BSP Abstract Submitted – 2026

Abstract title
High resolution molecular approaches to tracing *Cryptosporidium* transmission and virulence in cattle.

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The zoonotic protozoan parasite *Cryptosporidium parvum* is commonly found in young ruminants, with nearly 80-100% of neonatal dairy calves testing positive during the first few weeks of life (Bartley et al., 2024). Cryptosporidiosis – the diarrhoeal disease resulting from a *C. parvum* infection – can be fatal in neonatal calves as well as immunocompromised humans due to severe dehydration. In surviving calves, the initial bout of diarrhoea negatively affects the average daily weight gain, leading to significant economic consequences in the livestock industry. Alternatively, there are asymptomatic calves that act as a reservoir for the parasite, shedding infective oocysts into the environment and perpetuating transmission. Once excreted, oocysts persist in the environment for several months. Therefore, in outbreak scenarios reliable typing of *C. parvum* is vital to ascertain transmission pathways, identify the source of infection and negate further spread.

Cryptosporidiosis in calves is a non-notifiable disease despite being the primary cause of infectious diarrhoea in calves followed by rotavirus (Denholm, 2025). However, the reported prevalence statistics are derived from passive surveillance of gastrointestinal illness which is inherently biased. Currently, gp60 sub-genotyping and multiple locus VNTR analysis (MLVA) schemes are the preferred genetic approaches to identify the *C. parvum* isolates present in an outbreak. Public health labs have adopted a standardised MLVA scheme of seven validated loci to allow epidemiological data to be comparable between labs (Risby et al., 2023; Robinson et al., 2022).

However, throughout the literature, there is a lack of diverse genotypes reported within farms using these markers. We aim to test, whether higher-resolution genomic approaches to *C. parvum* genotyping are needed to further understand within-herd diversity and transmission. To answer this research question, we aim to understand within herd diversity and transmission of *C. parvum* and understand how genotypic diversity may affect clinical outcome in calves. Utilising a higher coverage MLVA scheme with next generation sequencing, we anticipate being able to identify more diverse *C. parvum* genotypes amongst neonatal calves on farms. In addition to furthering our understanding of *C. parvum* within-herd transmission, the active surveillance of other enteropathogens in calves will improve understanding of scour aetiology, thus aiding more targeted treatments.