

## **Occurrence of *Cryptosporidium* and *Eimeria* infections in UK sheep**

The protozoan parasites *Cryptosporidium* spp. and *Eimeria* spp. infect a wide range of animals across the world. Although the public and veterinary health significance of these parasites are different, they continue to remain infection challenges to the farming industry. As such, we investigated the occurrence of *Cryptosporidium* spp. and *Eimeria* spp. in sheep at two farm locations in North West England using a combination of classical parasitological and molecular approaches.

Throughout 2015-16, we collected a total of 552 faecal samples from female Swaledale and Texel sheep reared at two farms in South Cumbria. DNA extractions were performed on the sheep faeces and the presence of *Cryptosporidium* spp. and *Eimeria* spp. was confirmed by PCR amplification of the respective 18S rRNA gene. In total, 110 samples (=20%) were confirmed to be infected with *Cryptosporidium* spp. and 99 of these were typed to species level. The most common (n=65) 18S rRNA sequence corresponded to *C. xiao*/*C. bovis* and further analysis of the actin gene sequence confirmed that 42 of these were *C. xiao* infections. Also identified were *C. ubiquitum* (n=24), *C. sp.* (n=9) and *C. parvum* (n=1). Further analysis of the *C. ubiquitum* isolates by PCR amplification of the gene encoding GP60 confirmed that they were all subtype XIIa, which is a broad host range parasite. Infections in 70 of the 110 PCR-positive samples were also confirmed following staining and microscopy. A qPCR-based approach targeting the 18S rRNA gene was then utilized to assess parasite infection loads. The maximum, minimum and mean *Cryptosporidium* spp. infection loads (oocysts g<sup>-1</sup> faeces) were confirmed as 43,000, 10 and 5,000 respectively.

A subset of 158 faecal DNA extractions were PCR screened for *Eimeria* spp. infection and 78.4% were confirmed positive. DNA sequencing of these 18S rRNA amplicons

confirmed the dominance of *E. crandallis* (71%); other species identified were *E. ahsata* (27%) *E. faurei* (2%).

Overall, the data confirms that different *Cryptosporidium* and eimerian species are present in UK sheep at high prevalence levels and hence co-infections were also commonly observed (52%). The data allows for some potentially interesting associations between the parasite infections and intrinsic/extrinsic factors to be further investigated.