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Assessment of *Coxiella burnetii* within a Scottish dairy cattle herd: investigations prompted by stillbirth event reporting

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Objective: A series of stillbirths were reported by a British Holstein-Friesian dairy cattle herd in 2021. Clinical investigations of five stillbirths undertaken by the SRUC identified *Coxiella burnetii* as the likely contributing cause. The objective of this current study was to undertake a cross-sectional study at this farm to determine the distribution of *C. burnetii* exposure and infection in different management groups.

Methods: Blood samples and vaginal swabs were collected from animals in four management groups (target of n=25 per group) in Feb-March 2022: pre-bulling heifers at a separate heifer unit; pre-calving heifers including animals at the heifer unit and main farm; post-calving primiparous cows (one-to-30 days in milk); multiparous cows at any lactation stage. Sera were tested for evidence of exposure to *C. burnetii* by LSIVet Ruminant Q Fever- Serum/Milk ELISA at the Biobest Laboratories. Samples with a sample positive ratio (sp%) > 40 were classified as positive. Vaginal swabs were stored in DNA/RNA shield and heat treated at 70C for 1 hour prior to processing for DNA extraction at the University of Glasgow. Swab extracts were qPCR tested for *Coxiella burnetii* DNA using an assay that targeted the IS1111 insertion sequence (PMID: 21470457) A sample was considered positive for *C. burnetii* if positive and negative controls were valid and amplification with Ct < 35 was observed. Samples with Ct < 27 were further classified as "high load positive".

Results: A total of 97 animals were sampled Feb-Mar 2022. Twenty-nine out of 89 (32.6%) animals were seropositive for *C. burnetii* exposure. The highest seroprevalence (11 of 13, 84.6%) was observed in pre-calving animals in the main herd. Of the 97 samples tested by qPCR, 53 (54.6%) were classified as positive and 32 (33.0%) classified as "high load positive" for *C. burnetii*. Lower Ct values, indicating higher bacterial load were seen predominantly in heifers and adults in the main herd.

Conclusions: *C. burnetii* exposure and infection were widespread in this herd. The serological data are consistent with exposure of the majority of animals at the time that they move into the main herd. The qPCR data indicate high prevalence of shedding in the herd including animals shedding high concentrations of bacteria. These data can inform evaluation of the production impacts of *C. burnetii* in this herd and of possible control interventions.