



## Coxiella burnetii infection in horses: seroprevalence, environmental exposure and clinical expression

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### Introduction

Horses may be naturally exposed to *C. burnetii*. Their involvement in the infection epidemiology and Q fever clinical signs remain unclear despite experimentally induced infection resulting in clinical disease.

The objectives of the study were first, in an endemic area for humans and ruminants, to assess over two consecutive years horses serological status (ELISA assay), *C. burnetii* presence in their environment and clinical expression. Secondly, the aim was to measure nationwide the overall prevalence of *C. burnetii* detection in samples from aborted mares and horses with acute or chronic respiratory disease.

### Materials, methods and results

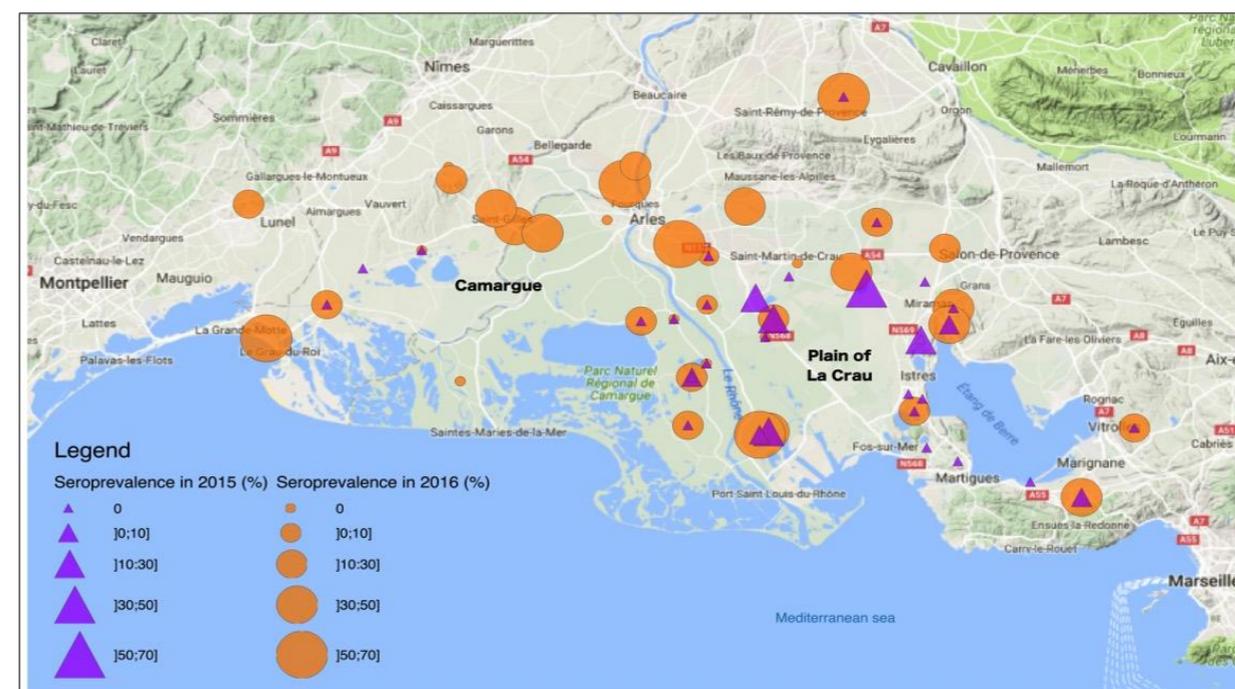
In the endemic area, 24 stables were investigated and 199 horses sampled yearly. Twenty-five horses distributed in 15 different stables were seropositive at least once. The seroprevalence tended to increase (5% in 2015 to 13% in 2016,  $p = 0.08$ ) (Figure 1). Among the seropositive horses, none displayed Q fever-compatible signs. *Coxiella* DNA was detected in almost 40% of collected ticks, occasionally in dust, but never in horse blood (Figure 2).

Two hundred and fifty-two samples from 178 aborted mares (placenta and/or fetus) were screened using non-quantitative PCR and 15 were positive (5,9%). Among 498 respiratory samples (broncho-alveolar or guttural pouch lavage, tracheal wash) from 456 horses, only one BAL sample was positive (0,2%).

### Conclusion

Horses are exposed to *C. burnetii* but most of them seroconvert without showing any clinical signs. Q fever abortive and respiratory forms appear to be uncommon in this species. Further studies are needed to accurately identify acute and chronic clinical expression in horses.

Figure 1 : Map showing intra-stable Q-fever seroprevalence in horses in 2015 and 2016





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Figure 2 : Map showing the distribution of ticks and dust samples collected in 2015 and 2016

