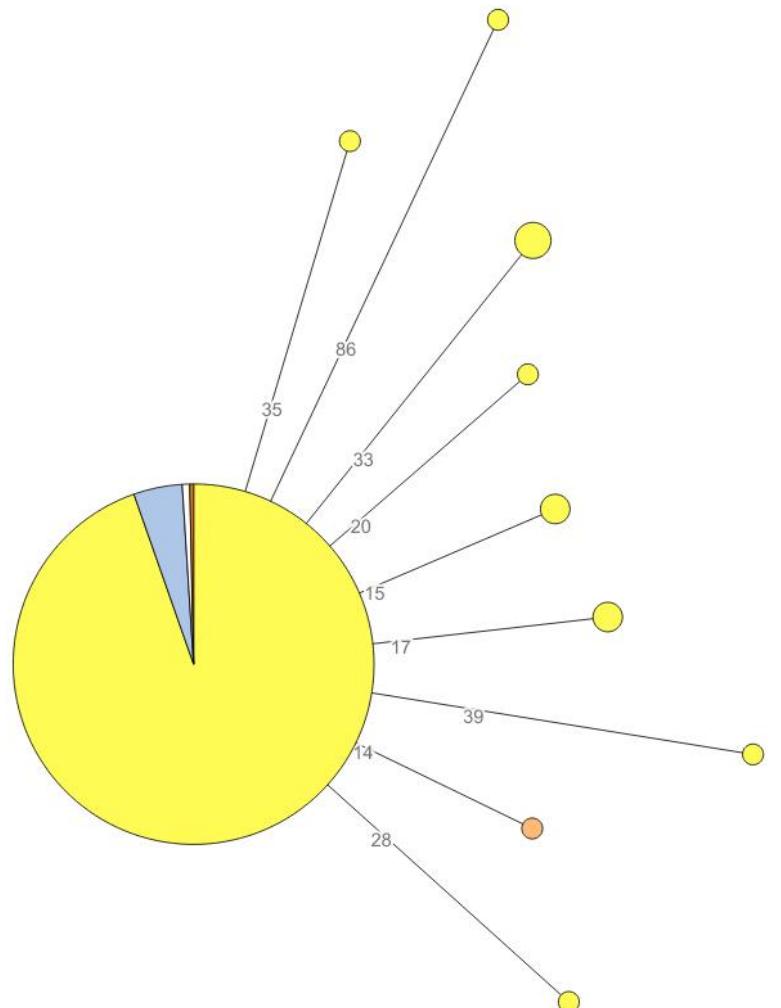
Machine learning & Source Attribution



Arning, N., Sheppard, S. K., Bayliss, S., Clifton, D. A., & Wilson, D. J. (2021). Machine learning to predict the source of campylobacteriosis using whole genome data. *PLoS genetics*, 17(10), e1009436.

Num. strains =298

- Host origine
- POLLO (294)
 - UOMO (13)
 - BALLERINA BIANCA (1)
 - PICCIONE SELVATICO (1)

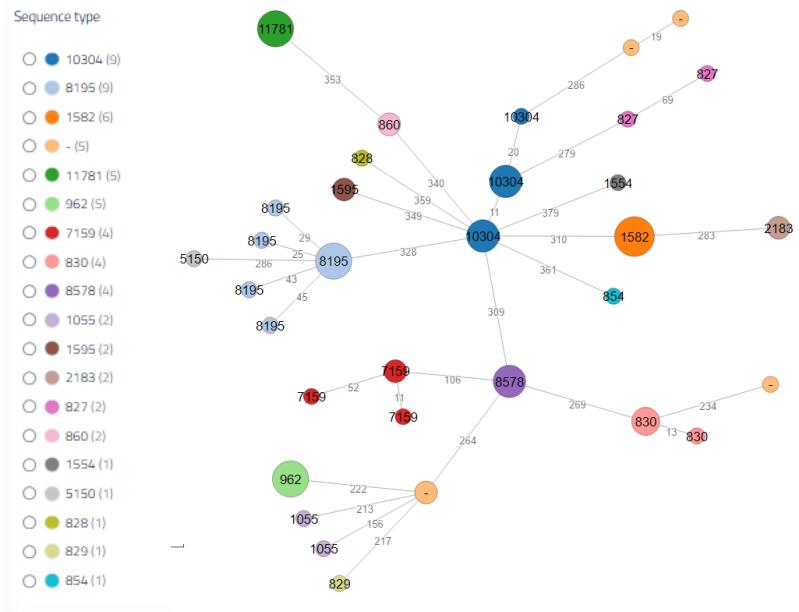


cgMLST C.jejuni ST2116 (num.311)

Data prelievo: 2008-2023

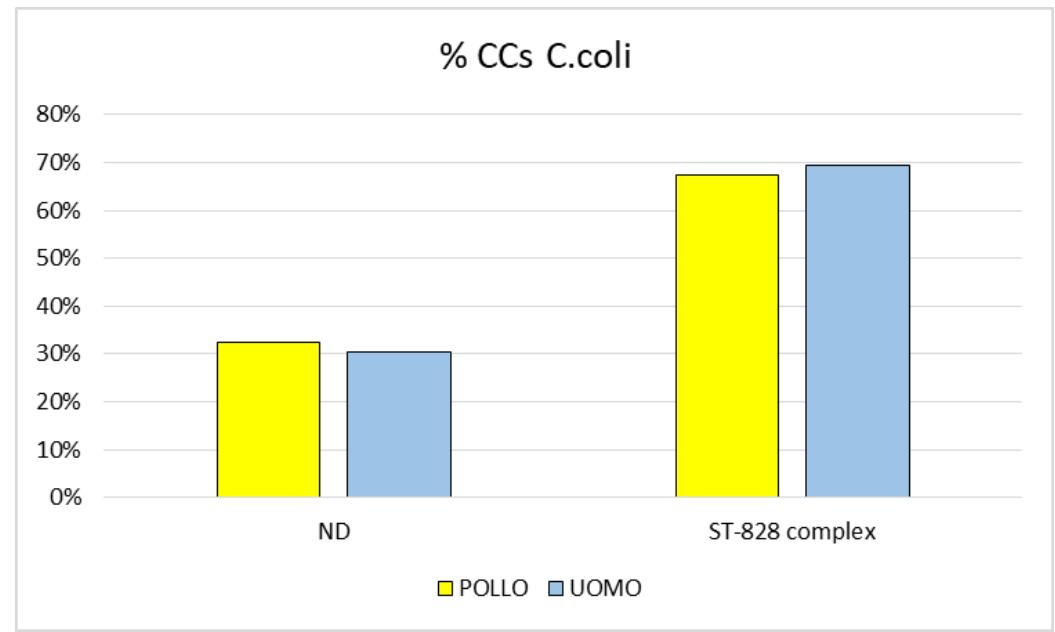


Year 2023 Surveillance *C. coli*



Poultry= 43
Humans= 23

1 CCs
1 CCs - shared





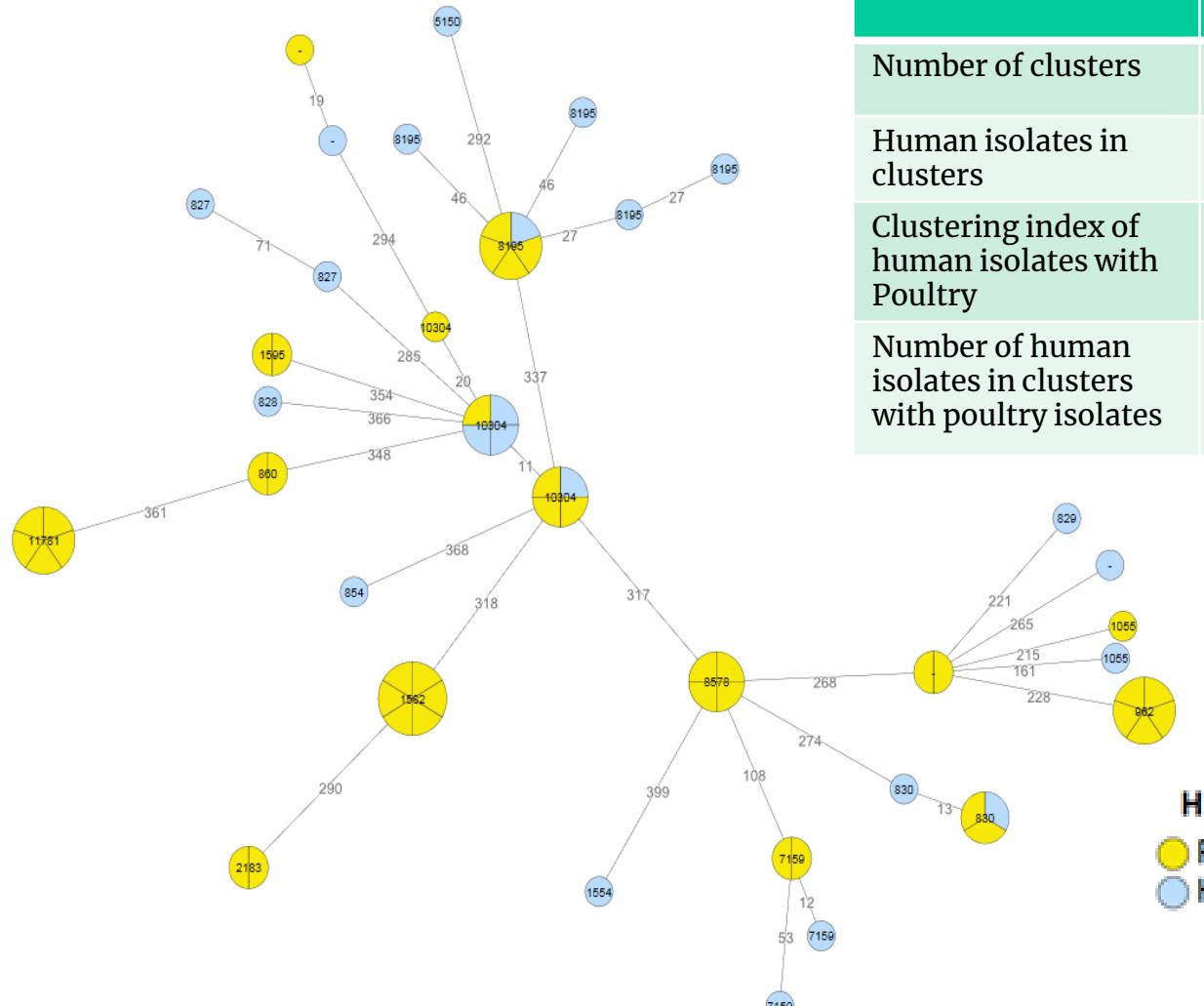
RESULTS

C. coli isolates

23 - Human

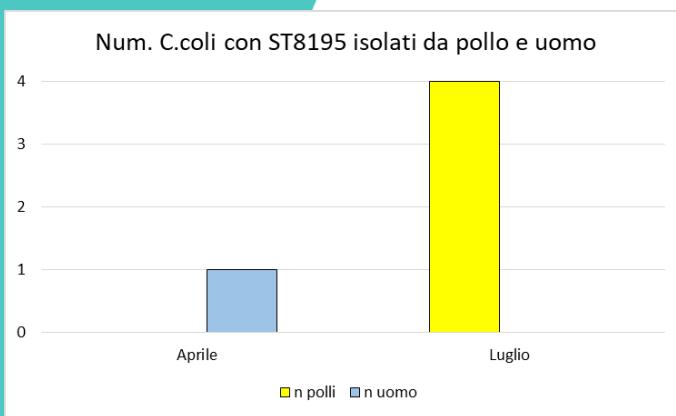
43 - Poultry

- ST1034
- ST8195
- ST830

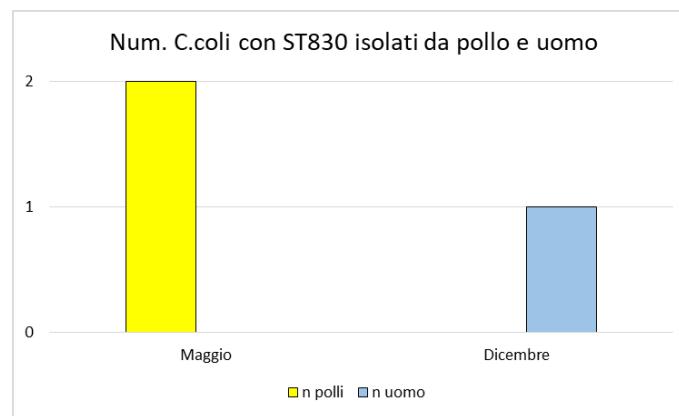


cgMLST _*C. coli*_528

<i>C. coli</i>	10 alleles cut-off
Number of clusters	13
Human isolates in clusters	6
Clustering index of human isolates with Poultry	26%
Number of human isolates in clusters with poultry isolates	6



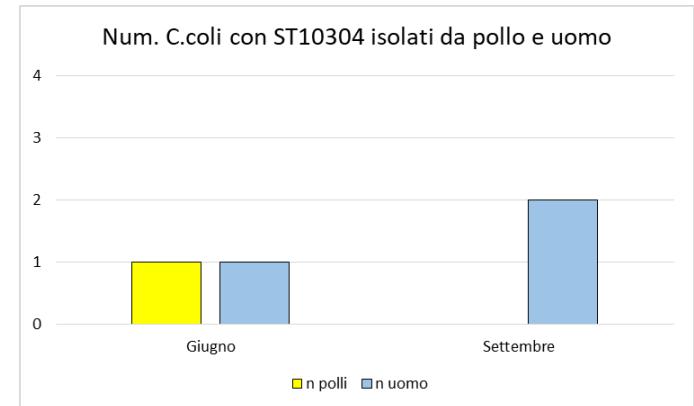
✓ 1 mattatoio – Emilia Romagna;
Casi – Marche.



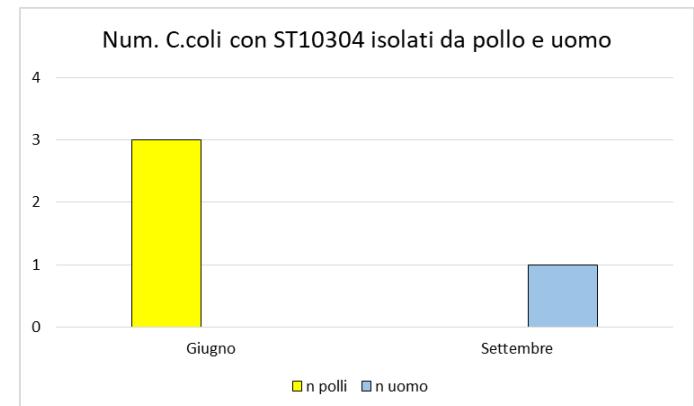
✓ 1 mattatoio – Emilia Romagna;
Casi – Piemonte-Umbria.

Cluster	Campioni	Origine	ST	Giorni
1	3	Pollo (2) Uomo (2)	830	220
2	5	Pollo (4) Uomo (1)	8195	80
3	4/5	Pollo (1) Uomo (3)/Pollo (4)Uomo (1)	10304	90/90

4 cluster - UOMO



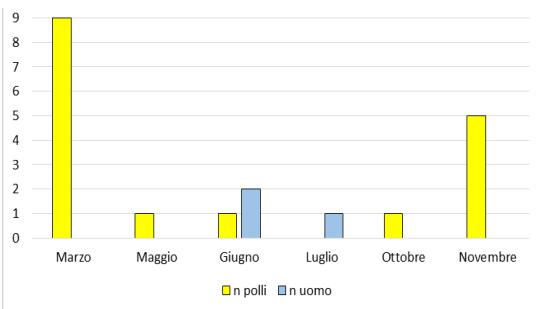
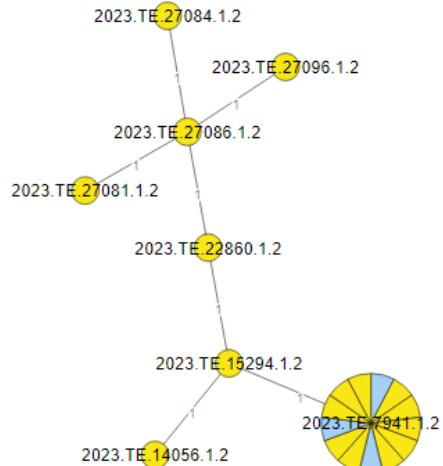
✓ 1 mattatoio –Emilia Romagna;
Casi –Piemonte, Bolzano.



✓ 2 mattatoi –Emilia Romagna;
Casi –Marche.

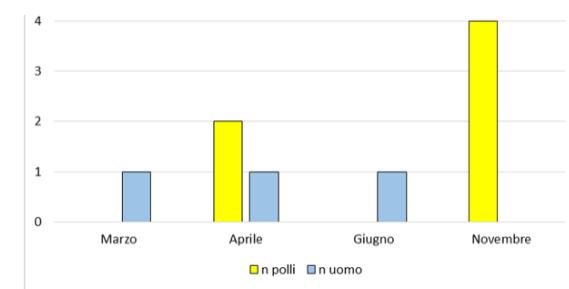
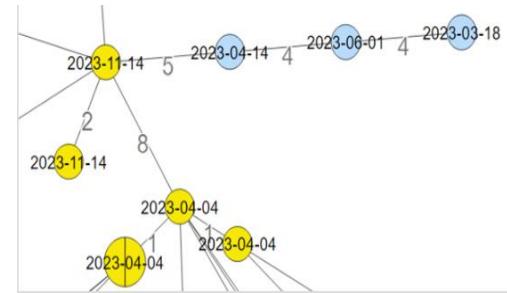
FOCUS ON CLUSTERS

C. jejuni ST2116



- 17 poultry isolates (Emilia Romagna/Lombardia)
- 3 human isolates (Piemonte)

C. jejuni ST50



- 6 poultry isolates (Emilia Romagna/Marche)
- 3 human isolates (**Piemonte/Marche/Umbria**)

Annex 1 – Working in progress

	SCHEMI (cgMLST)	C.JEJUNI					C.COLI			
		CLUSTER 1 ST-2116	CLUSTER 4 ST-2863	CLUSTER 5 ST-2863	CLUSTER 2 ST-50	CLUSTER 3 ST-50	Cluster 1 ST-830	Cluster 4 ST-10304	Cluster 3 ST-10304	Cluster 2 ST-8195
		H=no. 3 P=no. 17	H= no. 1; C= no. 4	H= no. 3; P= no. 1	H= no. 3; P= no. 6	H= no. 2; P= no. 1	H= no. 1; P= no. 2	H= no. 1; P= no. 3	H= no. 3; P= no. 1	H= no. 1; P= no. 4
	RIDOM (637 loci)	X (0-9 AD)	X (0-10 AD)	X (0-6 AD)	X (0-9 AD)	X (0-2 AD)	X (0-4 AD)	X (0-6 AD)	X (0-15 AD)	/
	GENPAT (678 loci)	X (0-4 AD)	X (0-12 AD)	X (0-12 AD)	X (0-10 AD)	X (0-5 AD)	X (0-7 AD)	X (0-12 AD)	X (0-12 AD)	X
	OXFORDSHIRE (1,343 loci)	X (0-1 AD)	X (0-11 AD)*	X (0-6 AD)	X (0-10 AD)	X (1-2 AD)	X (0-2 AD)	X (3-11 AD)**	X (2-7 AD)	X (0-5 AD)
	SNPs	X AD (1-6)	X AD (0-16)	X AD (1-6)	X AD (1-10)	X AD (2-7)	X AD (3- 23)	/ AD (14-21)	X AD (0-6)	/ AD(1-13)



CONCLUSIONS

Campylobacter Cases in Italy - 2023 Findings

Outbreaks overview: 39% of Campylobacter strains from clinical cases clustered together using WGS typing methods, suggesting hidden outbreaks.

Estimated Cases from Hidden Outbreak:

Range: **112,188 - 166,631** Confidence Interval (C.I.): 95%

Poultry-Linked Human Isolates: 12% of human isolates clustered with poultry isolates.
Likely linked to poultry meat.

Estimated Poultry-Linked Cases

Range: **23,246 - 54,552** Confidence Interval (C.I.): 95%

- Strategic implications and future outlook in Europe:
 1. ***Can we use focused investments in genomic surveillance to control Campylobacter?***
 2. ***Can Real-time application of WGS drive targeted interventions?***



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CAMPYLOBACTER



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Anna Janowicz
Roberta Di Romualdo
Teresa Romualdi
Federica Di Timoteo
Lisa Di Marcantonio
Katiuscia Zilli
Elisa Di Domenico

**THANK YOU FOR
YOUR ATTENTION!**



L. Villa
A. Garcia-Fernandez
I. Artuso



ISTITUTO ZOOPROFILATTICO SPERIMENTALE
DELL'UMBRIA E DELLE MARCHE "TOGO ROSATI"

M. Napoleoni

