Sequence conservation of *Cryptosporidium* invasion proteins which have potential as vaccine candidates against cryptosporidiosis in cattle and sheep

Bioinformatic analysis of four *Cryptosporidium* invasion proteins to develop understanding of whether these proteins could be potential vaccine candidates against cryptosporidiosis in cattle and sheep

Cryptosporidium causes the gastroenteric disease, cryptosporidiosis, which is a leading health, welfare and economic concern within the livestock sector, with the major aetiological agent being the pathogenic species, *C. parvum*. Despite this, treatment options are limited and there is currently not a vaccine available for either animals or humans. Specific proteins, considered to be involved in the attachment and invasion of this parasite to host cells, have since been investigated as potential vaccine candidates, but knowledge remains limited. A detailed understanding of the sequence variation and structures of these proteins allows a basis for the investigation of their potential as vaccine candidates. Bioinformatic analysis was performed on four *C. parvum* invasion proteins, Cpa135, CP2, CP15 and P23, comparing gene and amino acid sequence conservation both between *C. parvum* isolates and isolates from different *Cryptosporidium* species known to infect cattle and/or sheep. For each protein the amino acid sequences were highly conserved in *C. parvum* isolates, with some differences identified between *Cryptosporidium* species. Analysis of the Cpa135, CP2, CP15 and P23 protein structures across the *Cryptosporidium* species identified several domains and regions of interest. Cpa135, CP2 and P23 were all suggested to contain a signal peptide. Cpa135 was also identified to potentially contain a ricin-B, galactose-binding, fibrinogen-like and a limulus factor C cochlear (LCCL) protein domain. CP2 was found to contain multiple regions of coiling and disorder predictions and a region within the CP15 protein was identified as being a sequence which matched that of the ribosomal S19 family. Furthering the knowledge of these proteins allows for a way to investigate the presence of such in *Cryptosporidium* isolates and theorise their functions in infection along with their potential association with pathogenicity. All of which could then be used to advance vaccine production. This research provides a basis for the use of these proteins or their specific domains as potential vaccine candidates against cryptosporidiosis which could be developed upon through the production and expression of recombinant proteins.