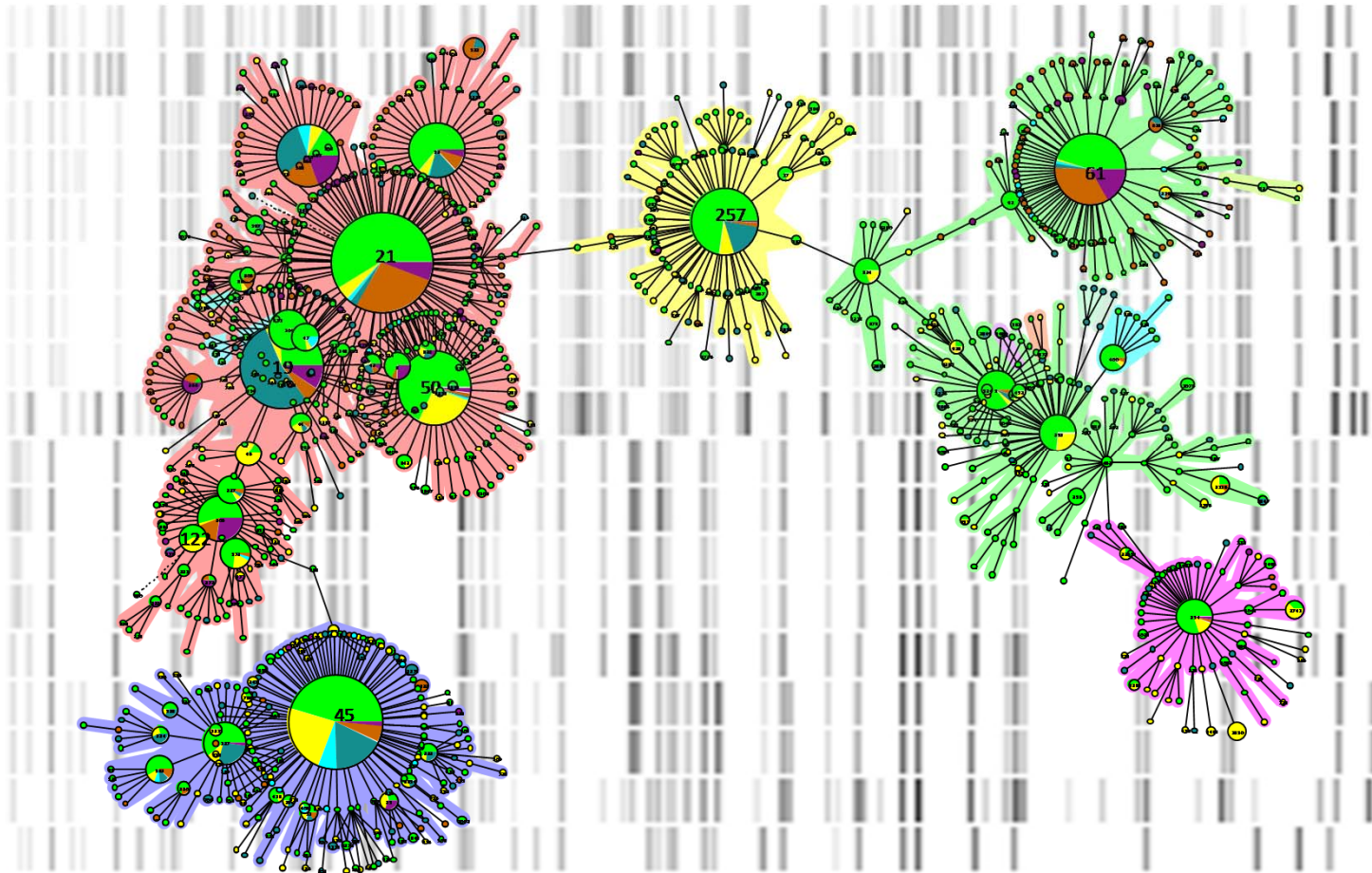


Epidemiologia molecolare di *Campylobacter* spp: dal fingerprinting ai metodi sequence-based



Dr. Antonio PARISI

Metodi

Fingerprinting

PCR RFLP FlaA typing
PFGE
AFLP
CGF

Sequence-based

Multi-Locus Sequence Typing
FlaA typing
PorA typing

NGS

Extended MLST
cgMLST
SNP

Epidemiologia molecolare

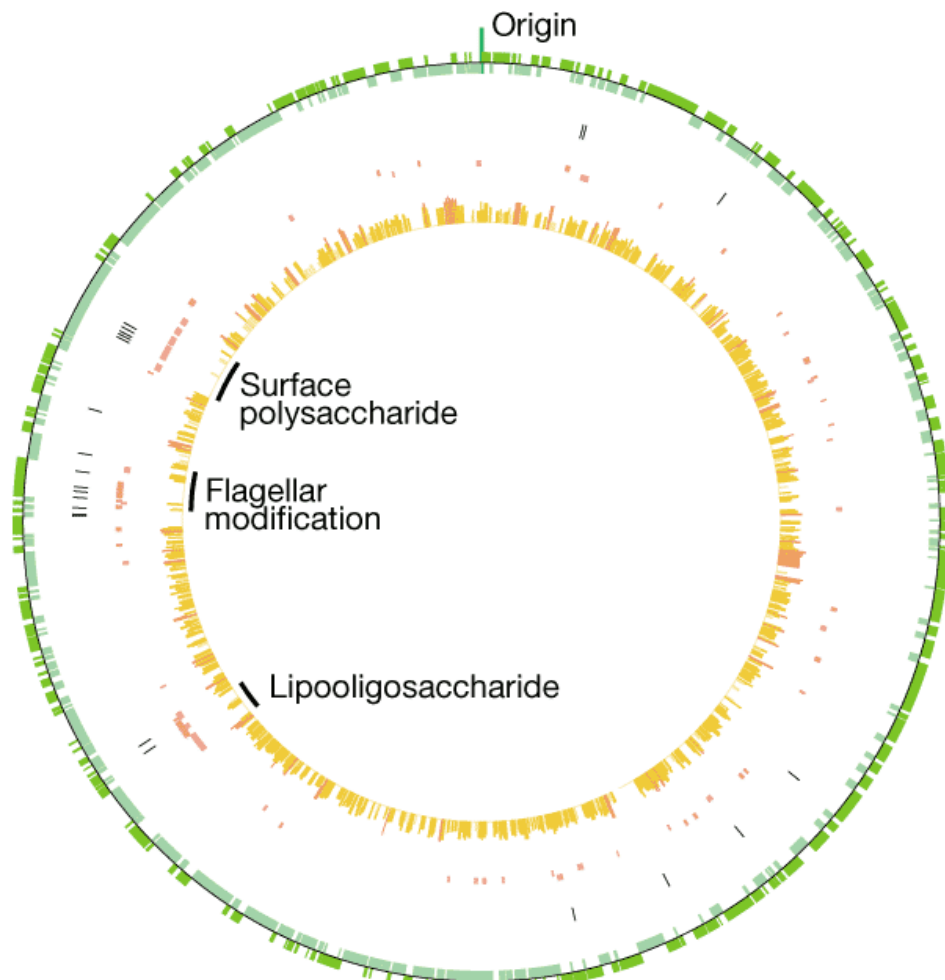
Outbreak
investigation

Global
epidemiology

Epidemiologia



Fingerprinting



C. jejuni genome

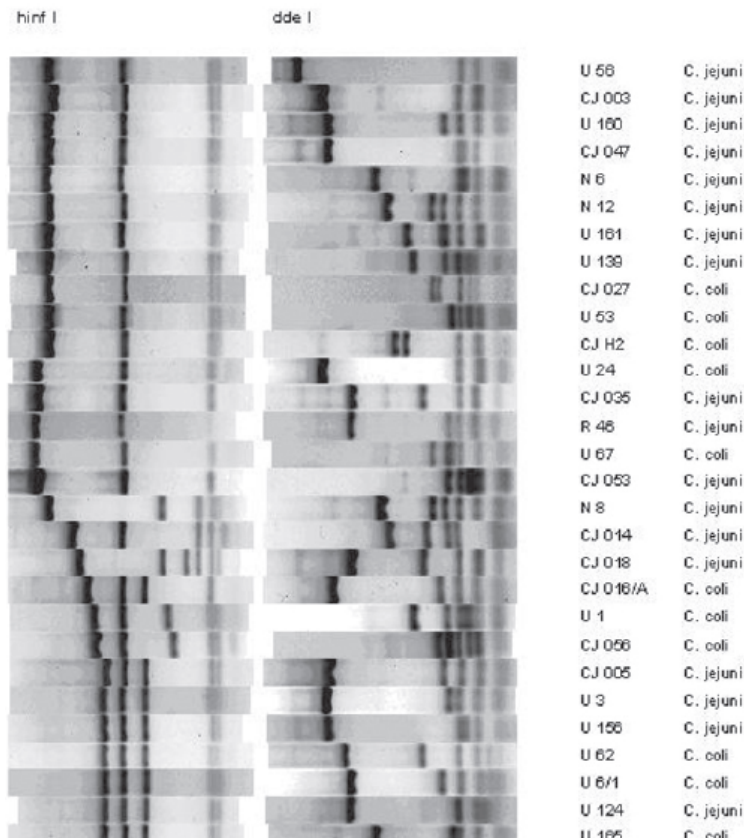
Campylobacter e alimenti

Industrie Alimentari - XLIV (2005) luglio-agosto

SI - N. ADDANTE - C. PEDARRA - C.O. MONTAGNA
profilattico Sperimentale della Puglia e Basilicata - Via Manfredonia 20 - 71100 Foggia - Italia

MANNO - T. MERICO
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per Casamassima Km 3 - 70010 Valenzano - BA - Italia

Contaminazione multipla campilobatteri termofili carne di pollo



Campylobacter e animali

Veterinary Research Communications, 31 (2007) 113–123
DOI: 10.1007/s11259-006-3404-3

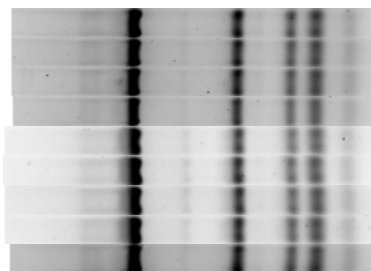
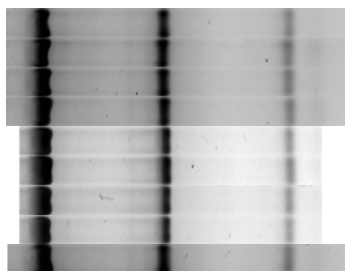
© Springer 2007

Prevalence, Molecular Characterization and Antimicrobial Resistance of Thermophilic *Campylobacter* Isolates from Cattle, Hens, Broilers and Broiler Meat in South-eastern Italy

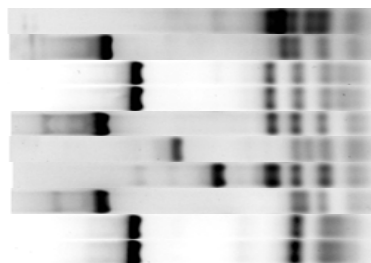
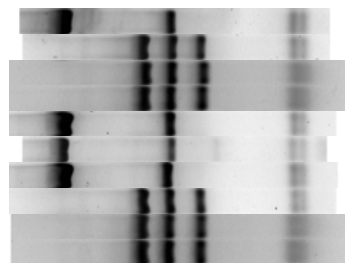
A. Parisi^{1,*}, S.G. Lanzilotta¹, N. Addante¹, G. Normanno², G. Di Modugno²,
A. Dambrosio² and C. O. Montagna¹

Hinf I

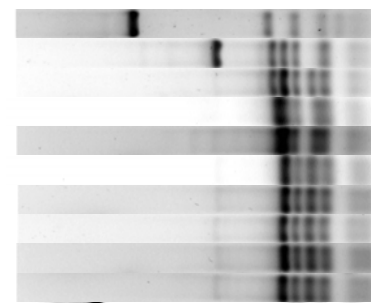
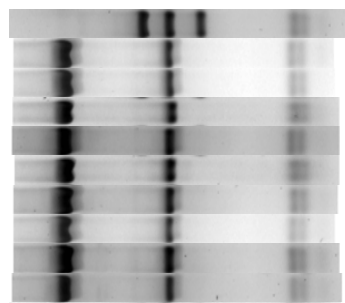
Dde I



U 77	A	C. jejuni
U 80	A	C. jejuni
U 79	A	C. jejuni
U 76	A	C. jejuni
U 85	A	C. jejuni
U 84	A	C. jejuni
U 87	A	C. jejuni
U 86	A	C. jejuni
U 82	A	C. jejuni

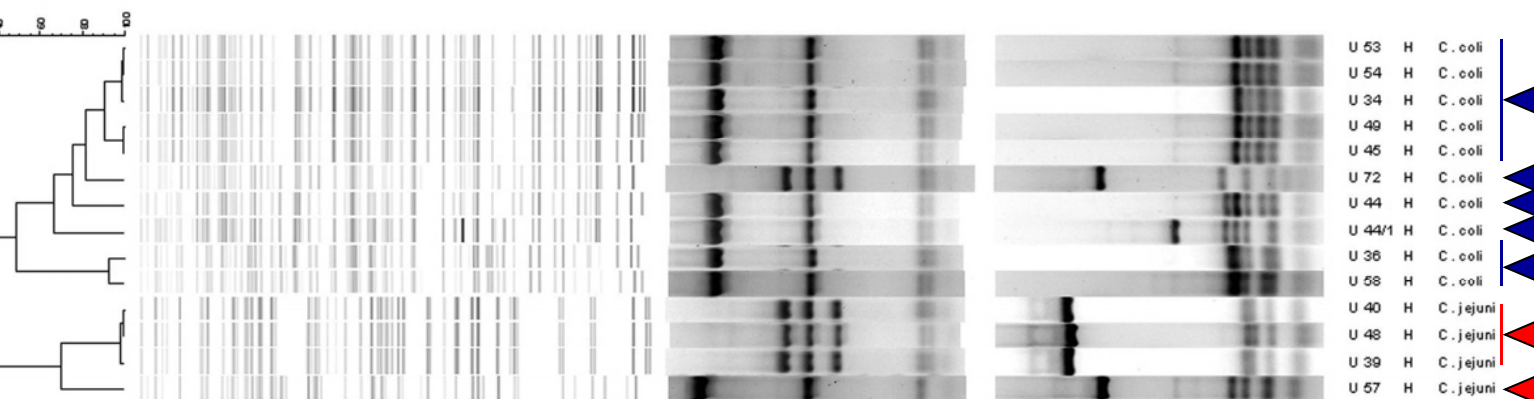
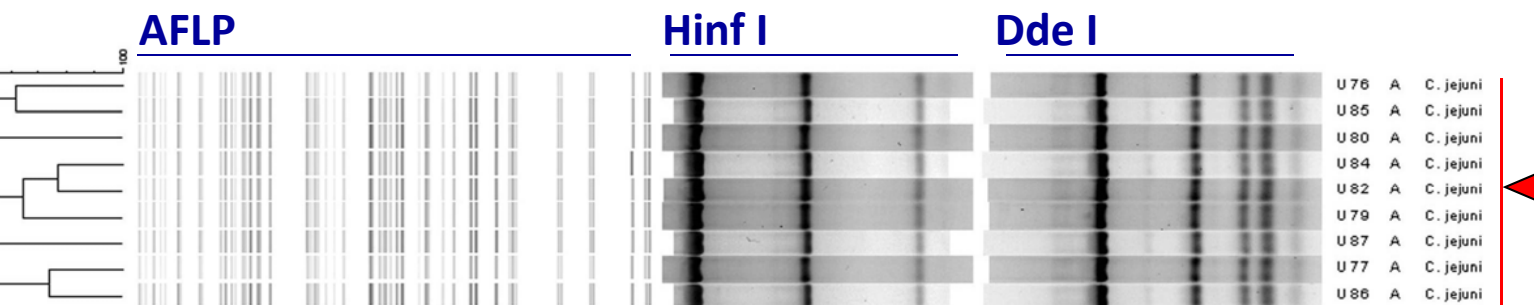


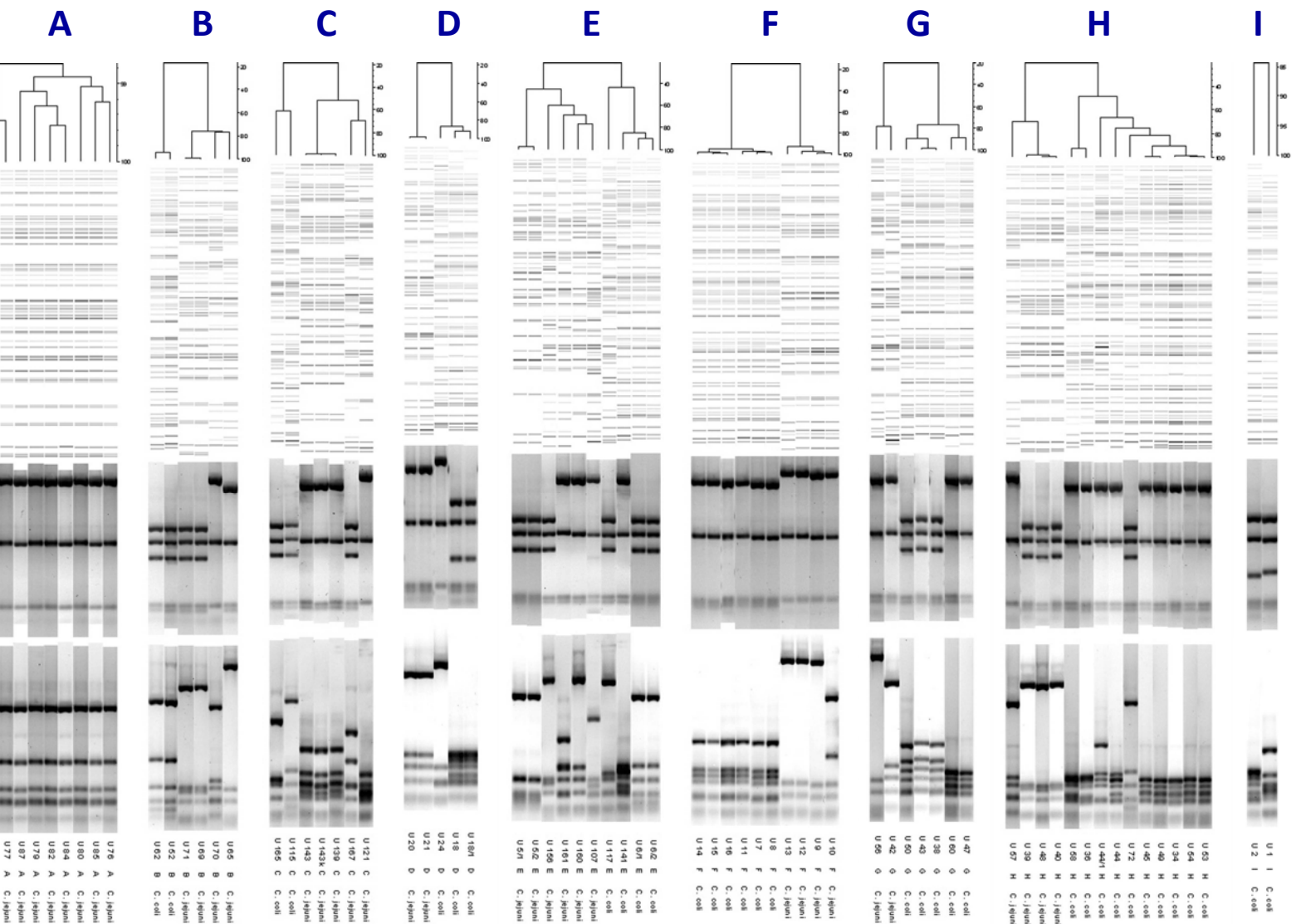
U 141	E	C. coli
U 117	E	C. coli
U 6/2	E	C. coli
U 6/1	E	C. coli
U 160	E	C. jejuni
U 107	E	C. jejuni
U 161	E	C. jejuni
U 156	E	C. jejuni
U 5/2	E	C. jejuni
U 5/1	E	C. jejuni



U 72	H	C. coli
U 44/1	H	C. coli
U 44	H	C. coli
U 36	H	C. coli
U 58	H	C. coli
U 34	H	C. coli
U 49	H	C. coli
U 45	H	C. coli
U 53	H	C. coli
U 54	H	C. coli
U 40	H	C. jejuni

Campylobacter e animali





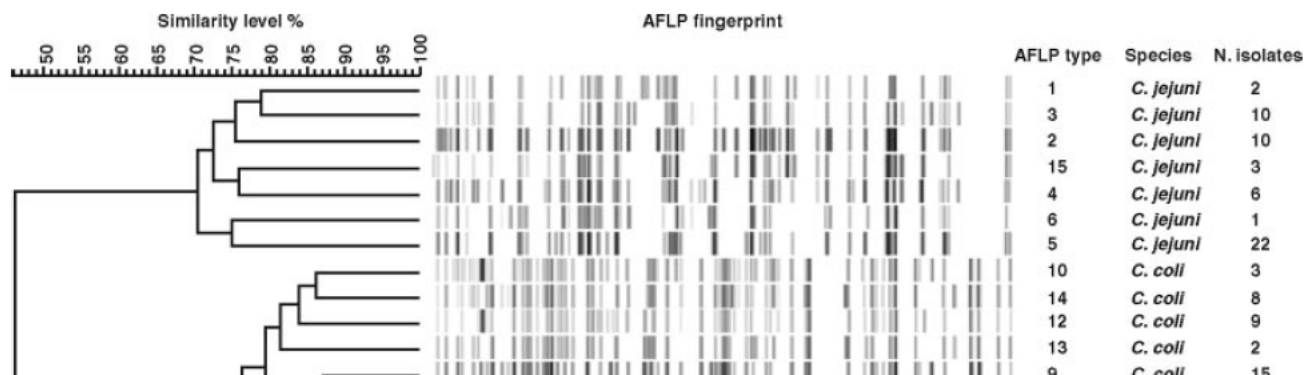
Campylobacter e animali

2008 Poultry Science 87:2152–2159
doi:10.3382/ps.2007-00441

GENOTYPING AND PHENOTYPING OF CAMPYLOBACTER BROILER ISOLATES

Genotypic and Phenotypic Diversity within Three *Campylobacter* Populations Isolated from Broiler Caeca and Carcasses

A. De Cesare*, A. Parisi†, V. Bondioli*, G. Normanno‡, G. Manfreda*¹



Campylobacter e animali

Applied and Environmental Microbiology 2014 Volume 80 Number 6



Prevalence in Bulk Tank Milk and Epidemiology of *Campylobacter jejuni* in Dairy Herds in Northern Italy

Valentina Bianchini,^a Laura Borella,^a Valentina Benedetti,^a Antonio Parisi,^b Angela Miccolupo,^b Eliana Santoro,^a Camilla Recordati,^c Mario Luini^a

Int. J. Environ. Res. Public Health **2014**, *11*, 7154-7162; doi:10.3390/ijerph110707154

Genotypes and Antibiotic Resistances of *Campylobacter jejuni* Isolates from Cattle and Pigeons in Dairy Farms

Valentina Bianchini¹, Mario Luini^{1,*}, Laura Borella¹, Antonio Parisi², Romie Jonas³, Anja Kittl³ and Peter Kuhnert³

Campylobacter e animali

Foodborne Pathogens and Disease - FPD-2015-2048.R2

of *Campylobacter jejuni* isolated from turkey by genotypic methods, antimicrobial susceptibility ence gene patterns: a retrospective study

G., Parisi A., De Cesare A., Mion D., Piva S., Zanoni R.G

typing method	N profiles	N isolates with unique profile	N isolates classified in cluster of profiles	Cluster size	DI (CI 95%)
MLST	33	11	113	2-15	0.947 (0.933-0.961)
PFGE	28	13	111	2-26	0.908 (0.882-0.933)
R-type	10	2	122	2-43	0.688 (0.633-0.743)
DNA	10	2	121	2-43	0.754 (0.700-0.799)

Campylobacter e uomo

J Clin Gastroenterol • Volume 45, Number 5, May/June 2011

Anna Maria Dionisi, BD*
Cinzia Milito, MD†
Helene Martini, MD†
Anna Maria Pesce, MD†
Milica Mitrevski, MD†
Guido Granata, MD†
Claudia Lucarelli, MD*
Antonio Parisi, BD‡
Ida Luzzi, BD*
Isabella Quinti, MD, PhD†

High Prevalence of Intestinal
Carriage of *Campylobacter*
coli in Patients With Primary
Antibody Deficiencies: A
Silent Infection That Could
Shift to a Life-threatening
Condition

Campylobacter e virulenza



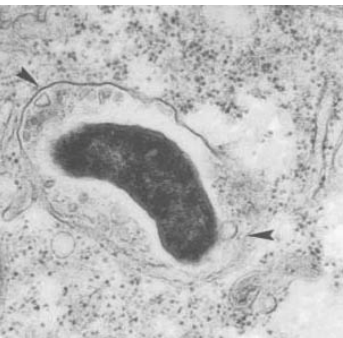
cadF

ceuE

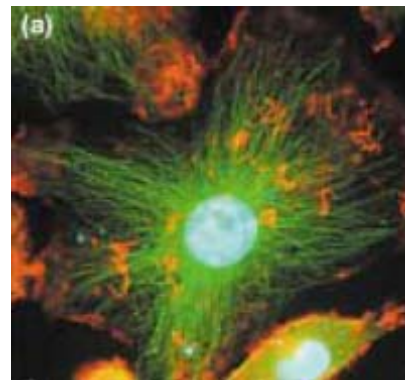
dnaJ

pldA

racR



virB11



cdtA

ciaB

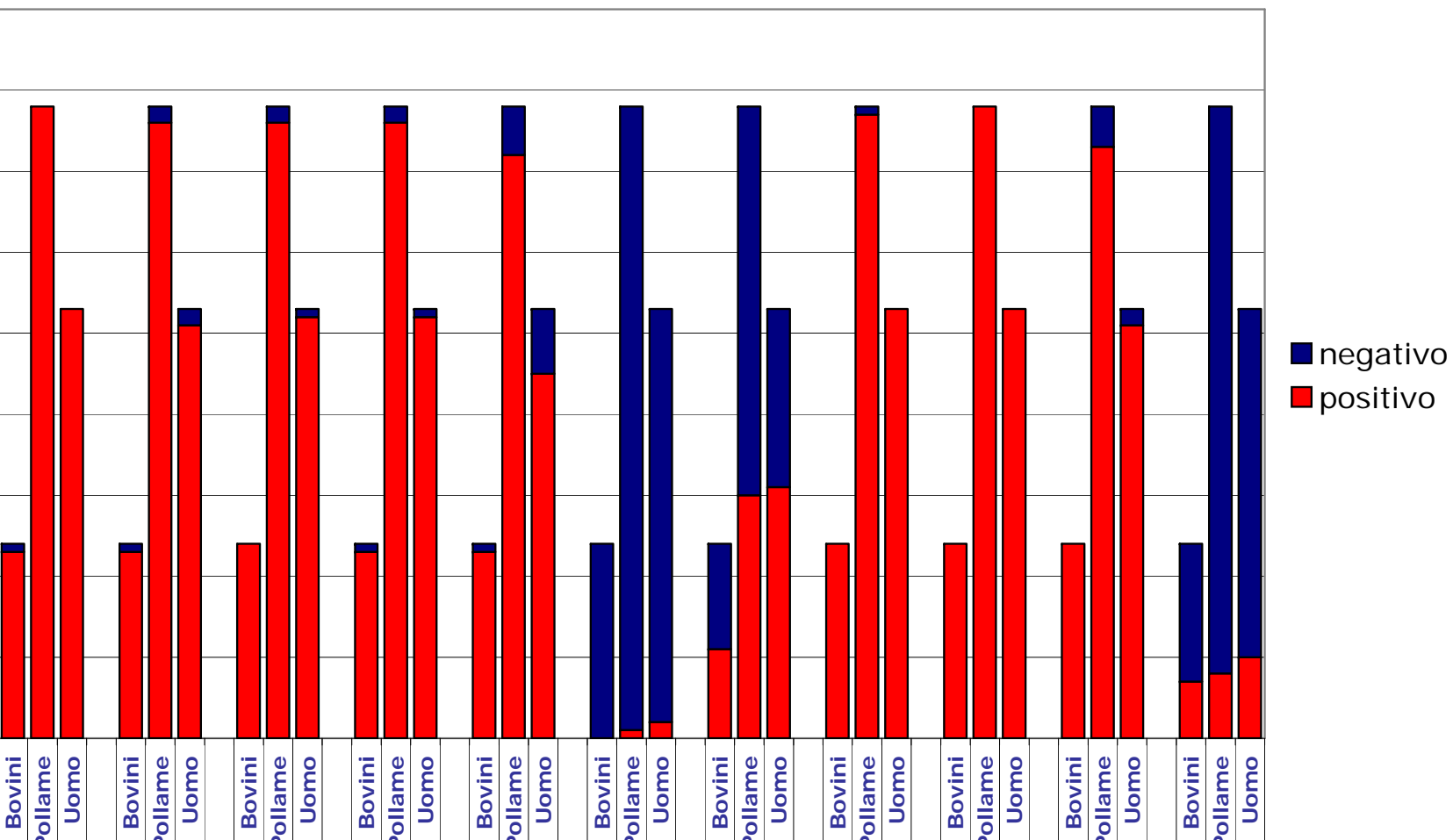
cdtB

cdtC

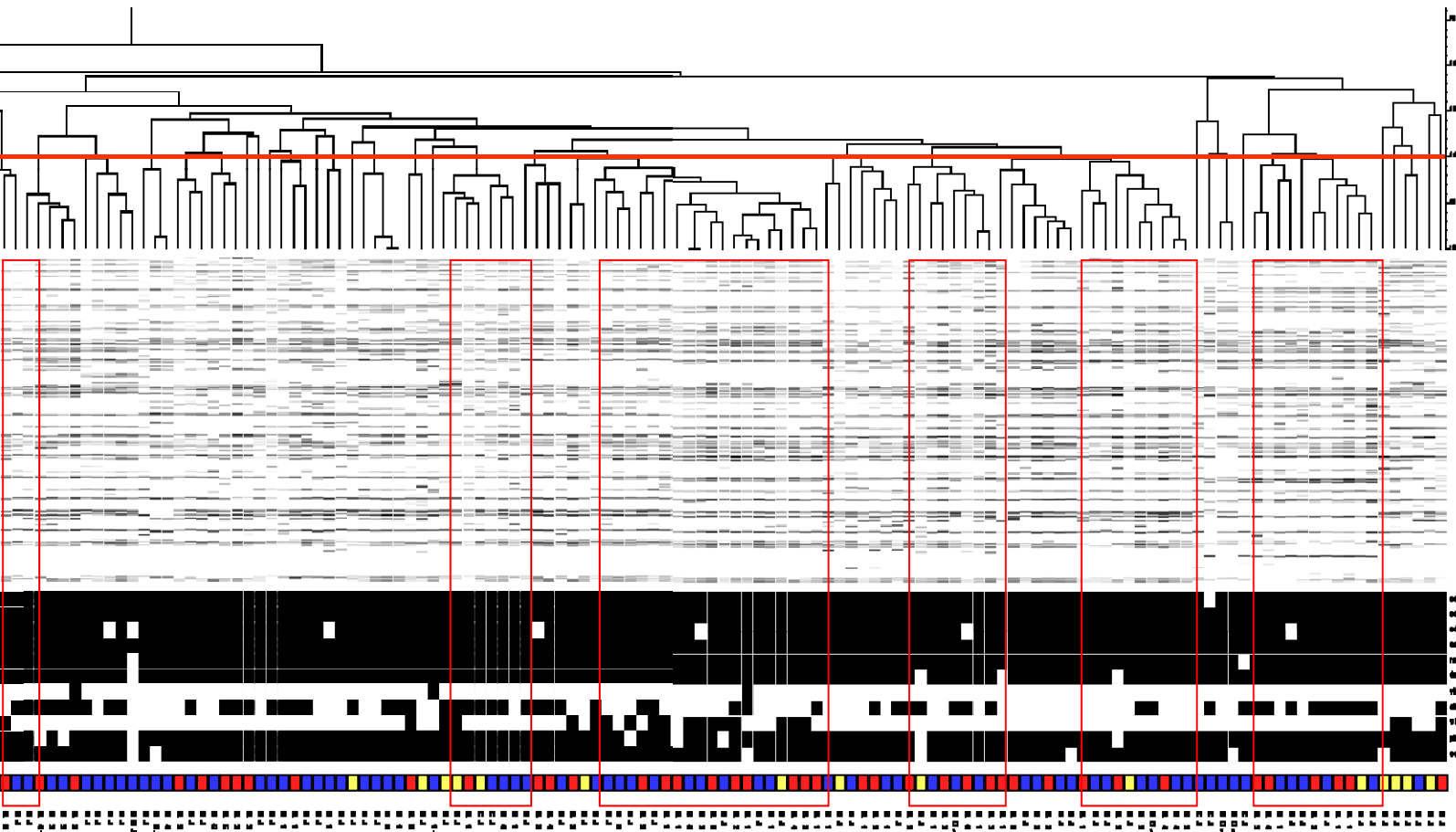


wlaN

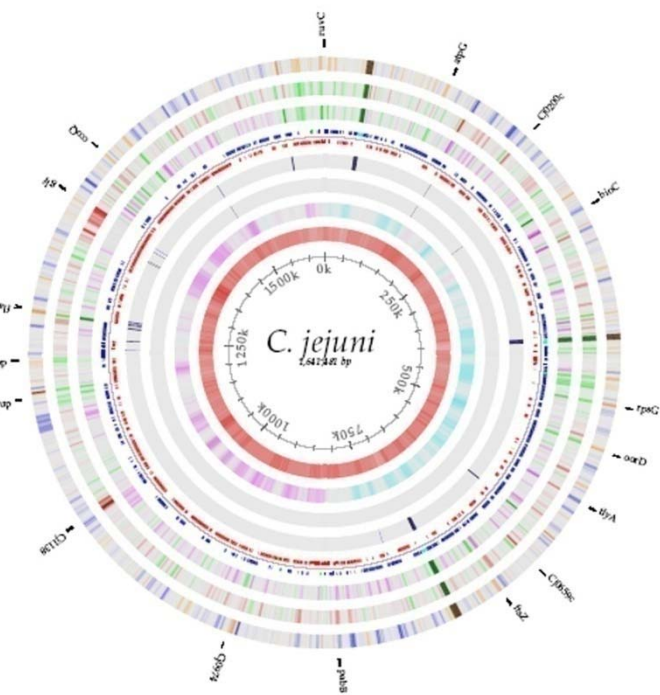
Campylobacter e virulenza



Campylobacter e virulenza



Multi-Locus Sequence Typing



aspA

glnA

gltA

glyA

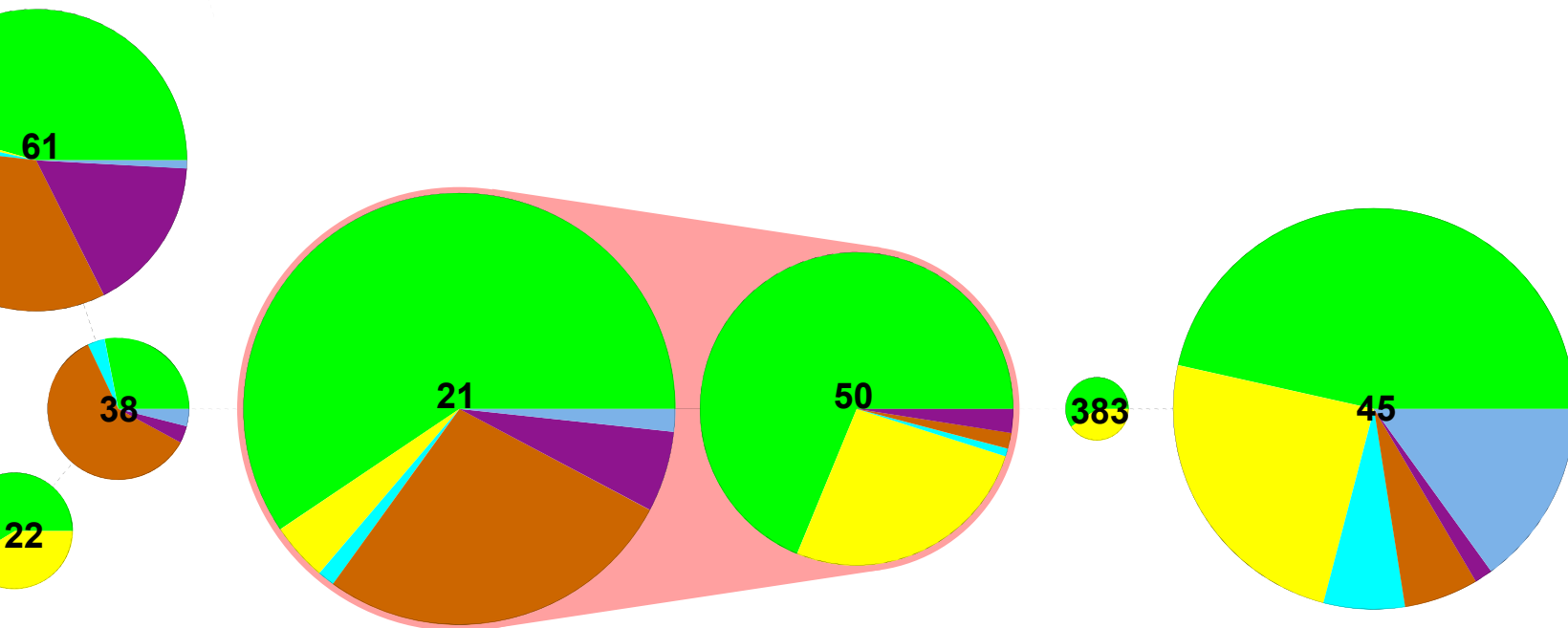
pgm

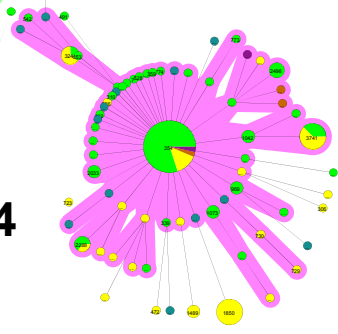
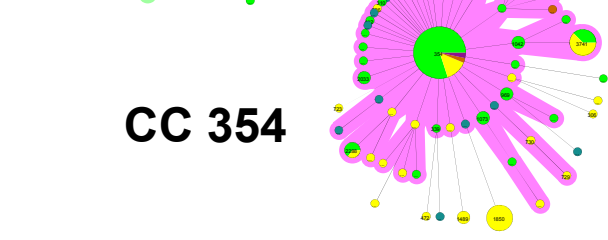
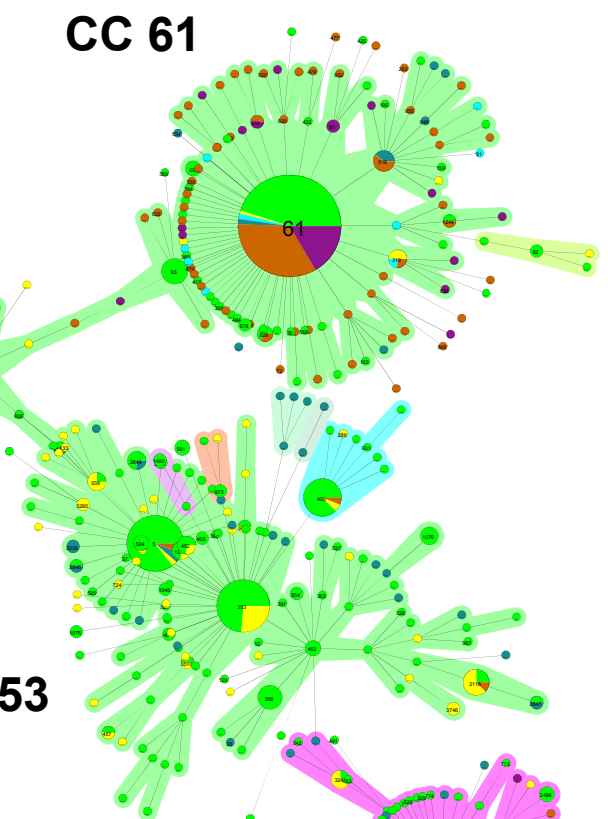
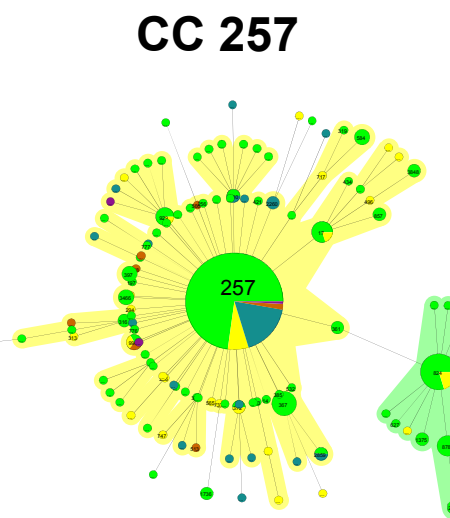
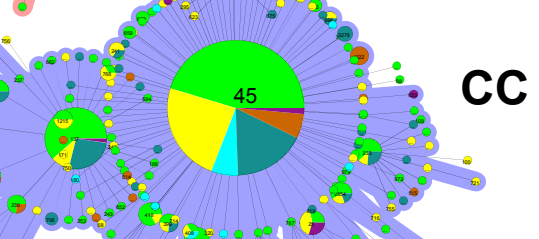
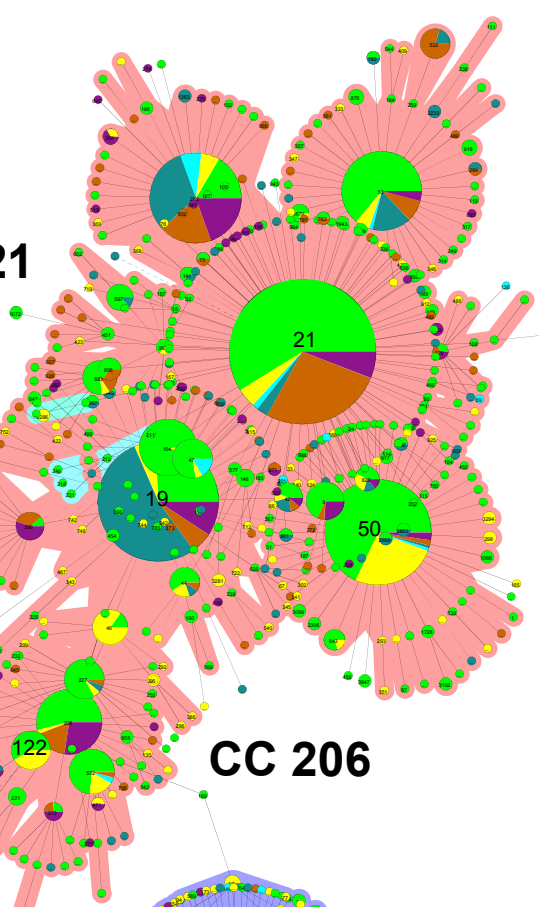
tkt

uncA

Multi-Locus Sequence Typing

Uomo Pollame Bovini Ovini Acque Altro



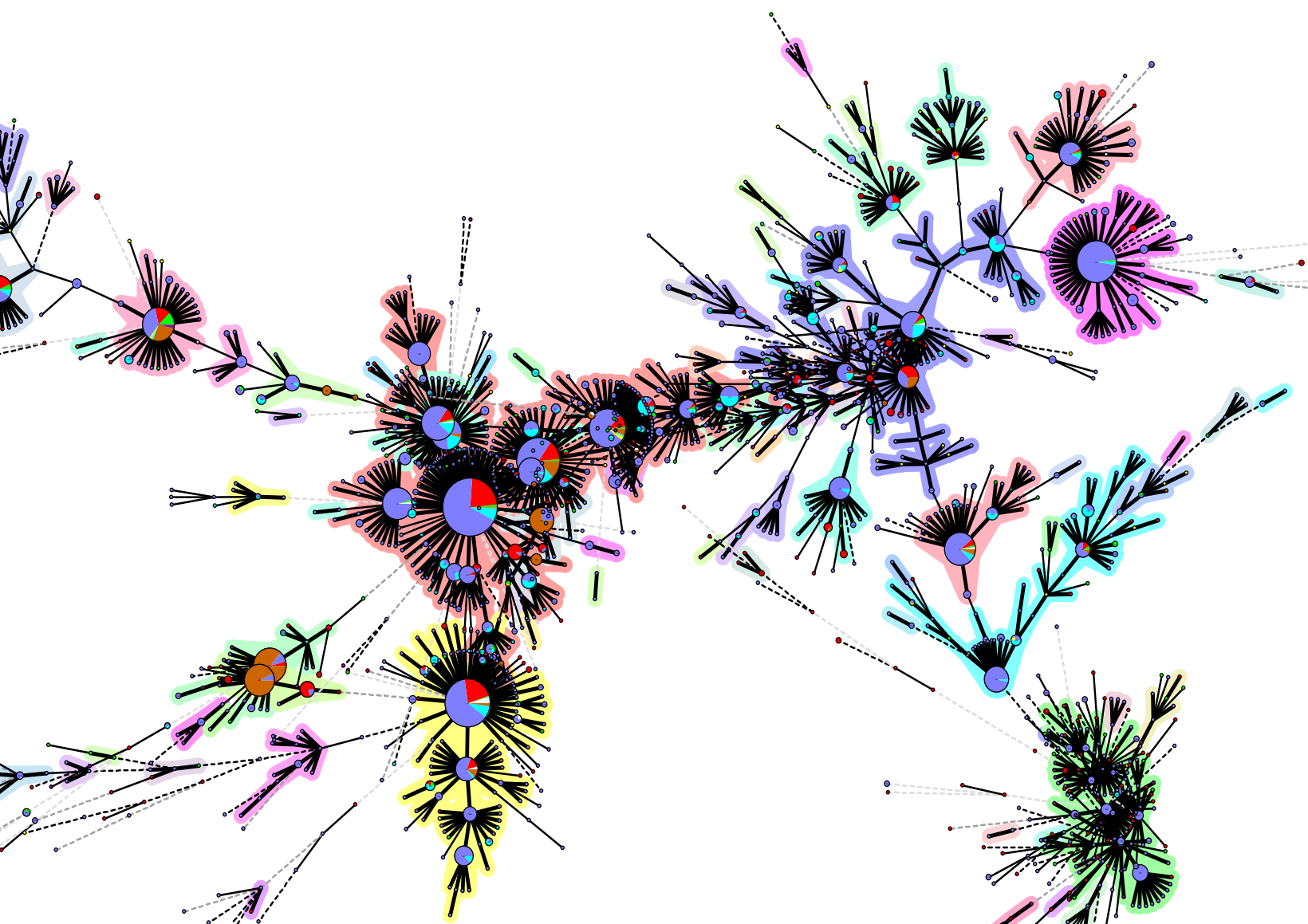


CC 45

CC 206

CC 353

CC 354



Conclusioni



Conclusioni



Conclusioni



SURVEILLANCE REPORT



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

Annual epidemiological report
*Reporting on 2009 surveillance data
and 2010 epidemic intelligence data*

2011

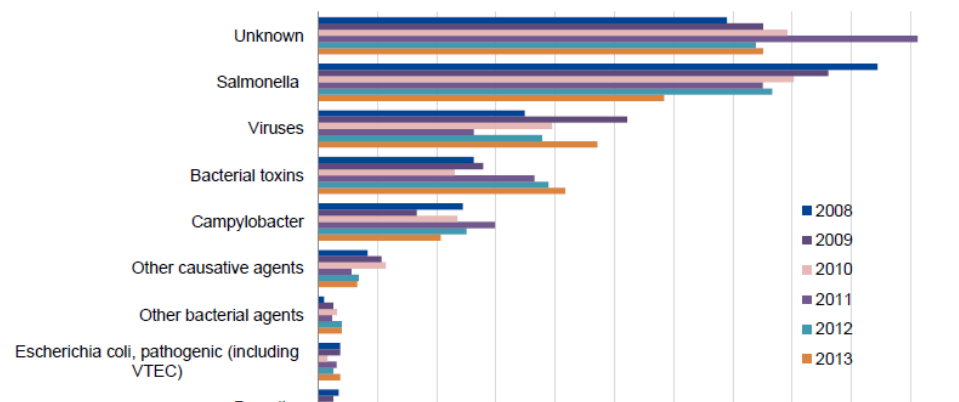
Conclusioni



Table 27. Number of outbreaks and human cases per causative agents in food-borne outbreaks in the EU (including strong evidence water-borne outbreaks), 2013

Causative agent	Strong-evidence outbreaks					Weak-evidence outbreaks					Total outbreaks	Total %
	N	%	Cases	Hospitalised	Deaths	N	%	Cases	Hospitalised	Deaths		
<i>Salmonella</i>	315	37.54	4371	1134	3	853	19.58	4338	1033	2	1168	22.48
Viruses	87	10.37	2023	126	0	855	19.62	7568	1841	0	942	18.13
Bacterial toxins	208	24.79	4006	163	1	626	14.37	5197	289	0	834	16.05
<i>Campylobacter</i>	32	3.81	478	15	0	382	8.77	1314	131	0	414	7.97
Other causative agents	76	9.06	520	46	1	56	1.29	445	27	0	132	2.54
Other bacterial agents	14	1.67	213	25	3	66	1.51	688	84	0	80	1.54
<i>Escherichia coli</i> , pathogenic - Verotoxigenic <i>E. coli</i> (VTEC)	12	1.43	154	36	0	62	1.42	353	70	0	74	1.42
Parasites	24	2.86	243	128	0	17	0.39	67	6	0	41	0.79
<i>Yersinia</i>	1	0.12	2	0	0	7	0.16	14	2	0	8	0.15
<i>Escherichia coli</i> , pathogenic (excluding VTEC)	1	0.12	128	0	0	0	0	0	0	0	1	0.02
Unknown	69	8.22	1386	138	1	1433	32.89	8454	652	0	1502	28.91
Total	839	100	13524	1811	9	4357	100	28438	4135	2	5196	100

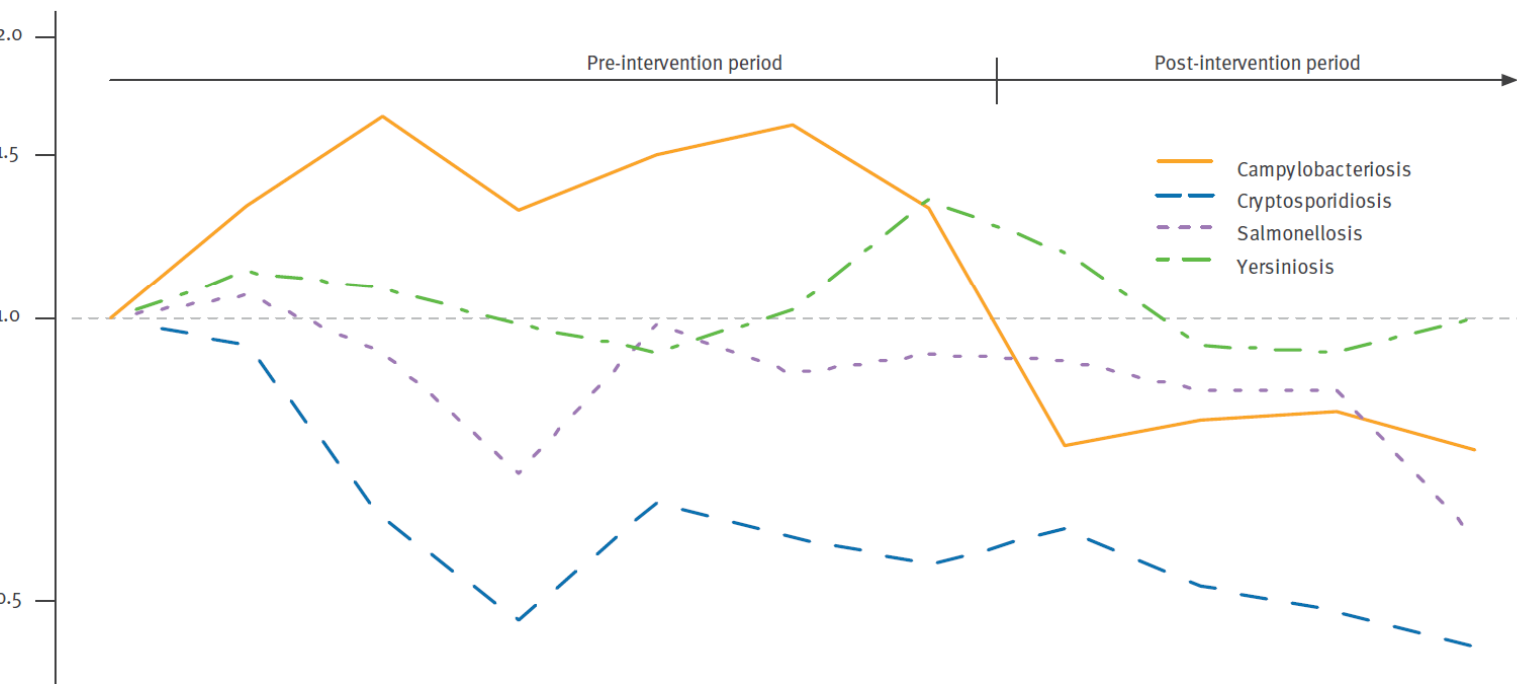
Figure 45. Distribution of all food-borne outbreaks per causative agent in the EU, 2013



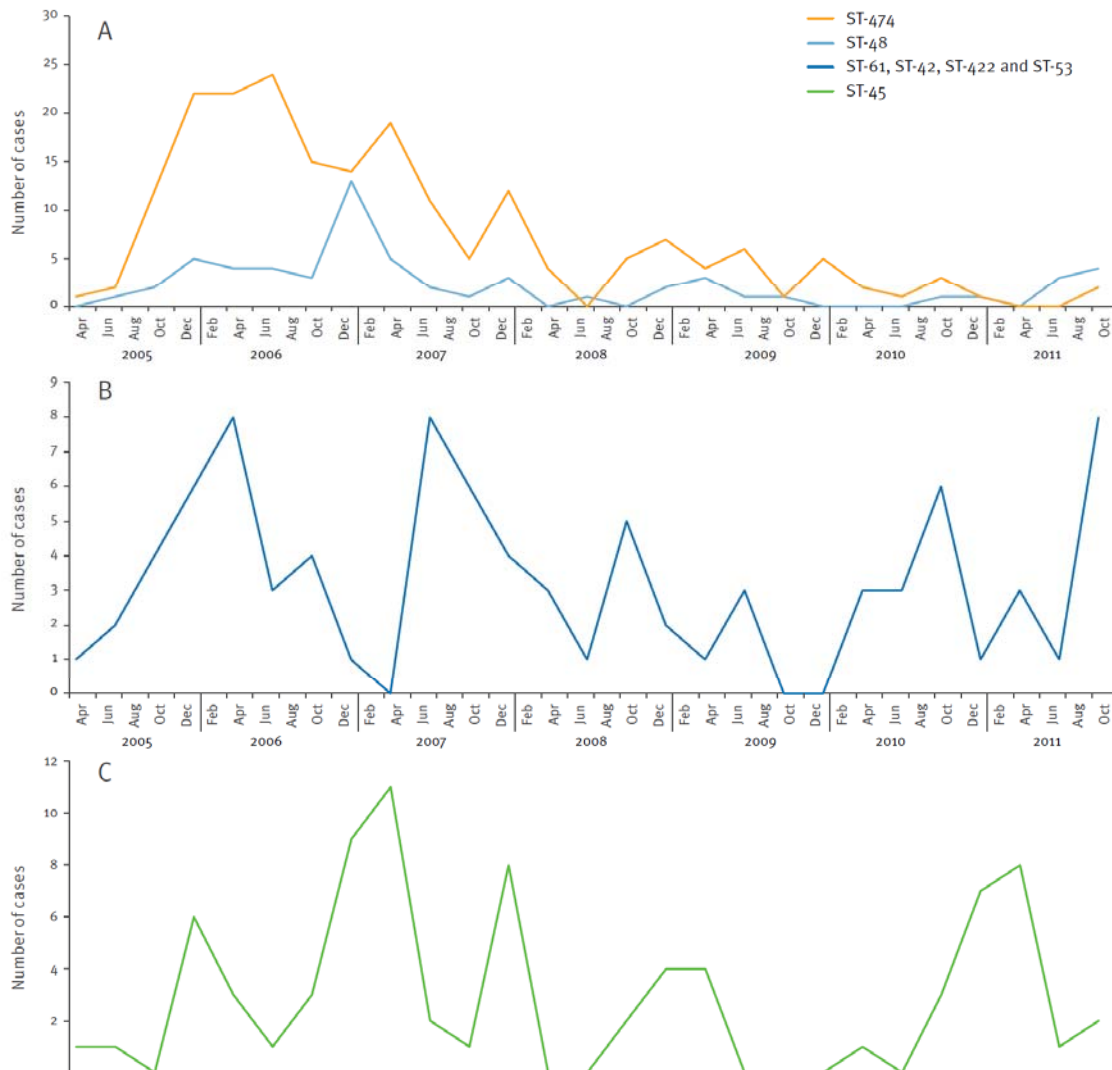
Molecular-based surveillance of campylobacteriosis in New Zealand – from source attribution to genomic epidemiology

P Muellner (petra@epi-interactive.com)^{1,2}, E Pleydell², R Pirie³, M G Baker⁴, D Campbell⁵, P E Carter³, N P French²

Notification rates^a of campylobacteriosis, cryptosporidiosis, salmonellosis and yersiniosis, New Zealand, 1999–2011 compared with 1999–2001



Human cases of campylobacteriosis caused by poultry- and ruminant-associated *Campylobacter jejuni* MLST types, as well as a ubiquitous ST in a sentinel surveillance site, New Zealand, 2005–2011



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