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alimentation, environnement, travail



Source attribution of French clinical isolates of *Campylobacter jejuni*

Pr Philippe Lehours

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Introduction: CNRCH activities

→ Isolates from 2017

	Stool	Blood	Others	Total
<i>C. jejuni</i>	5 399	64	12	5 475
<i>C. coli</i>	888	11	1	900
<i>C. fetus</i>	39	49	5	93
<i>A. butzleri</i>	78	0	0	78
<i>C. lari</i>	16	3	0	19
<i>C. upsaliensis</i>	7	1	0	8
<i>A. cryaerophilus</i>	7	0	0	7
<i>Helicobacter spp</i>	1	3	0	4
Other <i>Campylobacter</i>	6	2	3	11
Unknown	407	7	7	415
Total	6 848	140	22	7 010

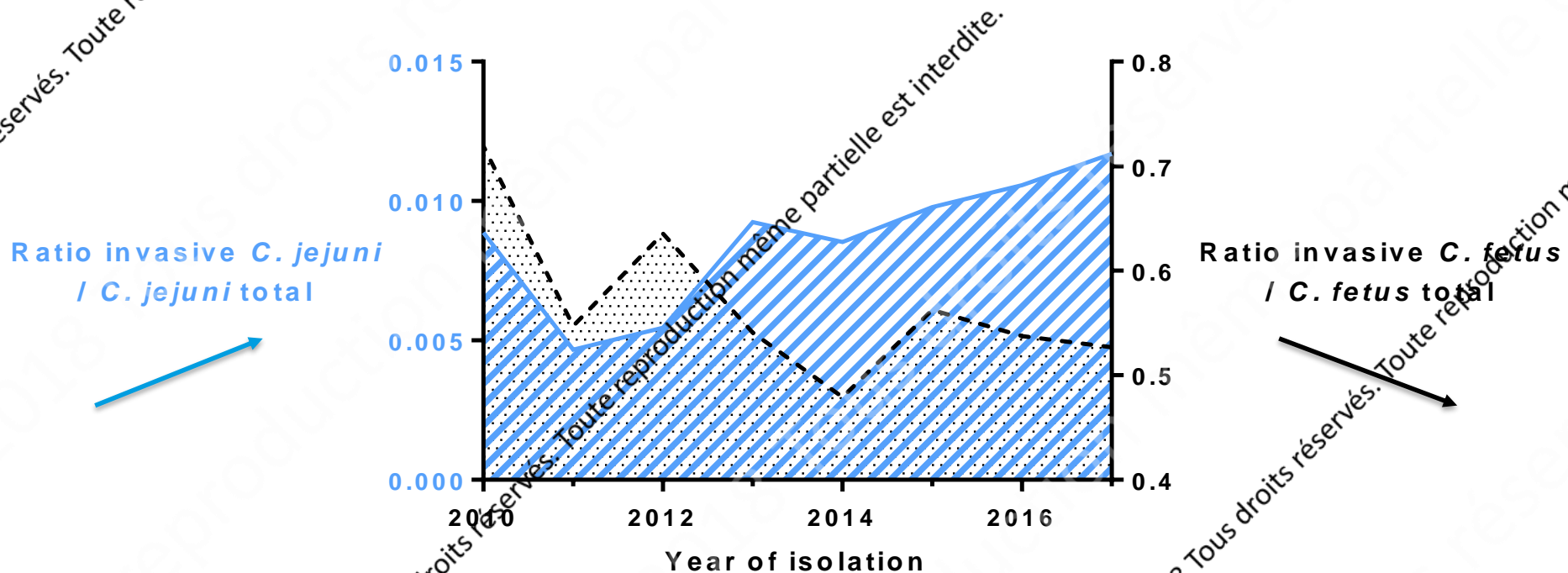
Introduction: invasive isolates

→ Isolates from 2017

	Stool	Blood	Others	Total
<i>C. jejuni</i>	5 399	64	1.17%	5 475
<i>C. coli</i>	888	11		900
<i>C. fetus</i>	39	49	52.7%	93
<i>A. butzleri</i>	78	0	0	78
<i>C. lari</i>	16	3	0	19
<i>C. upsaliensis</i>	7	1	0	8
<i>A. cryaerophilus</i>	7	0	0	7
<i>Helicobacter spp</i>	1	3	0	4
Other <i>Campylobacter</i>	6	2	3	11
Unknown	407	7	7	415
Total	6 848	140	22	7 010

Introduction: invasive isolates

- An increasing proportion of invasive *C.jejuni* are received every year since 2013

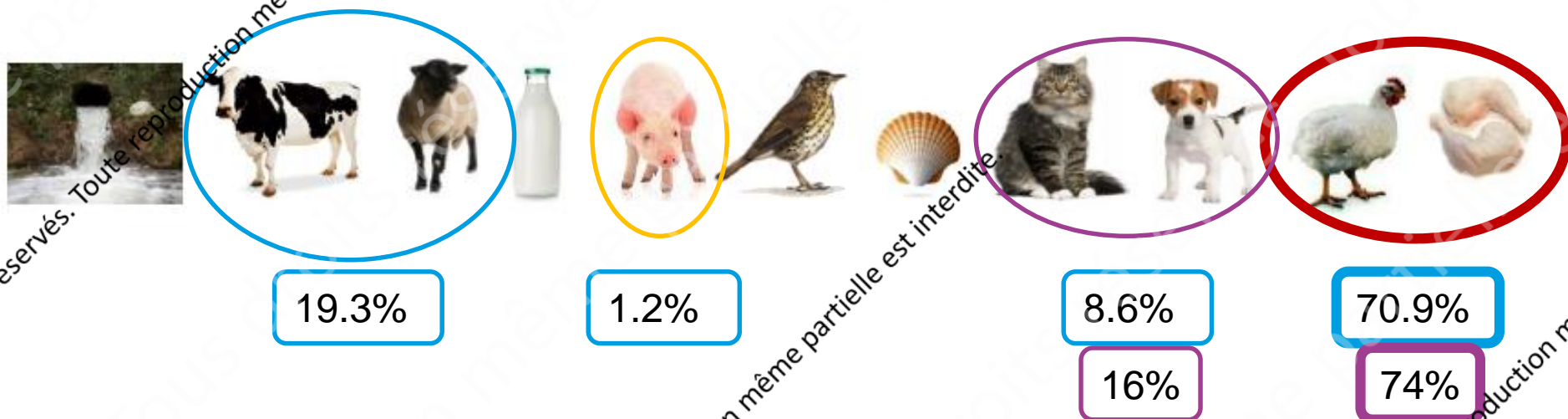


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Introduction: source attribution for *C. jejuni*

→ Origin of infection:



→ MLST based studies identify chicken as the main reservoir

[PLoS One](#), 2013 Nov 14;8(11):e81796. doi: 10.1371/journal.pone.0081796. eCollection 2013.

Source attribution of human *Campylobacter* isolates by MLST and flag-typing and association of genotypes with quinolone resistance.

[Kittl S¹](#), [Heckel G](#), [Korczak BM](#), [Kuhnert P](#).

[Sci Rep](#), 2017 Jul 11;7(1):5139. doi: 10.1038/s41598-017-05227-x.

A combined case-control and molecular source attribution study of human *Campylobacter* infections in Germany, 2011-2014.

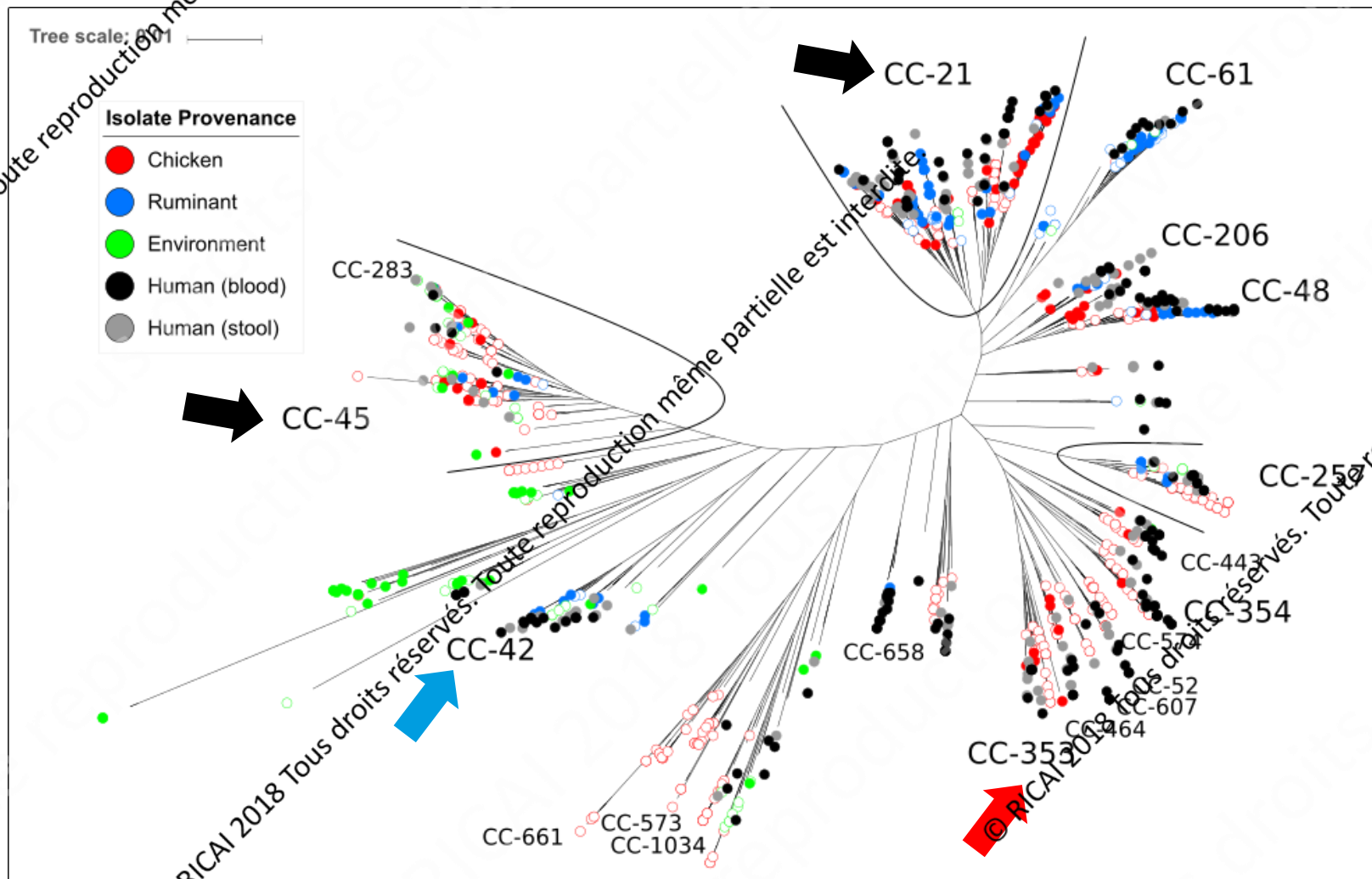
[Rosner BM¹](#), [Schielke A²](#), [Didelot X³](#), [Kops F⁴](#), [Spindlerbach J²](#), [Willrich N²](#), [Gölg G⁵](#), [Alter T⁵](#), [Stingl K⁶](#), [Josenhans C^{4,7}](#), [Suerbaum S^{8,9,10}](#), [Stark K¹¹](#).

Switzerland
2011-2012

Germany
2011-2014

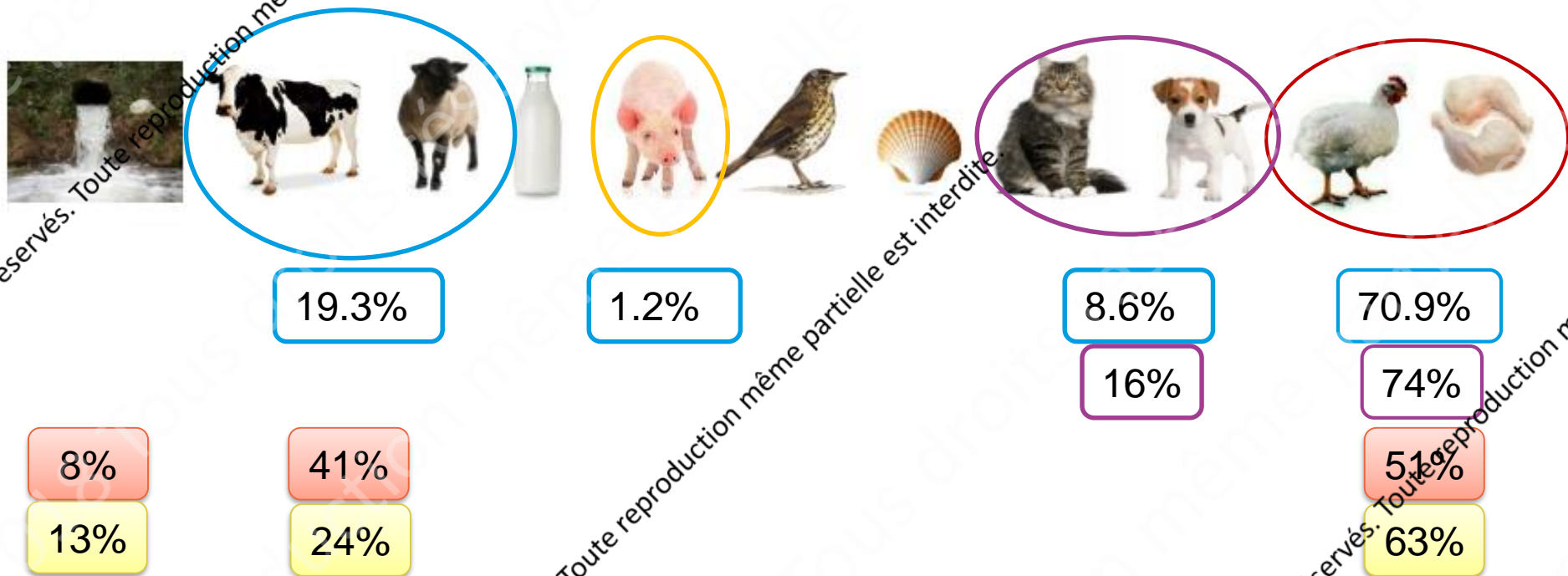
Introduction: MLST limits

Core genome tree



Introduction: source attribution for *C. jejuni*

→ Origin of infection:



→ Whole-genome based (15 markers) study identifies a role for ruminant

Sci Rep. 2018 Jun 18;8(1):9305. doi: 10.1038/s41598-018-27356-z.

Ruminant and chicken: important sources of campylobacteriosis in France despite a variation of source attribution in 2009 and 2015.

Thépault A^{1,2}, Rose V¹, Quesne S¹, Poissot J¹, Béven V³, Hirschaud E³, Touzain F³, Lucas P³, Méric G⁴, Mageiros L⁵, Sheppard SK^{4,6}, Chemaly M¹, Ring S⁷.



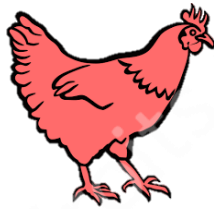
Facts and aims

- Increasing numbers of invasive *C. jejuni*
- Attribution studies based on non-invasive *C. jejuni*

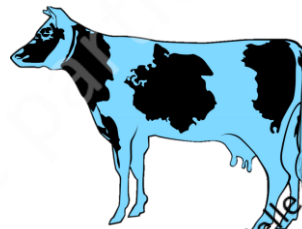
Is there a different origin for invasive strains ?

Material: reservoir strains

→ 583 strains publicly available from 3 main reservoirs



352



136



95

New Zealand
UK
USA
Belgium
Canada
The Netherlands
France

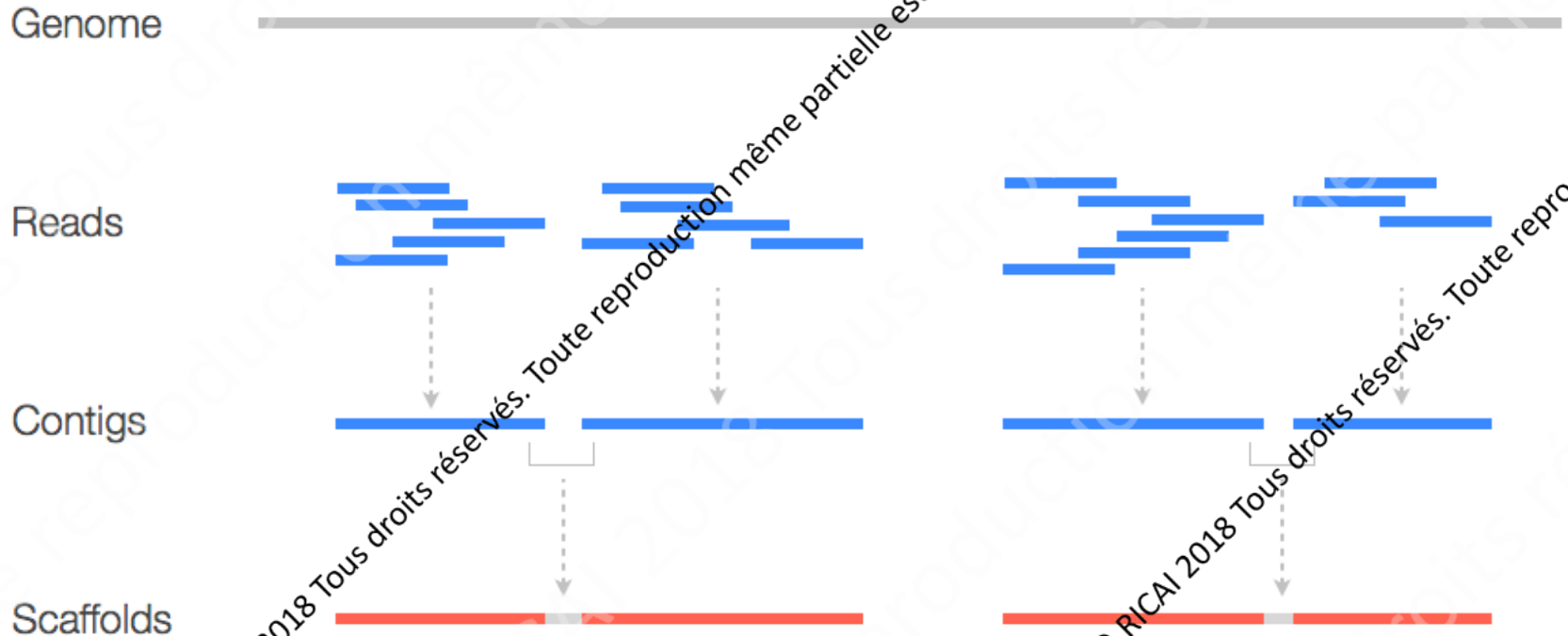
Material: clinical strains (n=316)

- 118 French clinical strains previously published
- 198 French clinical strains newly sequenced (Illumina NextSeq500)

	invasive 172	non invasive 143
2009	-	39
2011	17	-
2012	18	-
2013	33	-
2014	35	-
2015	32+1	78
2016	37	28

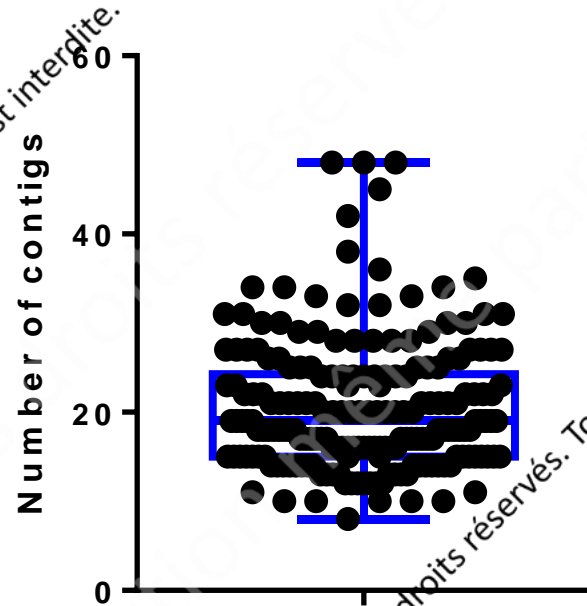
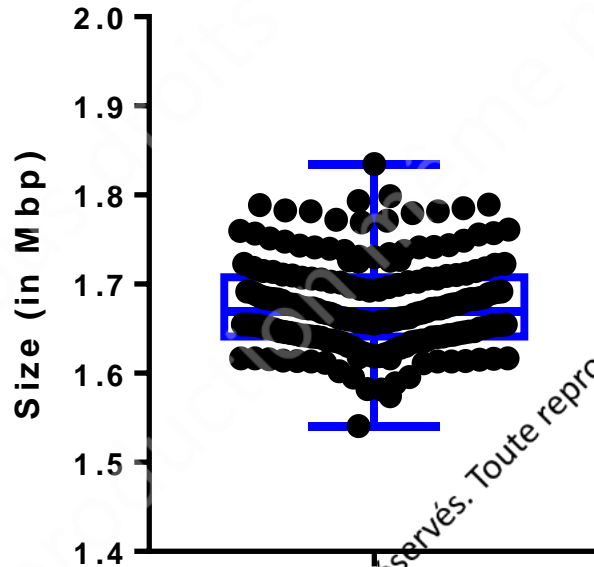
Material: newly sequenced clinical strains

- 198 strains newly sequenced strains
 - › Library prep (Nextera XT DNA Library Preparation Kit- Illumina)
 - › Sequencing (NextSeq500 - Illumina) (Helixio, Clermont Ferrand)
 - › *De novo* assembly (SPAdes)



Material: newly sequenced clinical strains

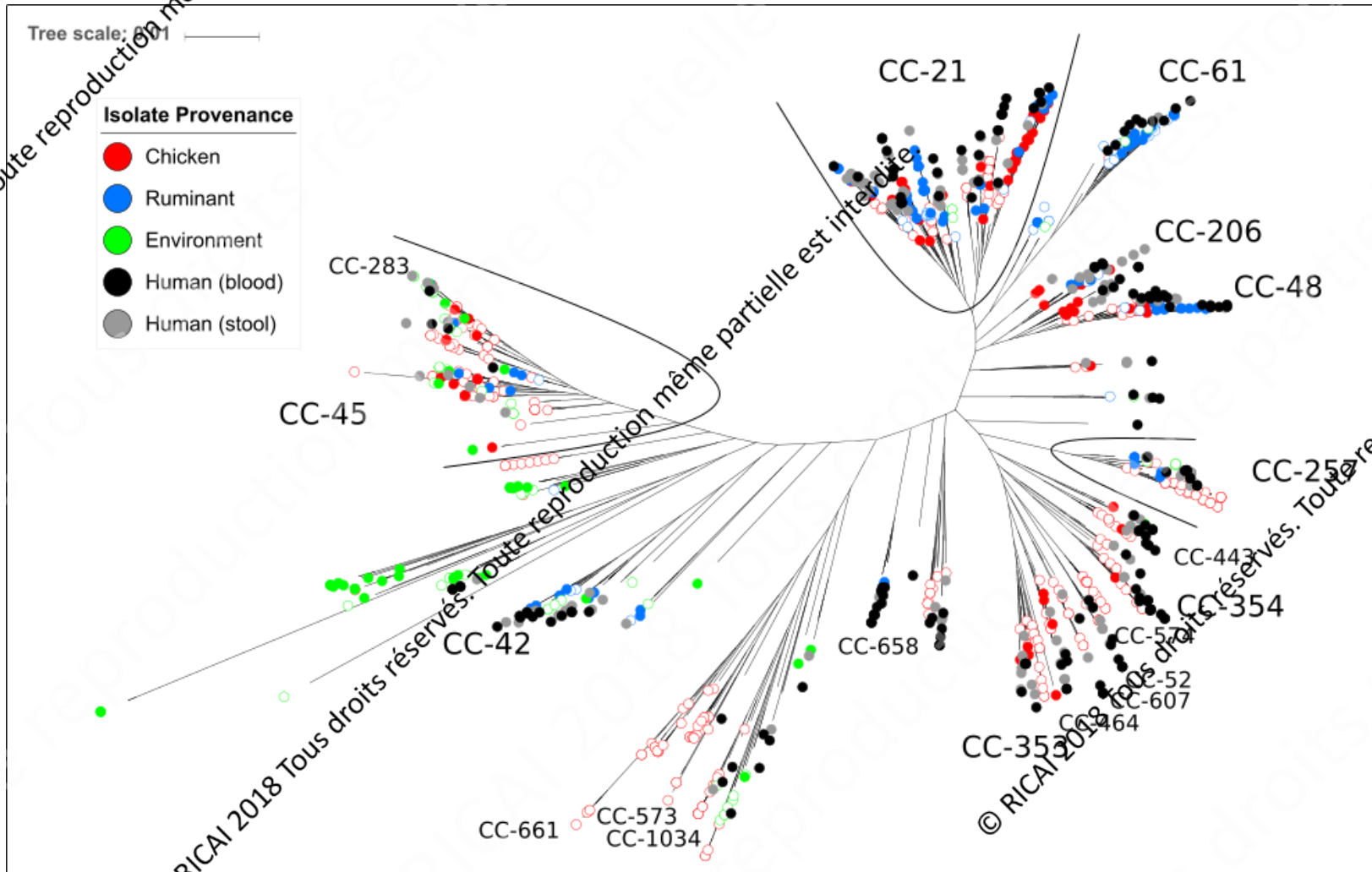
- 198 strains newly sequenced strains (Helixio)
 - › filtration of contigs (in-house script – CNRCH)



Material: dataset

Core genome tree

Plain circles = French isolates
Empty circles = World isolates



Methods

→ 15 host-segregating markers

Appl Environ Microbiol. 2017 Mar 17;83(7). pii: e03085-16. doi: 10.1128/AEM.03085-16. Print 2017 Apr 1.

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

Thépault A^{1,2}, Méric G³, Rivoal K¹, Pascoe B³, Mageiros L⁴, Touzain F⁵, Rose V¹, Béven V⁶, Chemaly M¹, Sheppard SK^{6,7}.

→ Use of BIGSdb to identify alleles present in each strain

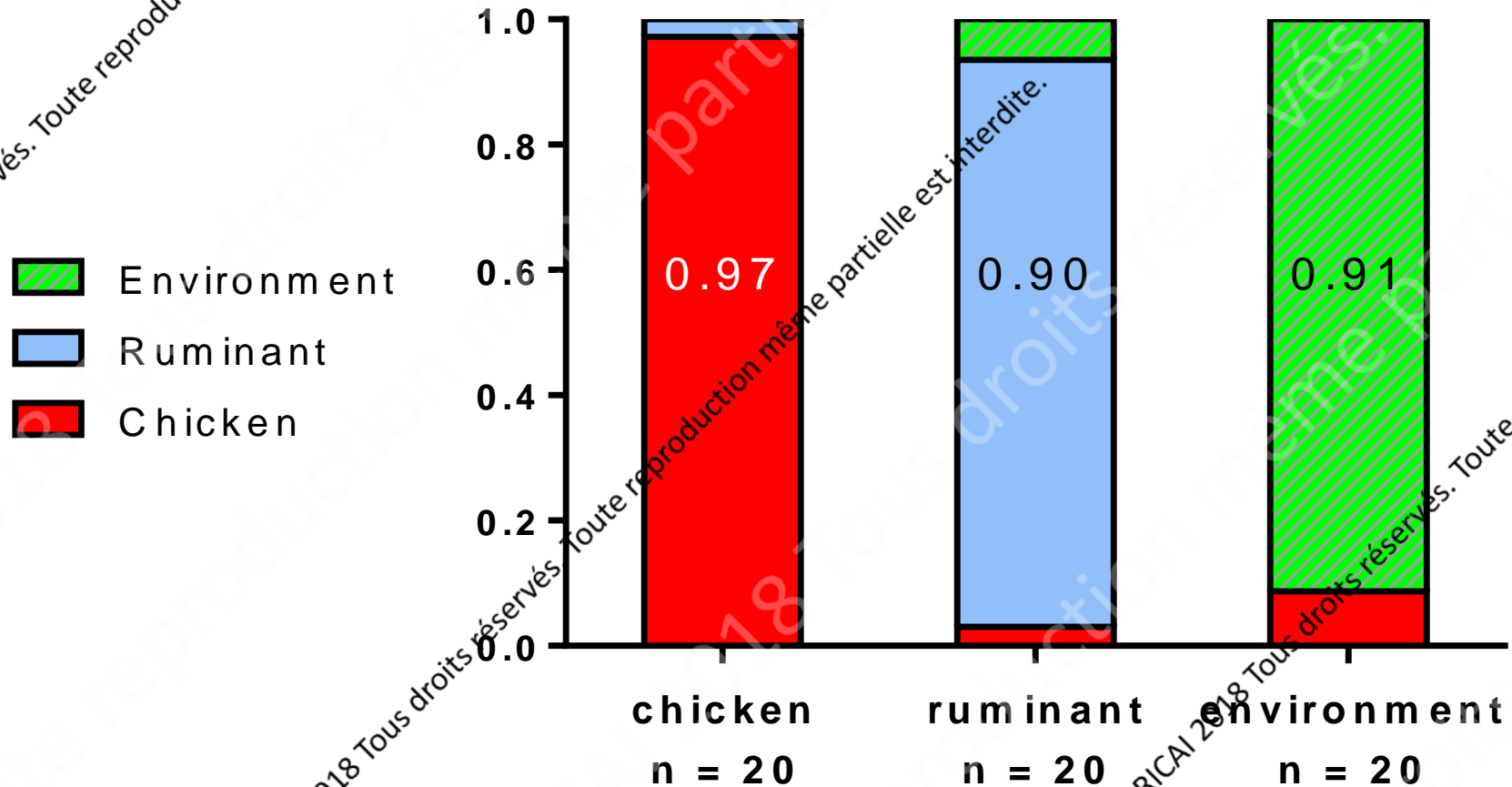
	marker 1	marker 2	marker 3	...	marker 14	marker 15
Strain 1	1	1	2	...	2	3
Strain 2	2	1	2	...	3	1

→ Use of Structure software to investigate population structure

- › 10 repetitions for each analysis

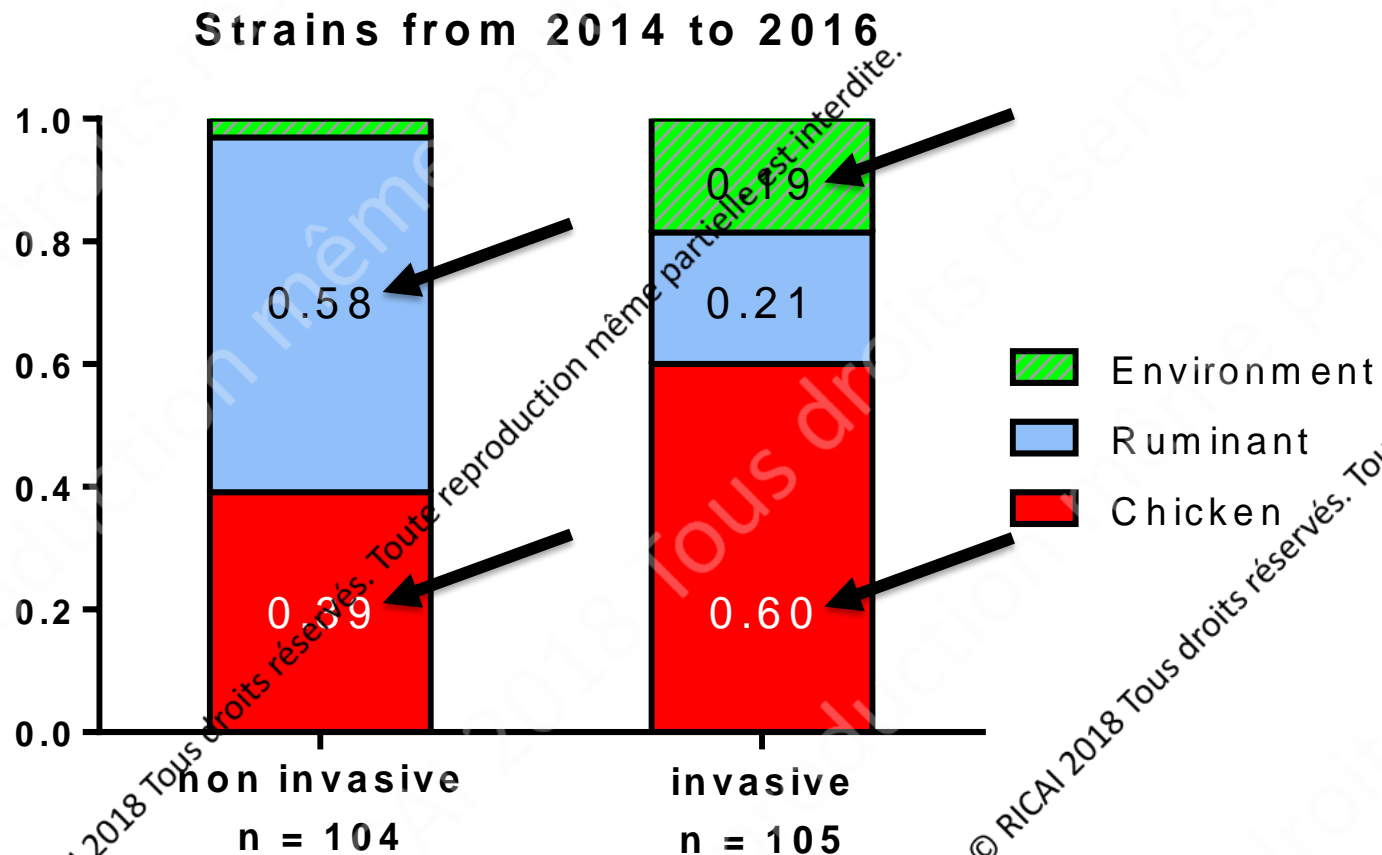
Results: self attribution

→ Self-attribution >90%



Results: source attribution of recent French isolates (2014-2016)

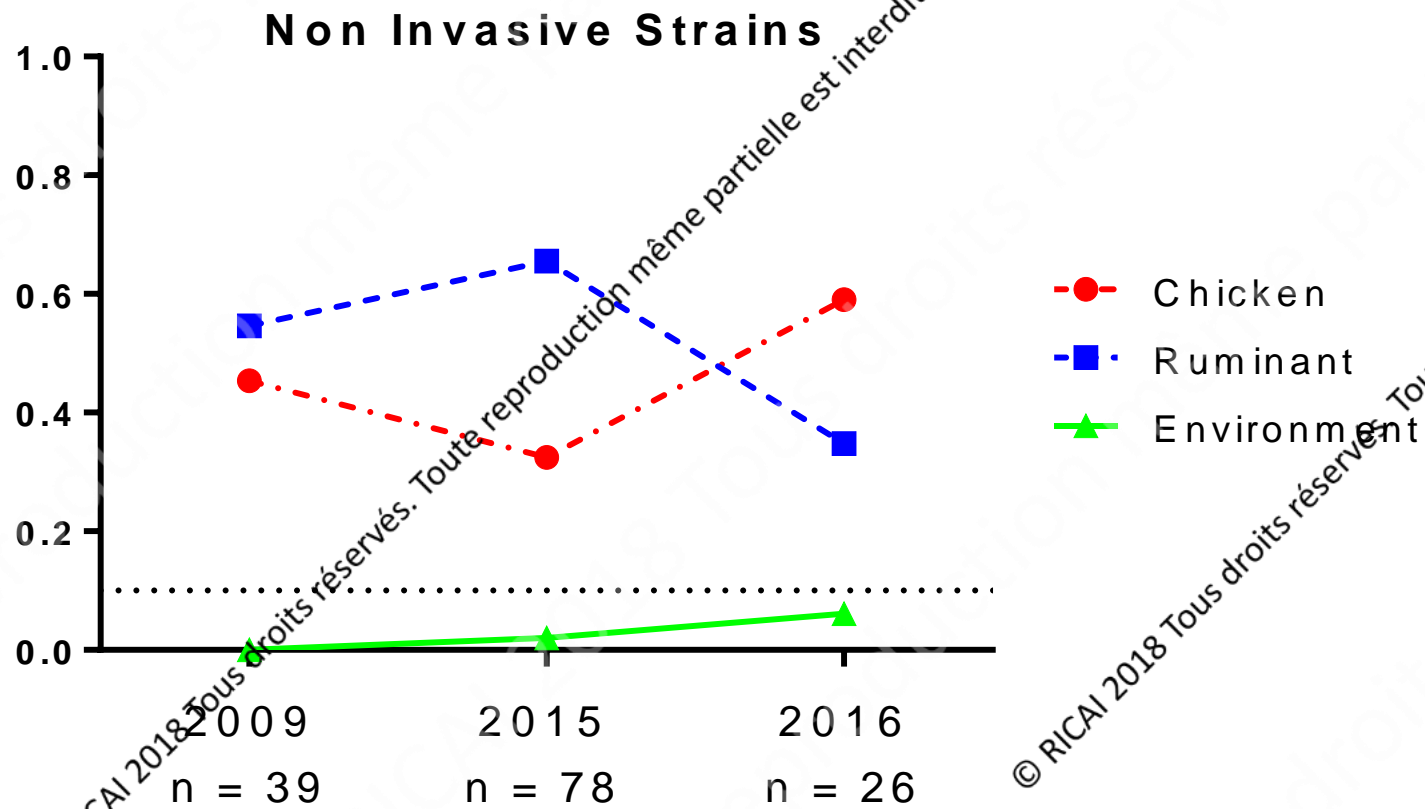
- Non invasive (ruminant and chicken)
- Invasive (mainly chicken)



Results: source attribution of non invasive strains

→ Non invasive

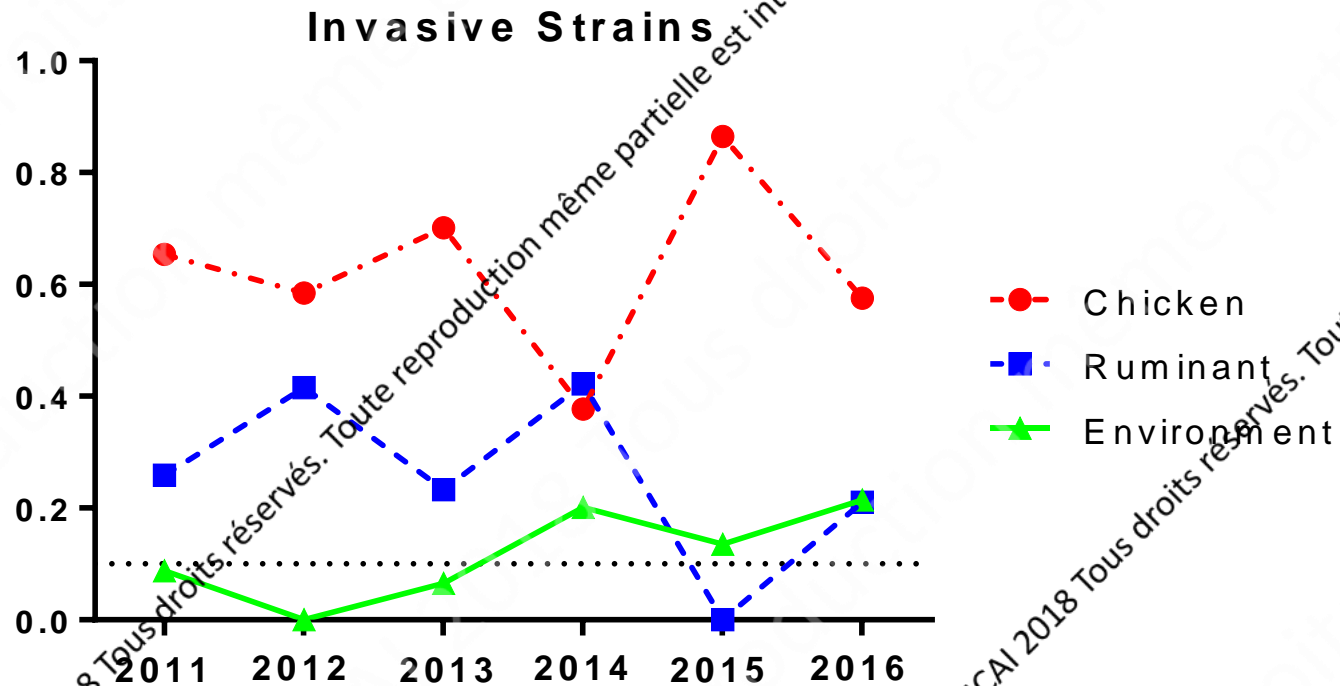
- › 50/50: chicken/ruminant
- › diminution of ruminant part after 2015
- › environment part always bellow 10%



Results: source attribution of invasive strains

→ Invasive:

- › mainly chicken
- › drop in ruminant part after 2014
- › environment increases (>10%) after 2014



Conclusion for non invasive strains

→ Chicken ↓ Ruminant ↗ in non invasive strains than thought



58%

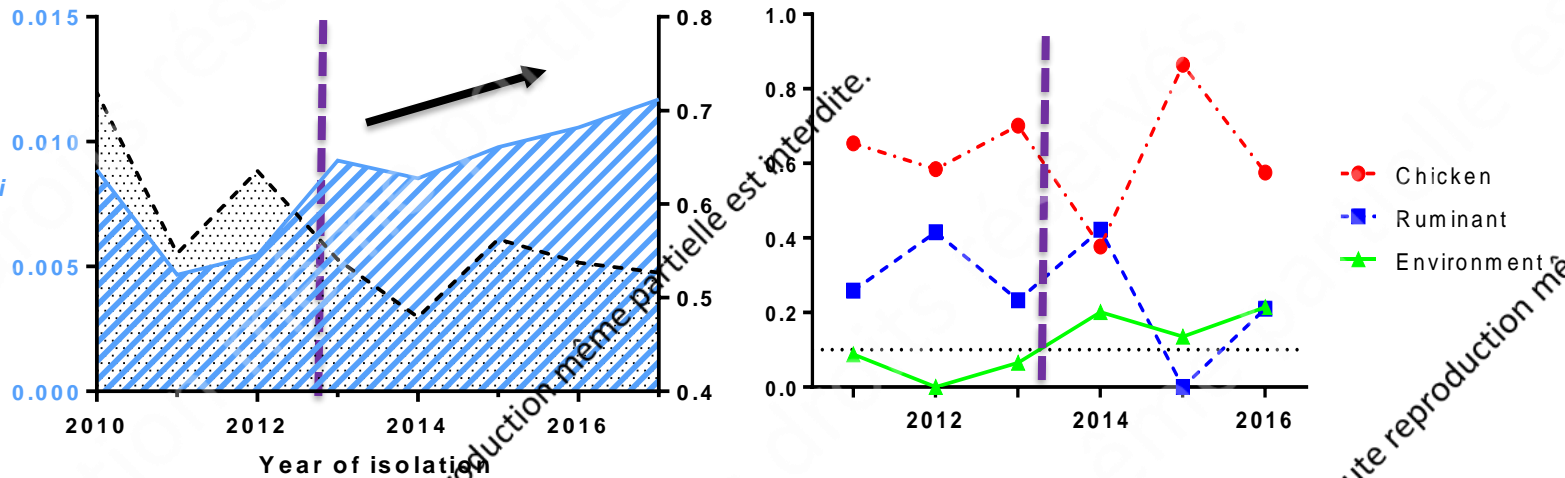


39%

› need for sampling campaign in bovine reservoir

Conclusion for invasive strains

→ Recent switch in invasive strains (mainly chicken)



→ Differences between invasive and non invasive strains
› genome Wide Association Study

Acknowledgements



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