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

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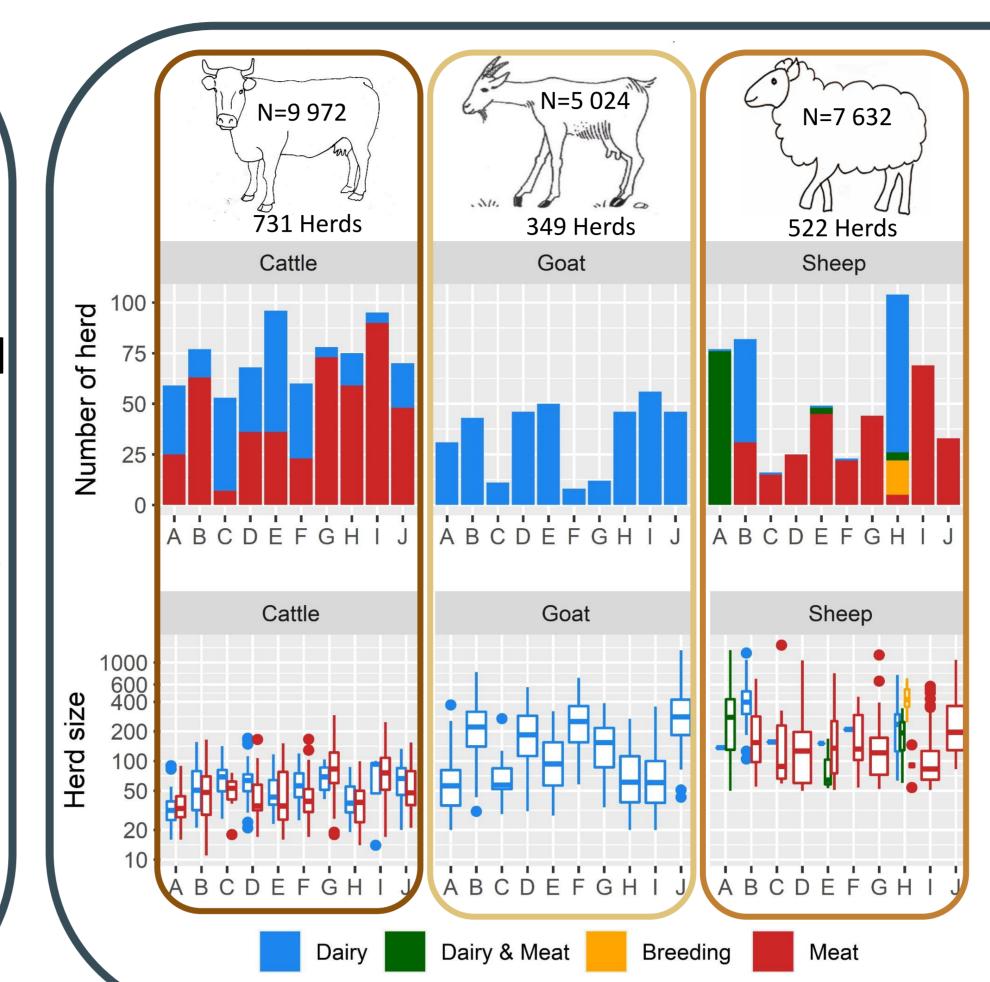
Context and objectives

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)



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 PriocheckTM ELISA test
- Additional informations
- \Rightarrow Herd size = number of : Females for cattle Animals for sheep and goats
- \Rightarrow Types of production

Dairy/meat/dairy & meat/breeding for sheep Dairy/meat for cattle and goats

Hierarchical logistic model

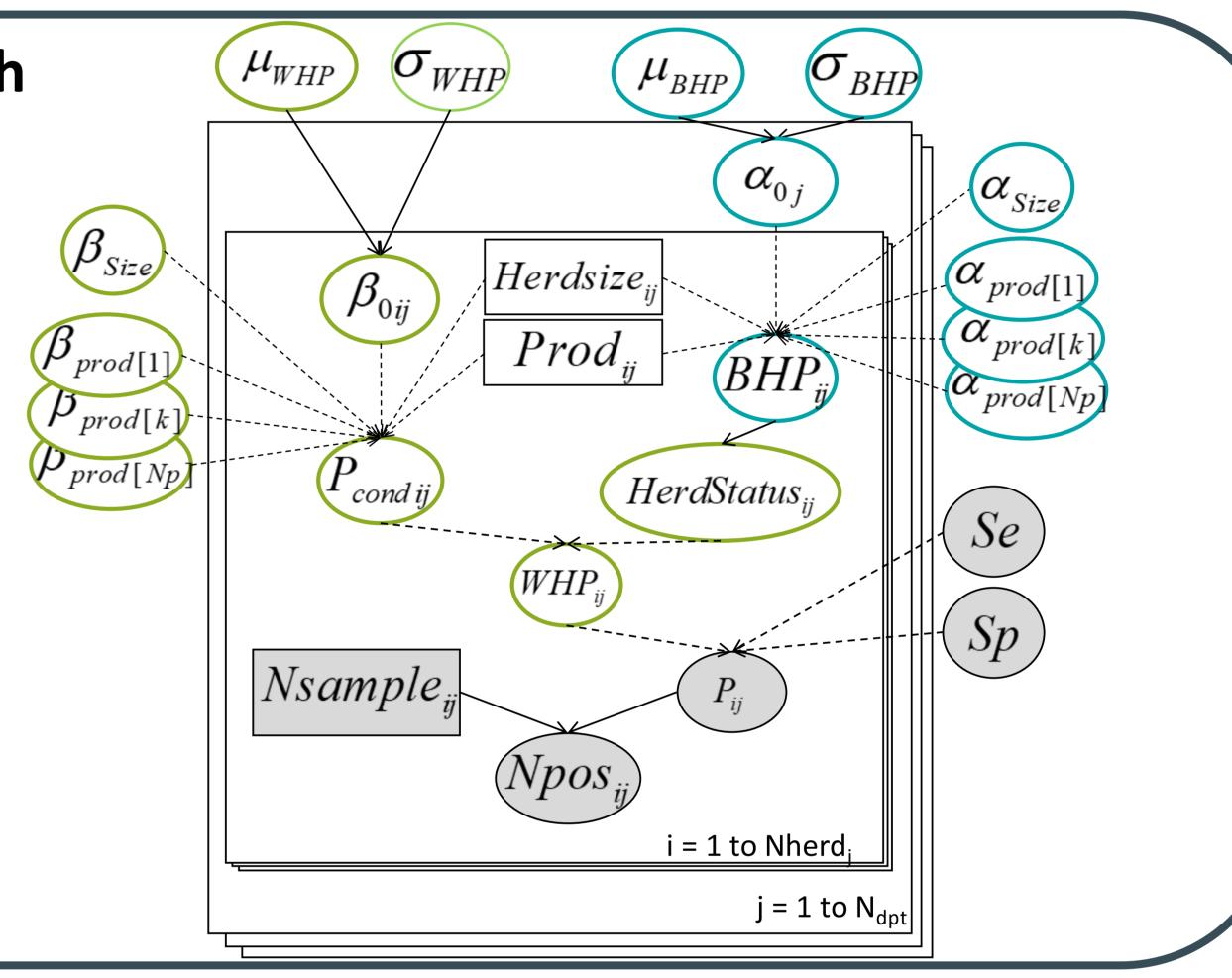
- Two intricated regression models:
- ⇒ Logistic regression with a random intercept a the departement level (α_{0i}) for the between-herd prevalence (BHP)
- ⇒ Zero inflated logistic regression with a random intercept a the herd level (β_{0ii}) for the within-herd prevalence (WHP)
- The number of tested seropositive animals $(Npos_{ij})$ in each herd was then supposed to follow a binomial distribution which depends on:
- \Rightarrow the number of animals sampled (Nsample_{ii})
- \Rightarrow the WHP (potentialy equal to 0)
- ⇒ the Sensitivity (Se) and Specificity (Sp) of the ELISA test

Model equation and directed acyclique graph

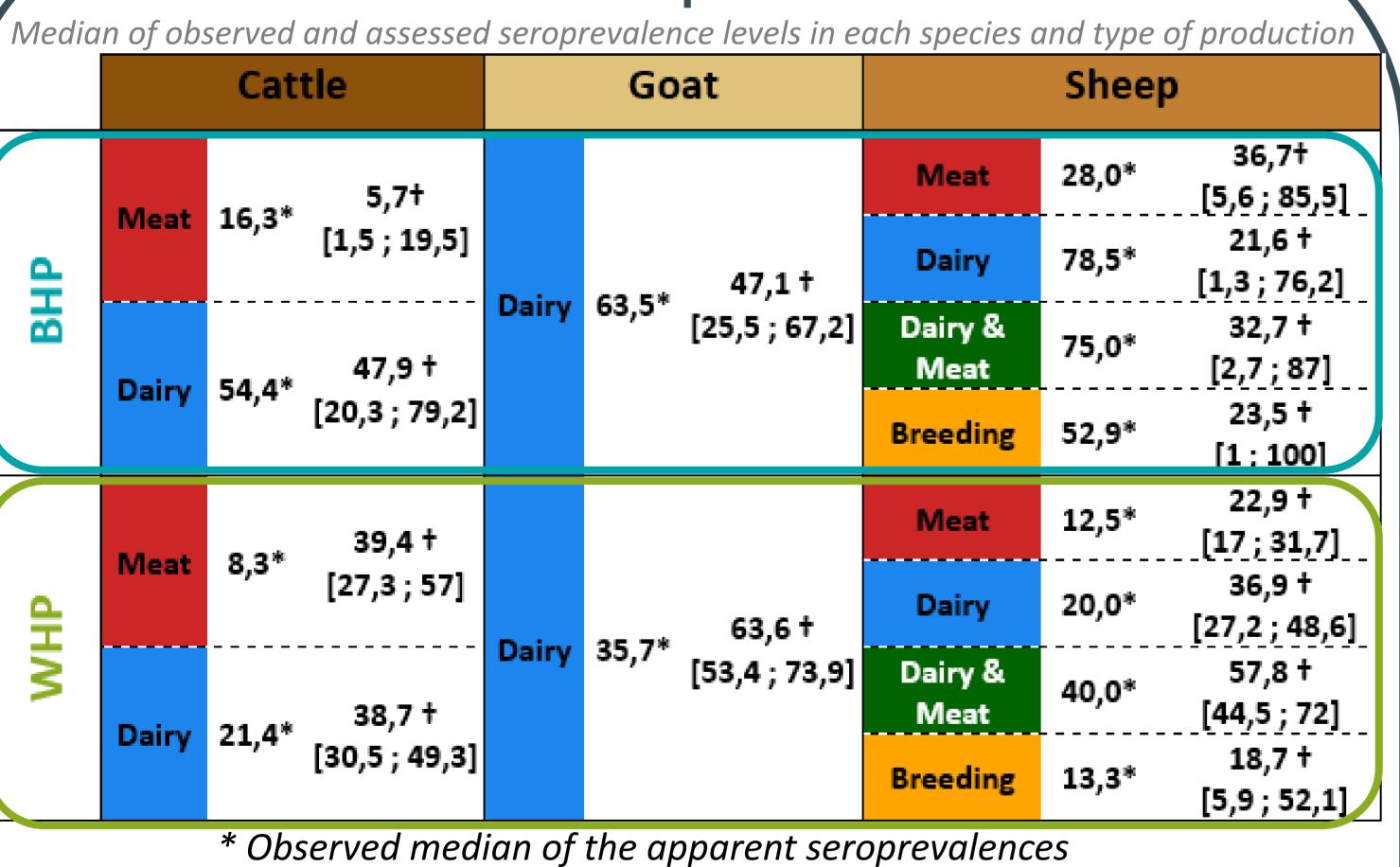
$$logit(BHP_{ij}) = \alpha_{0j} + \alpha_{size} \times Herdsize_{ij} + \alpha_{Prod[Prod_{ij}]}$$
$$\alpha_{0j} \sim Norm(\mu_{BHP_ref}, \sigma_{BHP})$$

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

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



Results: Seroprevalence



BHPs assessed† were lower than the observed apparent* BHPs

† Assessed median of the true seroprevalence

⇒ 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

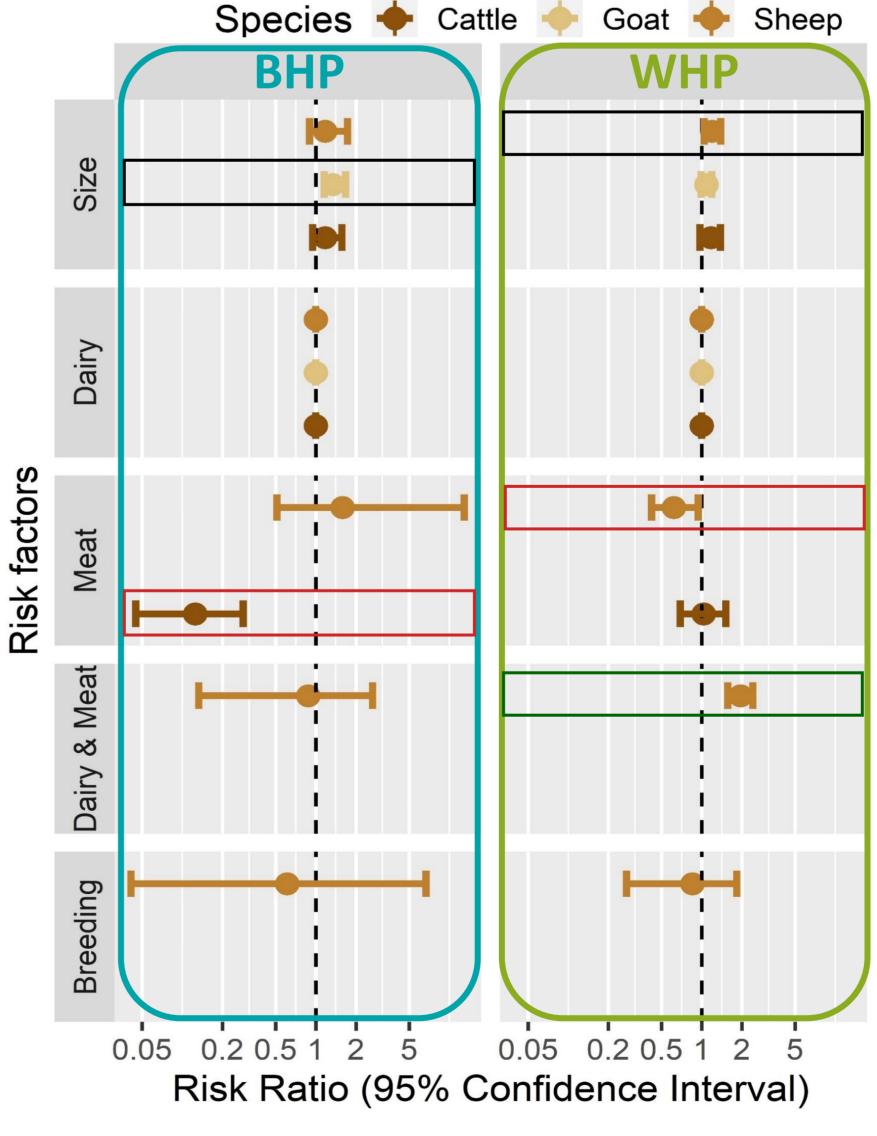
- Cattle
- 7.9x higher in dairy vs. in meat herds
- Goats
- 1.4x higher when herd size x2

WHPs

Sheep

size x2

- 1.6x higher in dairy vs. in meat
- 2.5x higher in dairy & meat vs. in meat 1.3x higher when herd



Goat 🔷 Sheep

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 nonrepresentativeness of the 10 'departments' included Random selection of herds without information on abortion occurrence

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



