

# Molecular epidemiology of *Coxiella burnetii* reveals the circulation of three main genotype clusters in French ruminants farms

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## I – Context and objectives

Q fever is a worldwide zoonosis caused by the bacterium, *Coxiella burnetii*. In domestic ruminants, Q fever main clinical manifestations are abortions and stillbirths. Human outbreaks are generally associated with infected ruminants and especially small ruminants. A molecular characterization of circulating strains within French ruminants herds is essential to trace the origins of Q fever outbreaks and investigate potential links between genotypes and virulence traits. This study aimed to :

- (1) Identify potential relationships between *C. burnetii* genotypes and domestic ruminant host species;
- (2) Assess the distribution of *C. burnetii* genotypes within major ruminant breeding areas with reference to other European countries.

## II – Material and Methods

### 1- Samples

Species		
Cattle	Goats	Sheep
160 (147)	65 (53)	76 (67)

Number of analyzed samples  
(number of interpretable genotypes)

### 2- Methodology:

#### ❖ Laboratory

MLVA genotyping<sup>(1)</sup>

➢ DNA sequencer → 15 markers < 500pb

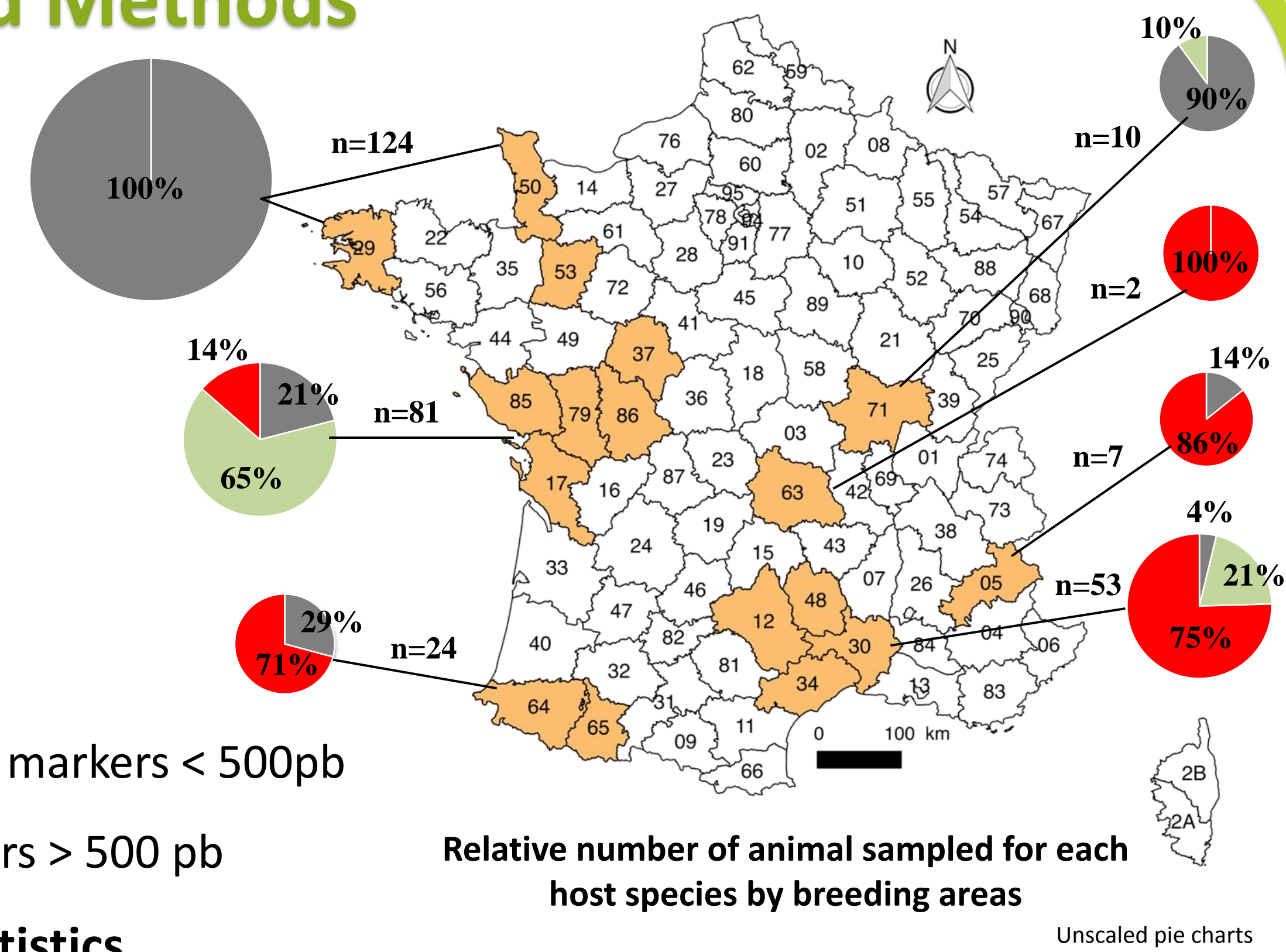
➢ DNA chips → 2 markers > 500 pb

#### ❖ Bioinformatics and statistics

➢ Ascending hierarchical classification → Genotype clustering

➢ Parsimony network → Proportion of host species per sub-cluster

➢ MANOVA → Genotypic diversity associated with ruminant species and/or breeding areas

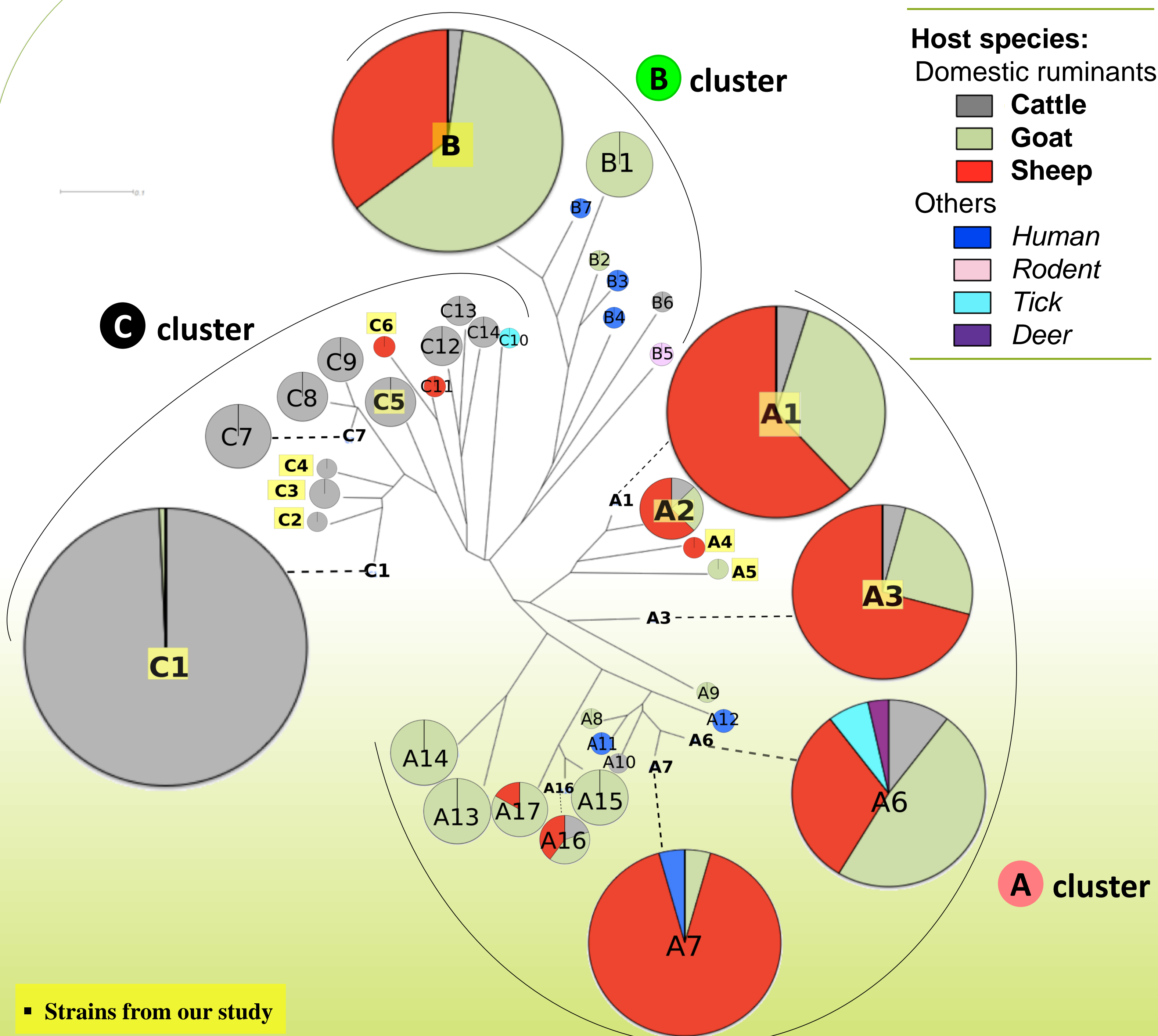


Relative number of animal sampled for each host species by breeding areas

Unscaled pie charts

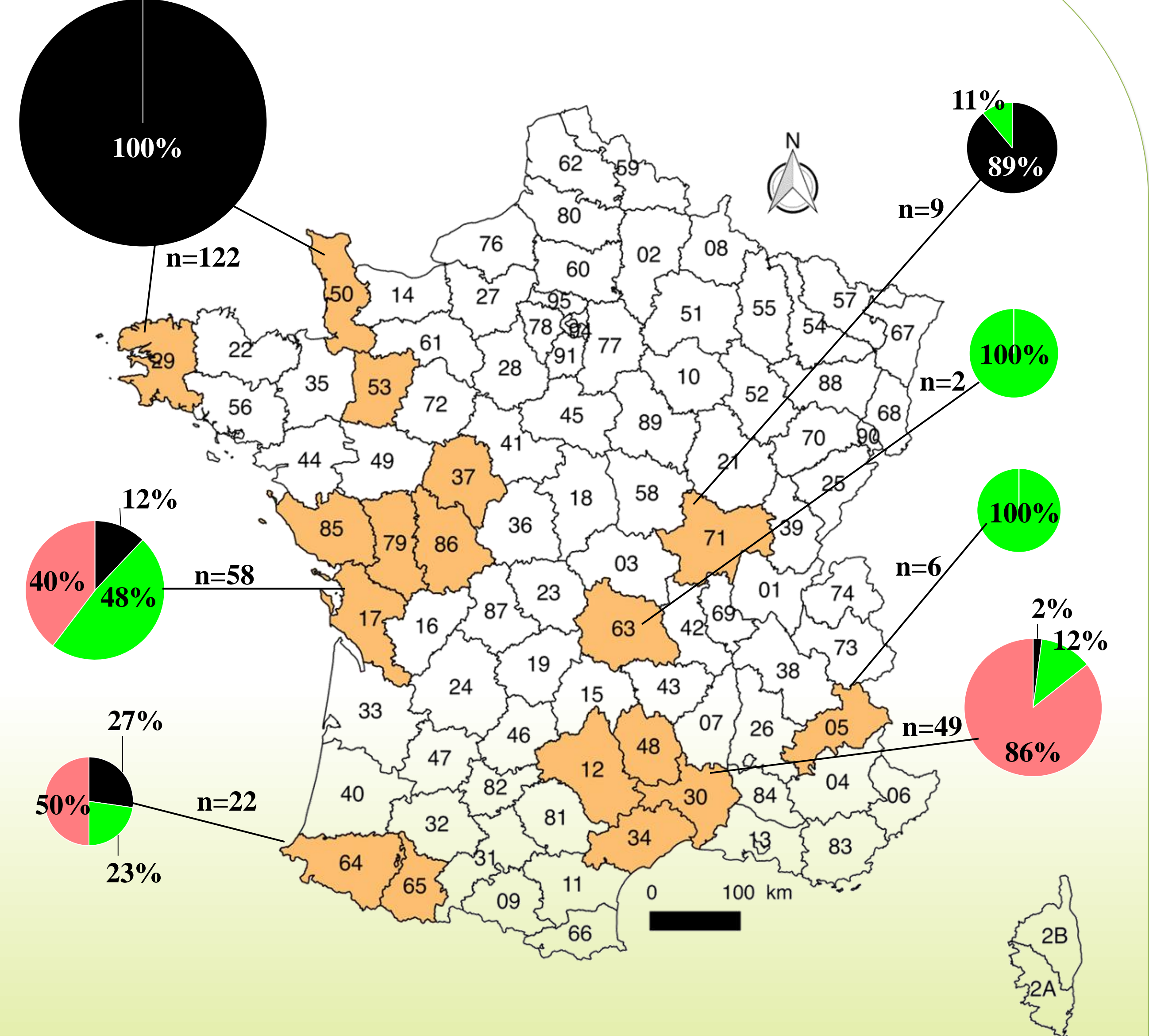
## III – Results

### Genotype distribution by host species



- Strains from our study
- Strains from others studies (2, 3, 4)

### Genotype distribution by breeding area



Clusters	Genotypes evidenced in other European studies						
	France <sup>(3)</sup>	Germany <sup>(2)</sup>	The Netherlands <sup>(2)</sup>	Switzerland <sup>(2)</sup>	Austria <sup>(2)</sup>	Slovakia <sup>(2)</sup>	Croatia <sup>(4)</sup>
A	x	x	x	x	x	x	x
B	x	x					
C	x	x					

### Data from our study

- 3 main clusters : **A** **B** **C** → ✓ 65% sheep belong to **A** cluster (n=76)
- 12 sub-clusters identified ✓ 63% goat belong to **B** cluster (n=48)
- ✓ 98% cattle belong to **C** cluster (n=144)

Genotypic diversity was significantly associated with both host species and breeding areas (Manova,  $p < 0.01$ )

## IV – Perspectives

Our species-associated patterns are consistent with those observed in other European studies<sup>(2,3,4)</sup>. Further epidemiological studies are needed to complete our findings. Phenotypic approaches will allow establishing links between virulence of genotyped strains and ruminant species.



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