Research report for Hannah Dairy Research Foundation Small Grant Scheme

Project title: Investigating the prevalence and impact of *Coxiella burnetii* infection in dairy herds in Scotland

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Research summary: *Coxiella burnetii* is a zoonotic pathogen that can cause febrile illness in people and reproductive disease including abortion and stillbirth in livestock. In the UK, *C. burnetii* appears to be widespread in dairy cattle herds [1] but the epidemiology and productivity impacts of infection remain poorly understood. Our study aimed to address this knowledge gap by generating data on *C. burnetii* infection patterns within dairy cattle herds, and to estimate production impacts of infection in these herds.

Working with two dairy farms in Scotland with prior evidence of *C. burnetii* infection, including one farm with recent abortions attributed to *C. burnetii* infection, we conducted investigations to determine the prevalence and impact of infection within these herds. Animals were recruited through two strategies: first, samples were collected from post-parturient cattle at routine health checks conducted 1-7 days post parturition (Farm 1). Second, a representative selection of animals was sampled across different management groups to investigate infection patterns across the herd (Farms 1 and 2). A variety of samples were collected including vaginal swab samples to investigate patterns of bacterial shedding by qPCR and serum to estimate the proportion of animals with antibodies against *C. burnetii.* Data on key performance indicators were collected to investigate the impact of infection on individual animal productivity and health.

We detected very high within-herd prevalence of *C. burnetii* infection with the highest prevalence of bacterial shedding detected in post-calving animals. At Farm 1; *C. burnetii* was detected in vaginal swab samples by qPCR in 319 (90.6%) of 352 animals sampled within 7 days of parturition. Of these, many animals demonstrated high bacterial loads, with higher loads detected in primiparous animals. Logistic regression models of *C. burnetii* infection and key performance indicators identified that animals that were shedding greater bacterial loads were significantly more likely to have experience one or more calving complications than animals with lower bacterial loads.

Cross-sectional surveys also demonstrated a high prevalence of infection. At Farm 1; *C. burnetii* was detected in vaginal swab samples by qPCR vaginal swab samples from 109 (66.9%) of 163 randomly selected animals from the main herd. A very similar number were also positive by qPCR on vaginal swab samples collected at Farm 2 (67 (69.0%) of 97) of randomly selected animals). At this farm, samples were collected across a range of different management groups including pre-bulling and pre-calving heifers and animals from the main herd. Seroprevalence showed striking variation between these different management groups (Figure 1). Both seroprevalence and bacterial shedding prevalence were associated with farm site (heifer rearing unit or main herd) and calving status (pre- or post- calving), with the highest prevalences observed in animals in the main herd and in post-calving animals.
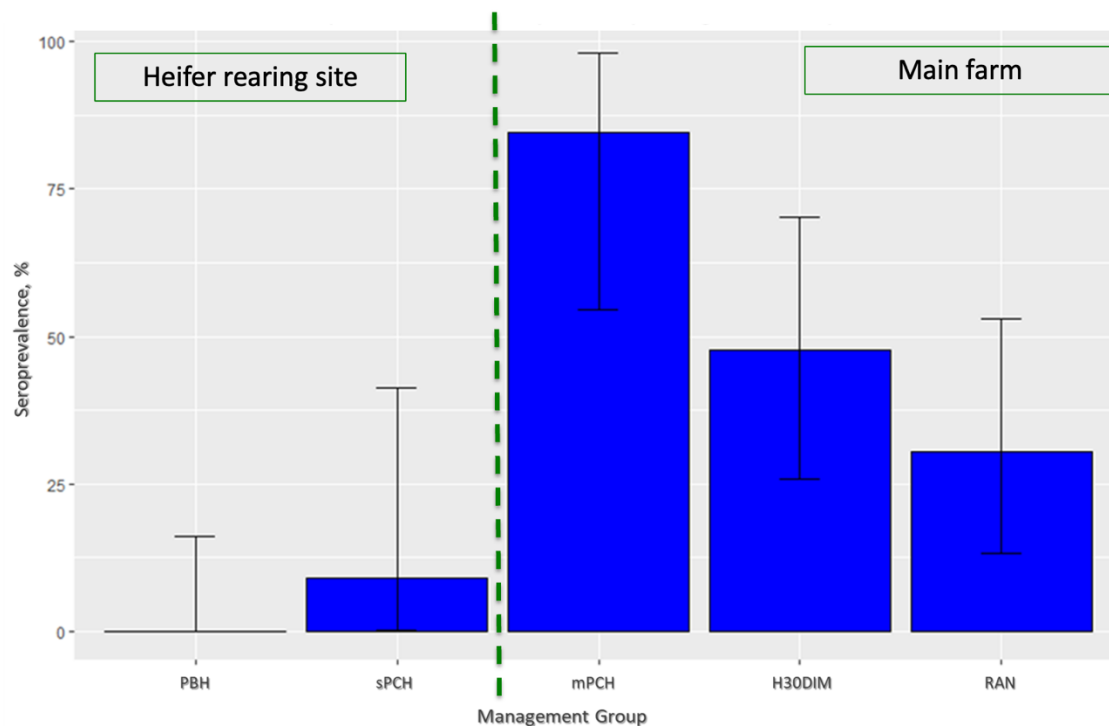
Figure 1: Seroprevalence in randomly selected animals from 5 different management groups (Farm 2).
Key: PBH = Pre-bulling heifer; sPCH = pre-calving heifer, heifer site; mPCH = pre-calving heifer, main farm; H30DIM = post-calving primiparous cow, 1-30 days in milk; RAN = adult cows, any lactation stage.

Evidence of widespread infection in animals in our study herds suggests the potential for negative reproductive impacts on both farms. Analysis of data from Farm 1 suggests that calving complications may be associated with higher levels of bacterial shedding, and the need for calving assistance in infected animals may also create a higher occupational risk for dairy farmers. Use good farm practices such as wearing waterproof gloves to handle potentially infected materials such as afterbirth or aborted foetuses is recommended to reduce the risk of zoonotic transmission [2].

Variation in prevalence between management groups on farms may be influenced by multiple factors including environmental infection pressures; life stage factors (e.g. heifers vs older animals) and reproductive cycle factors [3]. *C. burnetii* exploits the reproductive cycle of animal hosts and the amount of bacteria shed is known to vary with the reproductive cycle in female animals [4]. Heifer populations may be more vulnerable to adverse impacts of infection as demonstrated on Farm 2 prior to the start of our research study. The infection patterns demonstrated by this study indicate that vaccination prior to first pregnancy may help prevent may help to prevent *C. burnetii*-associated losses in the future.

Our study has revealed new insights into the infection patterns of *C. burnetii* within infected herds in Scotland. Until recently, *C. burnetii* has received relatively little attention in UK dairy herds but increased interest associated with legislative changes have highlighted important

knowledge gaps associated with this overlooked pathogen. This study provides a small but important piece of evidence to support the development of evidence-based herd health strategies for farmers and veterinarians as well as important data for the future development of human and animal health policy.

References:
1. Velasova, M., et al., *Herd-level prevalence of selected endemic infectious diseases of dairy cows in Great Britain.* J Dairy Sci, 2017. **100**(11): p. 9215-9233.
2. UK Health Security Agency. *Q fever: information for farmers.* 2024 [cited 2024; Available from: https://www.gov.uk/government/publications/q-fever-good-practice-for-farmers/q-fever-information-for-farmers#reduce-human-and-animal-health-risks-through-good-farm-practices.
3. Nogareda, C., et al., *Dynamics of Coxiella burnetii antibodies and seroconversion in a dairy cow herd with endemic infection and excreting high numbers of the bacterium in the bulk tank milk.* Res Vet Sci, 2012. **93**(3): p. 1211-2.
4. de Cremoux, R., et al., *Coxiella burnetii vaginal shedding and antibody responses in dairy goat herds in a context of clinical Q fever outbreaks.* FEMS Immunology & Medical Microbiology, 2012. **64**(1): p. 120-122.

Research Outputs:

Publications:
Weller GM (2024) *Examining the prevalence of Coxiella burnetii in a Scottish dairy herd and its impact on reproductive disease burden*. Master of Science in Veterinary Medicine (Research), University of Glasgow.

Halliday J, Aparicio-Chagolla A, Carter R, Vazquez R, Viora L, Mason, C., Allan KJ Widespread *Coxiella burnetii* distribution within a Scottish dairy cattle herd with a history of stillbirths. *In preparation*

Conference presentations and proceedings:
Aparicio-Chagolla A., Vazquez R., Allan K., Carter R, Halliday J, Viora L, Mason C. (2023). *Assessment of Coxiella burnetii within a Scottish dairy cattle herd: investigations prompted by stillbirth event reporting*. 6th European Meeting of Animal Chlamydioses and Zoonoses (EMAC-6).

Weller G., McKay C., Vazquez R., Pagnossin D., Carter R., Viora L., Allan K., Halliday, J. (2023) *Cross Sectional Investigation of Coxiella burnetii Following Parturition: A New Spotlight on a Neglected Zoonotic Disease in Scotland*. Hannah Dairy Research Foundation Conference 2023: Next Generation Quality Dairying.

Weller G, McKay C, Vazquez R, Carter R, Pagnossin D, Allan K, Viora L, Halliday J. (2023). *Investigation of Coxiella burnetii following parturition: a fresh spotlight on a neglected disease in Scotland*. 6th European Meeting of Animal Chlamydioses and Zoonoses (EMAC-6).

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Weller G., Vazquez R, Allan K, Viora L, Halliday J. (2023). *Investigating the prevalence and impact of Coxiella burnetii infection in dairy herds in Scotland*. European Buiatrics Congress and ECBHM Jubilee Symposium.