Coxiella burnetii within-and between-herd true seroprevalence assessment in domestic ruminants in France accounting for diagnostic uncertainty with latent class

T. Lurier, Florence Ayral, Carole Sala, Kristel Gache, Marie Laure Delignette-Muller, Elsa Jourdain, Elodie Rousset

Coxiella burnetii within- and between-herd true seroprevalence assessment in domestic ruminants in France accounting for diagnostic uncertainty with latent class

Thibaut Lurier[1, 2], Florence Ayral[2], Carole Sala[3], Kristel Gache[4], Marie Laure Delignette-Muller[5], Elsa Jourdain[1], Elodie Rousset[6]

1- UMR EpiA; 2- USC 1233; 3- EAS Unit ; 4- GDS France; 5- UMR 5558; 6- Q fever RNL

Context and objectives

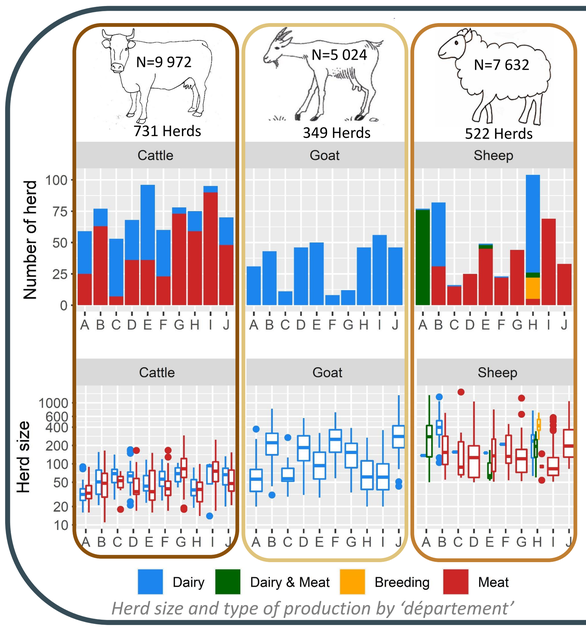
Q fever : a worldwide zoonosis still difficult to control

- **Human outbreaks** regularly occur over the world
- In Europe, most human cases are related to **domestic ruminant exposure**
- **Unbiased estimation of the prevalence** is crucial to detect and assess epidemiological changes
- In France, **only apparent seroprevalence** were assessed;
  Yet, based on Lurier et al. 2021, **Se varied from 54% to 75% and Sp from 97% to 99%**

Objectives of the study

✓ Reassess the **between-** and **within-herd seroprevalence** in cattle, sheep and goats from the results published by Gache *et al*. 2017

✓ Quantify the importance of two potential **risk factors of seropositivity** at the animal and herd level (type of production and herd size)



Herd size and type of production by 'département'

Data

- Sampling in 10 French 'départements'

- Random selection of 19 to 106 herds by département and species

- **Convenience sample** of 10 to 15 animals by herd
- **Serum analysis** in 10 veterinary laboratories with Priocheck™ ELISA test
- **Additional informations**

⇒ Herd size = number of :
Females for **cattle**
Animals for **sheep** and **goats**

⇒ Types of production
Dairy/**meat**/**dairy & meat**/**breeding** for **sheep**
Dairy/**meat** for **cattle** and **goats**

Hierarchical logistic model

- Two intricated **regression models** :

⇒ Logistic regression with a random intercept a the departement level (α_{0j}) for the **between-herd prevalence (BHP)**

⇒ Zero inflated logistic regression with a random intercept a the herd level (β_{0ij}) for the **within-herd prevalence (WHP)**

- The **number of tested seropositive animals** ($Npos_{ij}$) in each herd was then supposed to follow a binomial distribution which depends on :

⇒ the number of animals sampled ($Nsample_{ij}$)

⇒ the **WHP** (potentialy equal to 0)

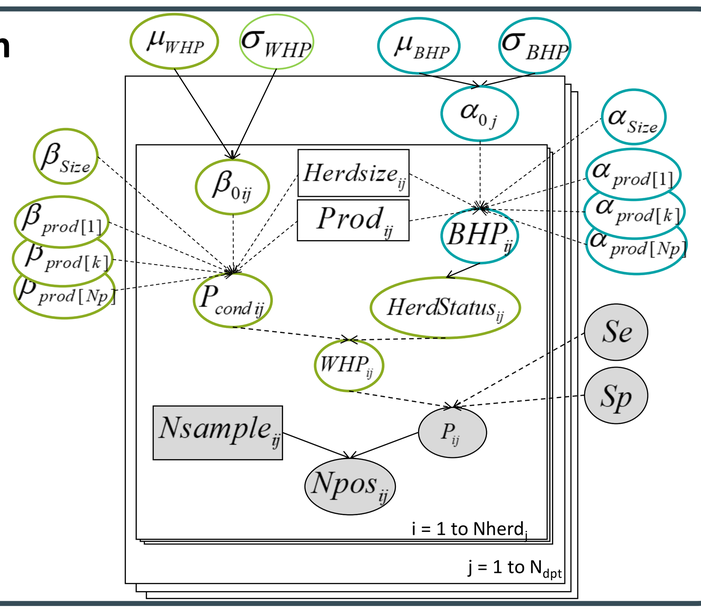
⇒ the **Sensitivity (Se) and Specificity (Sp) of the ELISA test**

Model equation and directed acyclique graph

$$\text{logit}\left(BHP_{ij}\right) = \alpha_{0j} + \alpha_{size} \times Herdsize_{ij} + \alpha_{Prod\left[Prod_{ij}\right]}$$
$$\alpha_{0j} \sim Norm\left(\mu_{BHP\_ref}, \sigma_{BHP}\right)$$

$$HerdStatus_{ij} \sim bern\left(BHP_{ij}\right)$$
$$\text{logit}\left(P_{cond\ ij}\right) = \beta_{0ij} + \beta_{size} \times Herdsize_{ij} + \beta_{Prod[\text{Prod}ij]}$$
$$\beta_{0ij} \sim Norm\left(\mu_{WHP}, \sigma_{WHP}\right)$$
$$WHP_{ij} = P_{cond\ ij} \times HerdStatus_{ij}$$

$$P_{ij} = WHP_{ij} \times Se + \left(1 - WHP_{ij}\right) \times \left(1 - Sp\right)$$
$$Npos_{ij} \sim binomial\left(Nsample_{ij}, P_{ij}\right)$$



Results : Seroprevalence

Median of observed and assessed seroprevalence levels in each species and type of production

		Cattle		Goat		Sheep		
BHP	Meat	16,3*	5,7† [1,5 ; 19,5]	Dairy	63,5*	47,1 † [25,5 ; 67,2]	Meat	28,0*	36,7† [5,6 ; 85,5]
	Dairy	54,4*	47,9 † [20,3 ; 79,2]				Dairy	78,5*	21,6 † [1,3 ; 76,2]
							Dairy & Meat	75,0*	32,7 † [2,7 ; 87]
							Breeding	52,9*	23,5 † [1 ; 100]
WHP	Meat	8,3*	39,4 † [27,3 ; 57]	Dairy	35,7*	63,6 † [53,4 ; 73,9]	Meat	12,5*	22,9 † [17 ; 31,7]
	Dairy	21,4*	38,7 † [30,5 ; 49,3]				Dairy	20,0*	36,9 † [27,2 ; 48,6]
							Dairy & Meat	40,0*	57,8 † [44,5 ; 72]
							Breeding	13,3*	18,7 † [5,9 ; 52,1]

** Observed median of the apparent seroprevalences*

† Assessed median of the true seroprevalence

BHPs assessed† were lower than the observed apparent* **BHPs**

⇒ Account for the **imperfect specificity** of the ELISA test

WHPs assessed† were higher than the observed apparent* **WHPs**

⇒ Account for the **moderate sensitivity** of the ELISA test

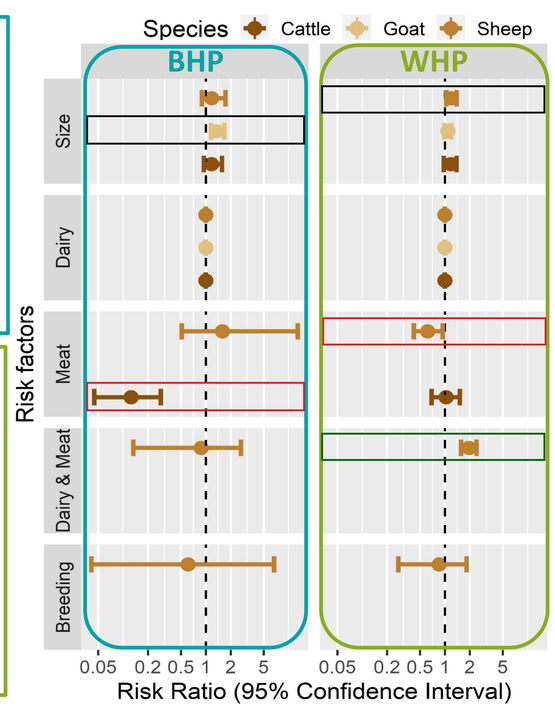
Results : Risk factors

BHPs

- **Cattle**
  - **7.9x higher in dairy** *vs*. in **meat** herds
- **Goats**
  - **1.4x higher** when **herd size x2**

WHPs

- **Sheep**
  - **1.6x higher in dairy** *vs*. in **meat**
  - **2.5x higher in dairy & meat** *vs*. in **meat**
  - **1.3x higher** when **herd size x2**



Risk ratio of seropositivity of the herd (between-herd) and of the animals in seropositive herds (within-herd). The reference herd is a dairy herd of medium size in each species

Conclusion

- **Better knowledge of the true within- and between-herd seroprevalence levels in France**
- **Identification and quantification of some relevant risk factors**

Discussion

- **Results must be carefully extrapolated**
  Potential non-representativeness of the 10 'departments' included
  Random selection of herds without information on abortion occurrence

⇒ **New insights into the epidemiology of *Coxiella burnetii* in domestic ruminants in France**

France
Auvergne Rhône Alpes

Thibaut.lurier@vetagro-sup.fr

Society for Bayesian Methods in Epidemiology and Diagnostics - Conference 2024, January 30 2024, Brussels (Belgium)