

Characterising *Cryptosporidium* invasion proteins and developing a workflow to investigate their potential as vaccine candidates against cryptosporidiosis.

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The protozoal parasite, *Cryptosporidium*, is responsible for the gastroenteric disease, cryptosporidiosis. Within the livestock sector, this disease is of great health, welfare, and economic importance, where high morbidity levels can be found, and fatal outcomes are particularly common for neonatal ruminants. The zoonotic pathogen, *C. parvum*, is the most commonly identified aetiological agent of cryptosporidiosis in cattle and sheep. Despite the veterinary importance of this parasite for livestock, treatment options are limited, and a vaccine is currently not available for either animals or humans. Proteins involved in the attachment to and invasion of host cells have been previously suggested as potential vaccine candidates against the disease, such proteins include: Cpa135, CP2, CP15 and P23. This research aims to develop the understanding of these invasion proteins, to determine their potential as putative vaccine candidates. This investigation started with bioinformatic analysis to explore sequence structure and conservation of these invasion proteins between both *C. parvum* isolates and from isolates of other *Cryptosporidium* species that infect ruminants. Regions of these putative invasion proteins have been selected for expression as recombinant fusion proteins to identify whether particular domains are associated with a protective immune response in the host. DNA was extracted from *Cryptosporidium* positive ruminant faecal samples, and the specific regions of DNA amplified and cloned into TA plasmids. Positive clones are being selected and inserts incorporated into a pTrcHis expression plasmid to generate fusion proteins which will be used to determine the protective immune response they may provide to the host. Being able to identify and work with these proteins, and their coding sequences, both bioinformatically and *in vitro*, will allow for a developed understanding into the interaction between the parasite and the host and how this interaction can provide prophylactic benefit for targeted hosts against a parasitic disease.