

Can contacts between cattle farms explain genetic variability in *Cryptosporidium* parasites?

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Previous research on *Cryptosporidium* spp. has tended to concentrate on parasites that clinically affect cattle. We investigated parasite subgenotypic diversity in cattle herds of unknown disease status within a discrete study area using molecular PCR 'fingerprinting' techniques. Genetic variation was compared with between-farm contacts to provide additional insight into the epidemiology and transmission of the pathogen.

Fifty-five out of 215 calf faecal samples collected were found to be *Cryptosporidium* positive; 46 of these positive samples amplified across all five 'fingerprinting' micro/minisatellite loci. Twenty nine different multilocus genotypes were found with six genotypes occurring more than once, highlighting considerable diversity within the population. Some of the genetic variability in the *Cryptosporidium* isolates could be explained by contact types between farms; the use of dealers ($P=0.004$) and markets ($P=0.04$) by producers appeared to promote diversity. Farms with truly closed herds tended to have fewer multilocus genotypes relative to the number of *Cryptosporidium* positive samples ($P=0.09$) than farms with truly open herds. The number of multilocus genotypes found per farm appeared to be somewhat related to farmers' attitudes towards biosecurity; farmers who thought the preventive practices were 'very useful' tended to have fewer multilocus genotypes than those who thought the practices 'not very useful' ($P=0.09$).

Great variation was seen in the sub-species genetic structure of *Cryptosporidium* spp. in this population. Previous studies isolating parasites from clinically affected animals displayed less variation. The diversity observed here may be explained by the extensive contact structures that exist locally between farms in the UK; this may assist in furthering knowledge on how pathogens are transmitted through populations and ultimately how they can be controlled. Using a combination of approaches, such as molecular biology and epidemiology, provides novel methods for investigating pathogen transmission.