Cattle*Review*

Introduction: This edition of Cattle Review considers recent papers on liver and rumen fluke, fertility is seasonal calving Irish dairy herds and calf diarrhoea pathogens in the American Midwest.

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Liver and rumen fluke

The liver fluke, *Fasciola hepatica*, is common in many parts of Great Britain. To detect liver fluke infection and to assess whether fasciolicide treatment has been successful, the faecal egg count (FEC) and faecal egg count reduction test (FECRT) are widely used. Rumen fluke is also increasingly reported, but its species identity is yet to be determined. Liver fluke and rumen fluke eggs are morphologically similar, which may lead to erroneous diagnoses of liver fluke infection or treatment failure. As an alternative to FEC, a coproantigen ELISA (cELISA) can be used. The potential for this test to cross-react with rumen fluke species from Great Britain has not been evaluated. Rumen fluke specimens from cattle and sheep in Scotland were identified to species level using DNA sequencing by Gordon et al (2013) (*Veterinary Parasitology* dx.doi.org/10.1016/j.vetpar.2013.01.014). Subsequently, rumen and liver fluke obtained from naturally co-infected sheep were subjected to immunohistochemistry using antibodies from a commercially available cELISA kit for *F. hepatica*. Finally, faecal samples from naturally co-infected sheep flocks were examined by FEC and cELISA. Rumen fluke from imported and home-bred cattle and sheep in Scotland belonged to the species *Calicophoron daubneyi*, rather than *Paramphistomum cervi*, the species presumed to be most common in Great Britain. Intense staining of the gastrodermis was observed in *F. hepatica* but cross-reactivity with *C. daubneyi* was not seen. Faecal samples that contained rumen fluke eggs but not liver fluke eggs were all negative by cELISA. The authors conclude that *C. daubneyi* is the most common rumen fluke of domestic ruminants in Scotland and that cELISA reduction testing may be a valuable alternative to FECRT in herds or flocks that are co-infected with liver and rumen fluke.

Fertility in seasonal herds

Herd management record analysis facilitates accurate assessment of the current herd reproductive status; a crucial decision making tool to implement effective change. To determine the relative importance of cow and management factors on reproductive indices in moderate-yielding Irish seasonal-calving dairy herds, breeding records of 1173 cows were collected from 10 seasonal calving herds between 2007 and 2009 by Lane et al (2013) (*Animal Reproduction Science* **141**: 34–41). Backward-stepwise multivariable logistic regression analysis was utilised to determine the effect of cow factors including parity, calving timing, days post partum, heat detection accuracy and herd factors including herd size and heat detection efficiency on key reproductive indices. Mean farm 6 week pregnancy and end of season not-in-calf rate were 46% (range 14–72%) and 22% (range 3–40%), respectively. Oestrous detection efficiency ($p<0.001$), timing of calving ($p<0.001$) relative to start of breeding, history of abnormal repeat intervals ($p<0.001$) and length of post partum interval ($p<0.001$) were each associated with lower 6 week pregnancy rates. Timing of calving ($p<0.001$) and history of abnormal repeat intervals ($p<0.001$) were associated with higher not-in-calf rates. Herd size and cow parity were not associated with either outcome when factors including existing calving pattern and heat detection accuracy and efficiency were accounted for. The existing spread in calving pattern, heat detection quality and length of voluntary waiting period were the most influential factors that reduced fertility performance in seasonal-calving herds.

Calf diarrhoea

Calf diarrhoea is a major economic burden to the cattle industry worldwide. A variety of infectious agents are implicated in calf diarrhoea and co-infection of multiple pathogens is not uncommon in diarrhoeic calves. This case–control study undertaken in the United States by Cho et al (2013) (*Veterinary Microbiology* **166**: 375–85) was conducted to assess infectious aetiologies associated with calf diarrhoea in Midwest cattle farms. A total of 199 and 245 faecal samples were obtained from diarrhoeic and healthy calves, respectively, from 165 cattle farms. Samples were tested by a panel of multiplex polymerase chain reaction (PCR) assays for 11 enteric pathogens: bovine rotavirus group A (BRV-A), bovine coronavirus (BCoV), bovine viral diarrhoea virus (BVDV), bovine enterovirus (BEV), bovine norovirus (BNoV), Nebovirus, bovine torovirus (BToV) *Salmonella* spp, *Escherichia coli* K99+, *Clostridium perfringens* with b toxin gene and *Cryptosporidium parvum*. The association between diarrhoea and detection of each pathogen was analysed using a multivariate logistic regression model. More than half of the faecal samples from the diarrhoeic calves had multiple pathogens. Statistically, BRV-A, BCoV, BNoV, Nebovirus, *Salmonella*, *E. coli* K99+, and *C. parvum* were significantly associated with calf diarrhoea. Among them, *C. parvum* and BRV-A were considered to be the most common enteric pathogens for calf diarrhoea with high detection frequency (33.7% and 27.1%) and strong odds ratio (173 and 79.9). Unexpectedly BNoV (OR = 2.0) and Nebovirus (OR = 16.7) were identified with high frequency in diarrhoeic calves, suggesting these viruses may make a significant contribution to calf diarrhoea. While from a UK perspective the finding of *C. parvum* and BRV-A would be no surprise; finding BNoV and Nebovirus would be. However, we are not commonly looking for these pathogens and one wonders whether we should be in light of these US data. LS