

Genome-wide identification of host-segregating epidemiological markers for source attribution in *Campylobacter jejuni*

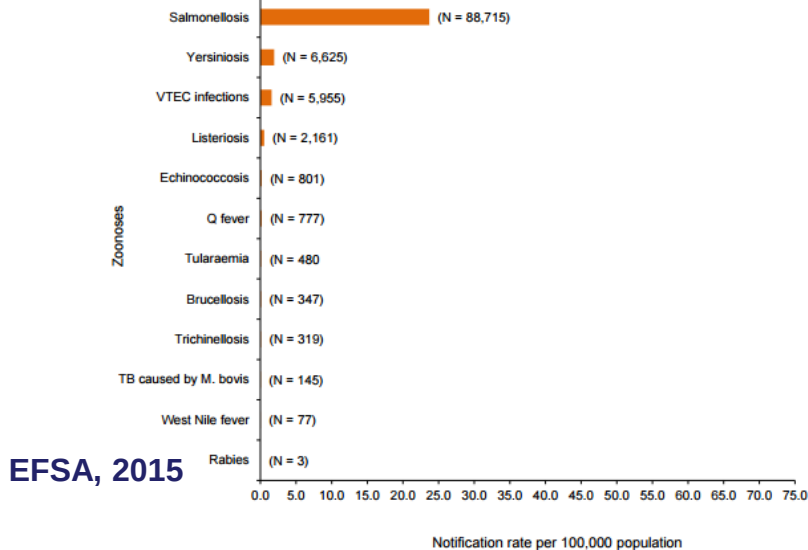
Gilles Salvat, 5 November 2018, Nanyang Technological University, Singapore

Amandine Thépault, M. Chemaly, G. Méric, L. Mageiros, T. Poezevara,
S. Quesne, V. Rose, V. Béven, F. Touzain, S. K. Sheppard & K. Rivoal

French Agency for Food, Environmental and Occupational Health and Safety (Anses)
Unit of Hygiene and Quality of Poultry and Pig Products

Campylobacteriosis

Campylobacteriosis N=236,851



236,851

420,000,000

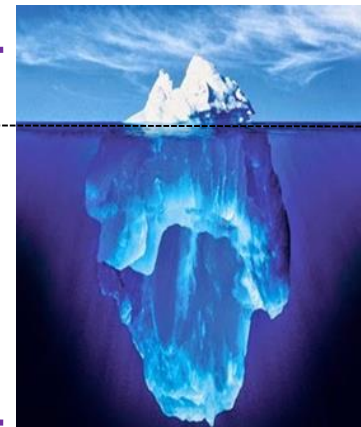
ECDC, 2015



5,958

528,780

Van Cauteren
et al., 2015



Numerous potential sources of contamination



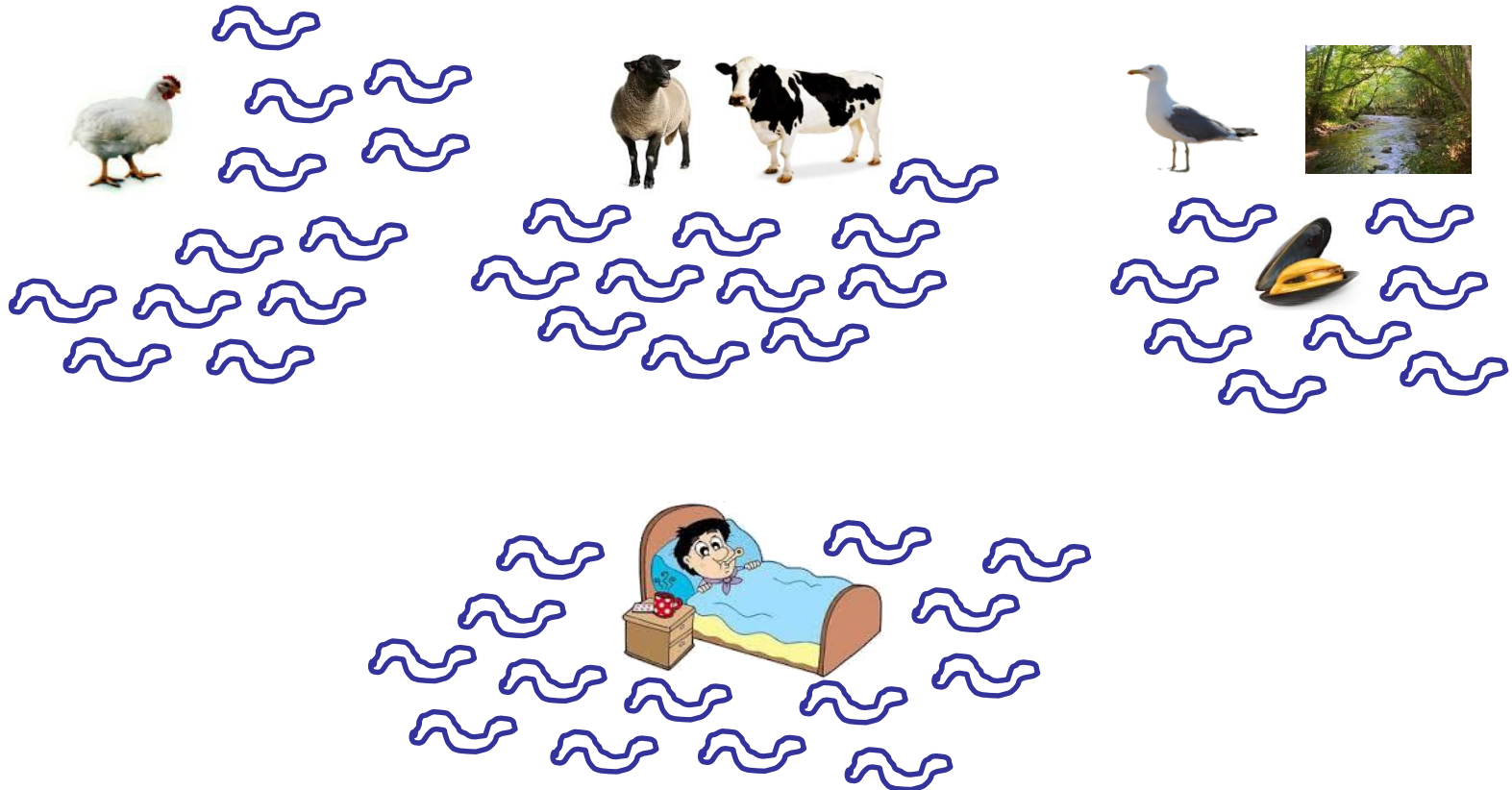
Chicken as the main source of human contamination (Sheppard *et al.*, 2009; Wilson *et al.*, 2009; Müllner *et al.*, 2010; Kittl *et al.*, 2013; Mossong *et al.*, 2016)

Main risk factors: consumption of undercooked broiler meat and cross contaminations (Luber *et al.*, 2009; Hermans *et al.*, 2012; EFSA, 2013)

Source attribution

“Source attribution can identify the most important reservoirs for a pathogen of interest and to set priorities to focus control strategies” (WHO, 2007)

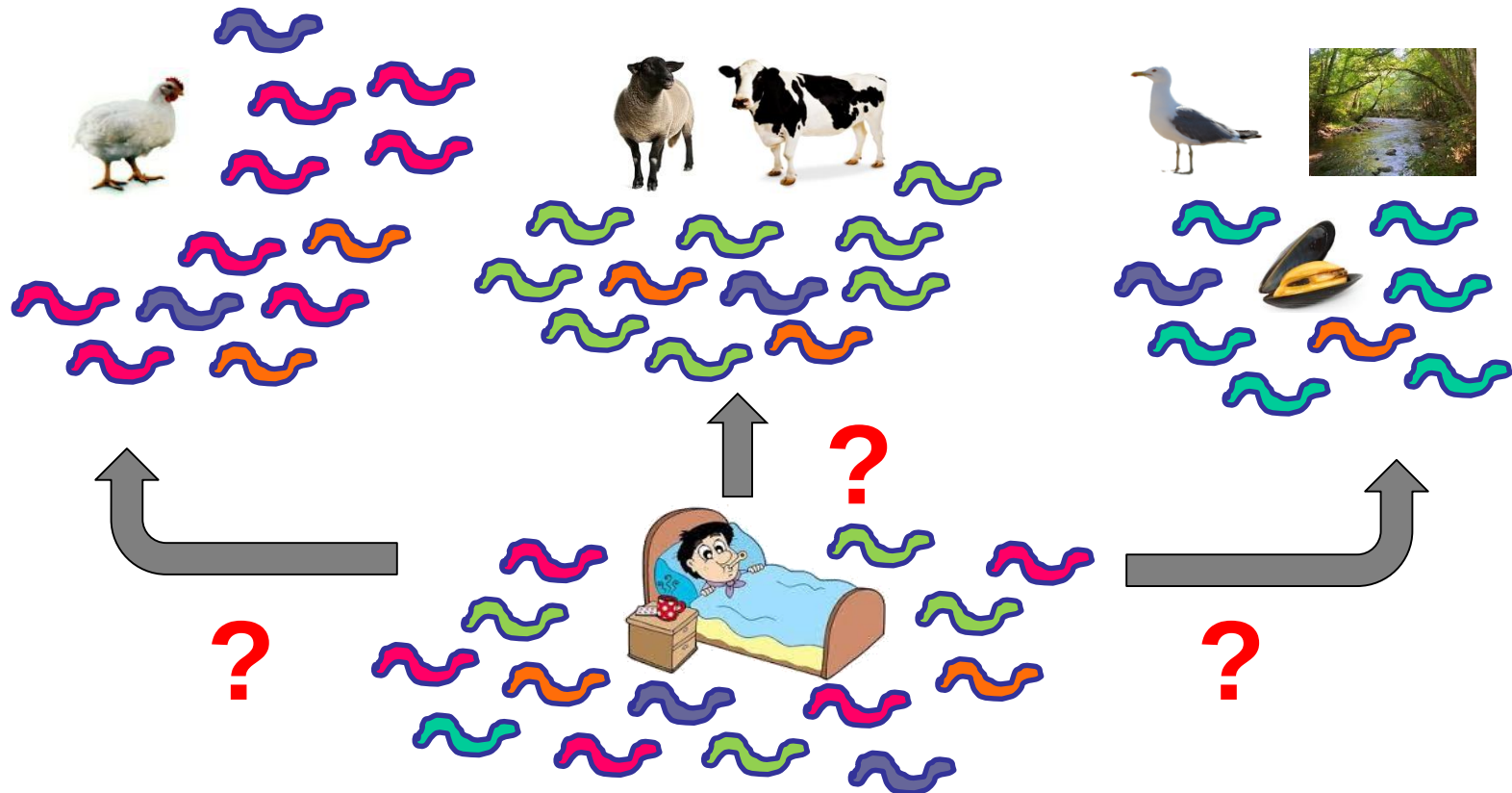
Microbial subtyping approach



Source attribution

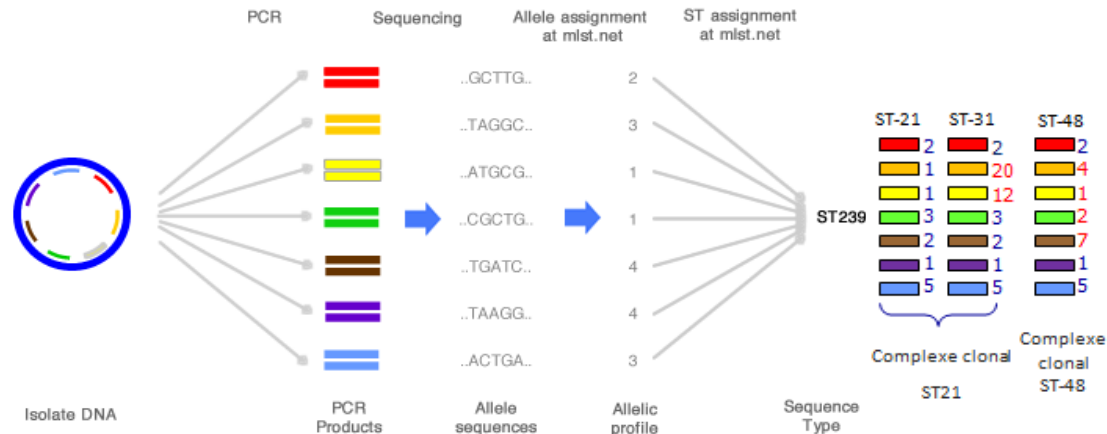
“Source attribution can identify the most important reservoirs for a pathogen of interest and to set priorities to focus control strategies” (WHO, 2007)

Microbial subtyping approach



Genotyping methods

MLST : gold standard for genotyping and source attribution in *Campylobacter*



Limitation: Assignment of clinical isolates from host generalist clonal complexes

Whole genome sequencing : possibility of studying the genetic variability within more than 7 genes

- ➔ Whole genome MLST (wgMLST) = MLST on all the genes
- ➔ Promising tool to increase the sensitivity of source attribution?

Genotyping methods



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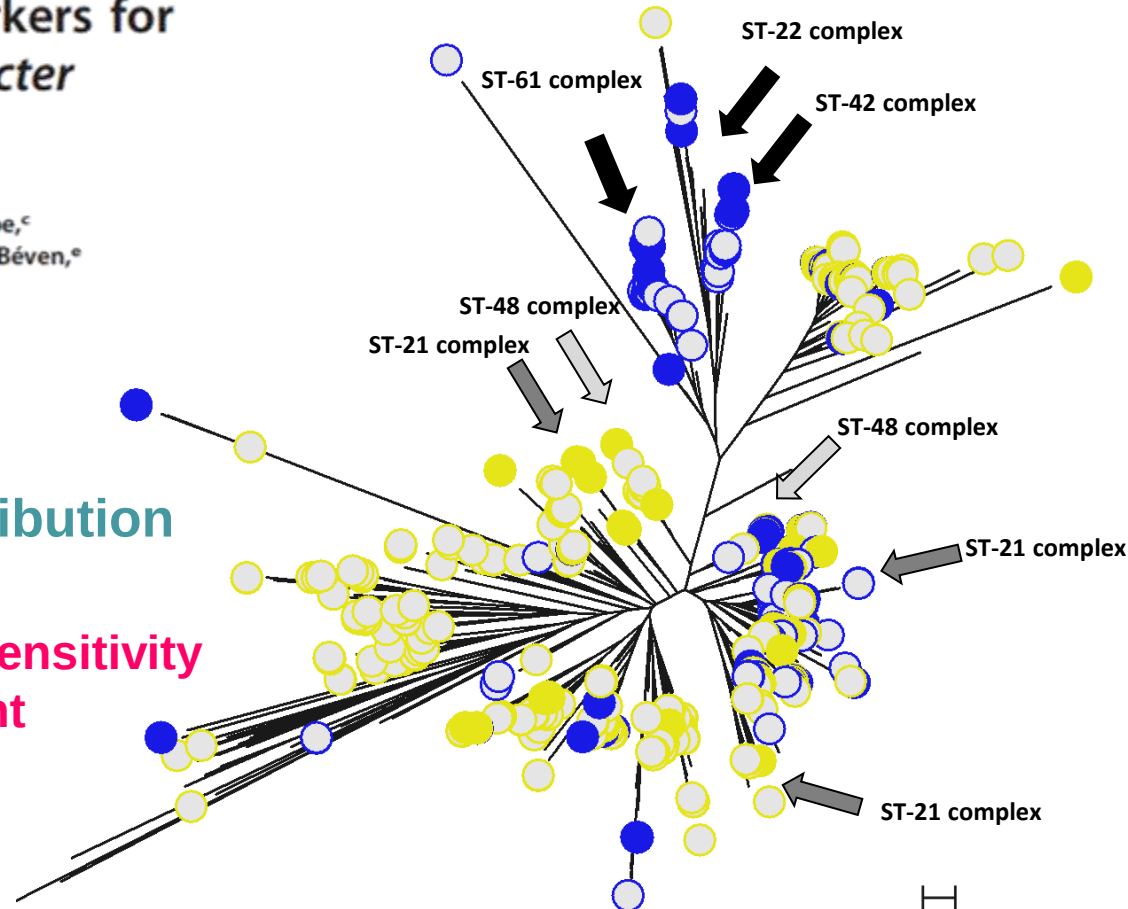
Genome-Wide Identification of Host-Segregating Epidemiological Markers for Source Attribution in *Campylobacter jejuni*

Amandine Thépault,^{a,b} Guillaume Méric,^c Katell Rivoal,^a Ben Pascoe,^c Leonardos Mageiros,^d Fabrice Touzain,^e Valérie Rose,^a Véronique Béven,^e Marianne Chemaly,^a Samuel K. Sheppard^{c,f}

15 HS markers for source attribution

→ Potential improvement of sensitivity in the probabilistic assignment

● FR chicken ● FR ruminants
○ UK chicken ○ UK ruminants



0.001
ances

Genotyping methods

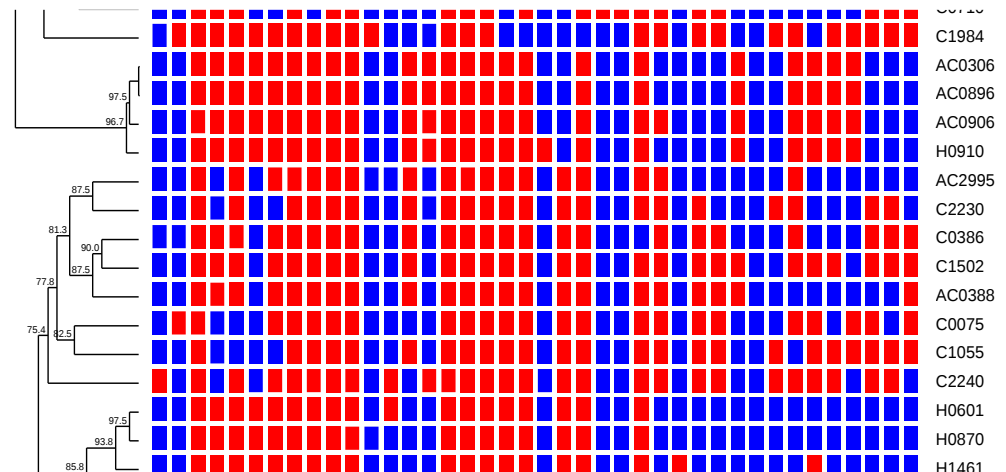
Comparative Genomic Fingerprinting (CGF40) (Taboada *et al.*, 2012)

Amplification of 40 accessory genes

Binary CGF40 data

Concordant with MLST

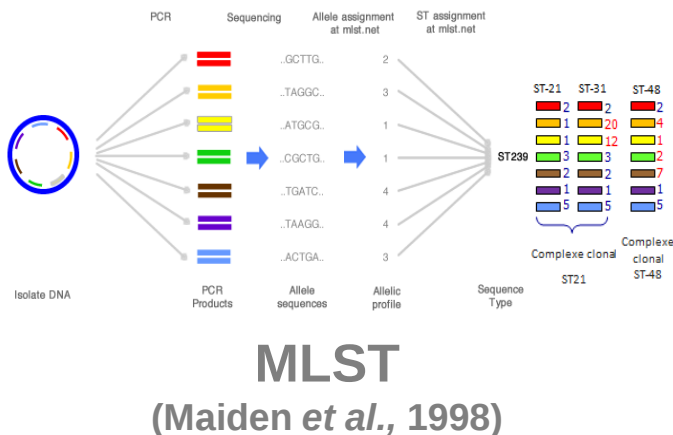
Easily deployable



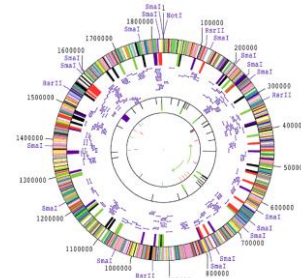
➔ Interesting genotyping method for source attribution?

Aim of the study

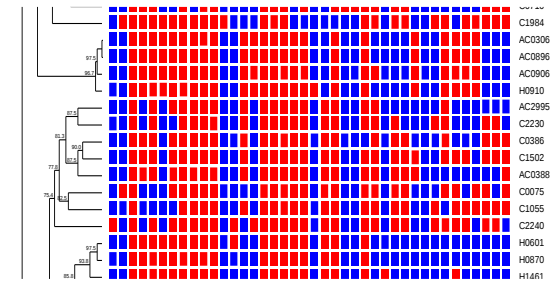
Assess the ability of three genotyping methods in source attribution to identify the origin of human campylobacteriosis in France



Whole Genome Sequencing
15 HS markers
(Thépault *et al.*, 2017)



CGF40
(Taboada *et al.*, 2012)



Genotyping of *C. jejuni* isolates

					 
				Ifremer	2009 2015
CGF40	644	691	161	122	143 371
MLST	644	119	55	39	143 79
WGS (Ion torrent technology)	392	195	55	98	42 79

Clinical cases from the 10 most populated departments in France

Data analysis and source attribution

Bionumerics (Applied Math v6.5) & **PubMLST** database

→ MLST alleles designations

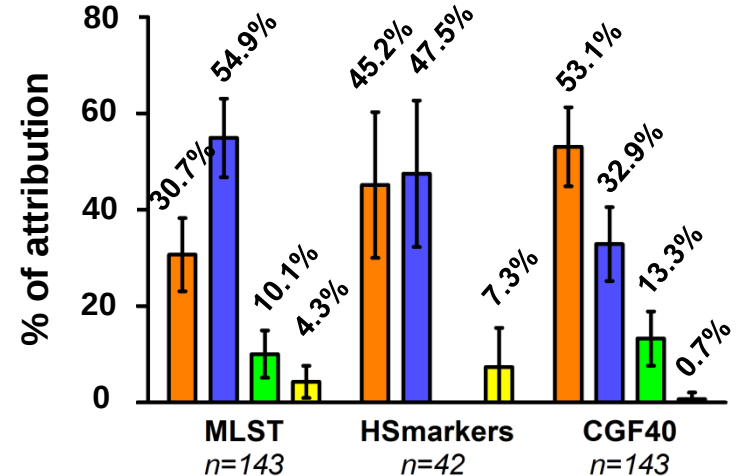
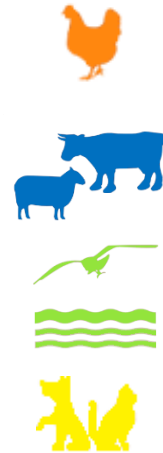
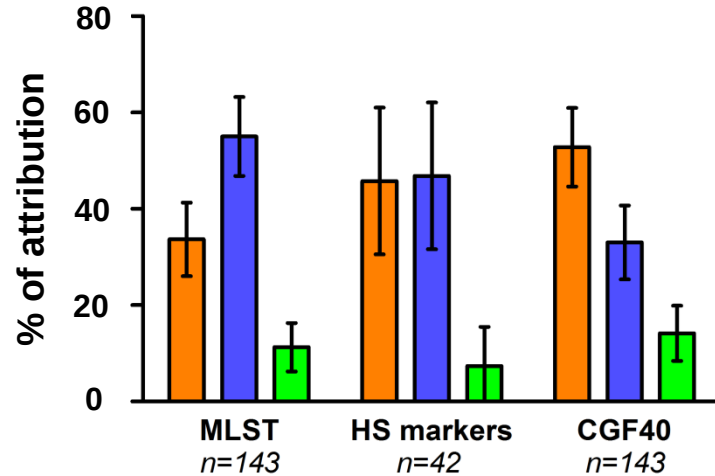
BIGSdb (Jolley & Maiden, 2010) : Bacterial Isolate Genome Sequence database

→ Genome Comparator for wg MLST

Structure (Pritchard *et al.*, 2010) : Clustering method based on a Bayesian model

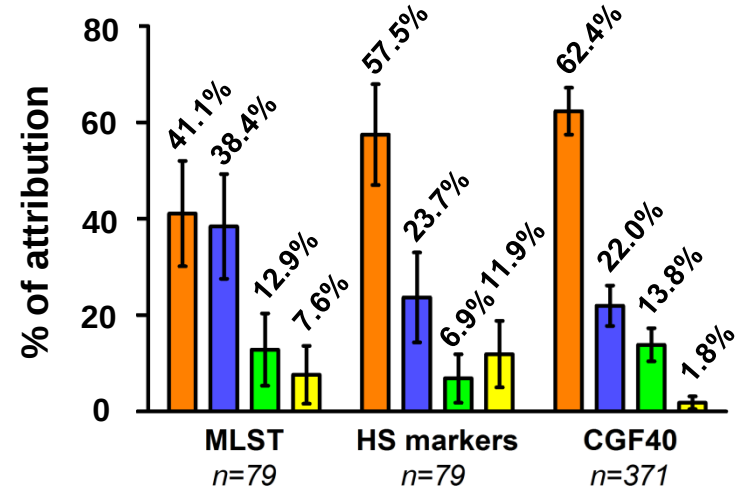
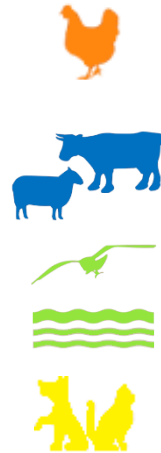
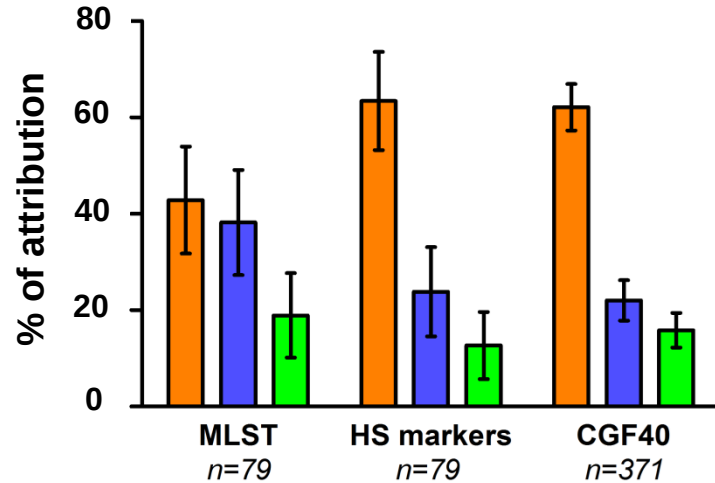
→ Probabilistic assignment of human isolates to a source

Source attribution of French cases from 2009



- ➔ **MLST** - Higher implication of ruminants (55%) compared with chicken (33.7%) or environment (11.3%)
- ➔ **HS markers** - Equivalent implication of ruminants (46.9%) and chicken (45.8%); environment (7.3%)
- ➔ **CGF40** - Higher implication of chicken (52.8%) compared with ruminant (33%) or environment (14.2%)
- ➔ **Addition of pets as a potential reservoir** : same trends in source attribution except using the HS markers

Source attribution of French cases from 2015



- ➔ **MLST** - Equivalent implication of ruminants (38.2%) and chicken (42.9%); Higher compared with environment (18.9%)
- ➔ **HS markers** - Higher implication of chicken (63.4%) compared with ruminant (23.9%) or environment (12.7%)
- ➔ **CGF40** - Higher implication of chicken (62.1%) compared with ruminant (22.0%) or environment (15.9%)
- ➔ **Addition of pets as a potential source:** same trends in source attribution except using the HS markers

Conclusions

- Differences in attribution between the 3 genotyping methods :
 - MLST vs HS markers : improvement of sensitivity using the HS markers
 - CGF40 : “not suitable to perform source attribution study as it does not provide enough detailed genotyping information” (Ravel et al., 2017)
- Differences in the source attribution according to the year
 - Source attribution on a regular basis
- Environment (0%-13%) and pets implication (7%-12%)
- Chicken is highly implicated in human contamination (Sheppard et al., 2009; Mullner et al., 2009; Strachan et al., 2009; Kittl et al., 2013, Mossong et al., 2016, Rosner et al., 2017)
- Ruminant reservoir plays a significant role in French campylobacteriosis

Acknowledgment



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Katell RIVOAL
Marianne CHEMALY



**Unit GVB -
Sequencing Platform**

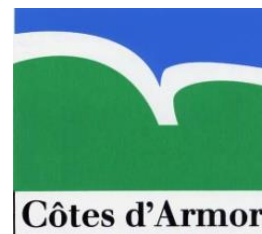


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