

Molecular epidemiology of bovine coccidiosis in northern Miyagi prefecture, Japan

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SUMMARY

Coccidiosis, which is caused by the apicomplexan parasite *Eimeria* spp., is a widespread infectious disease in livestock of various kinds, including cattle. Recently, some clinical reports shown that the parasite obtains drug-resistance capability and that their pathogenicity becomes highly toxic. However, no experimental basis exists to explain such cases. This study clarifies adaptation of the bovine coccidian parasite. We performed an epidemiological survey around the Tohoku area in Japan. Rectal feces were collected from 122 beef cattle and 123 dairy breeds that were bred at four farms. Feces derived from cattle showing coccidiosis symptoms were collected and provided by a NOSAI veterinarian. At three dairy farms, the ratios of infection are low, and the frequency range was from 4.3% to 14.7%. In contrast, at the other farm, no clinical sign of bovine coccidiosis was observed, but about half of the beef cattle were infected. It is particularly interesting that the dominant coccidian species clearly differs between among farms and samples from coccidiosis cattle. *Eimeria bovis* was dominant in some, but *Eimeria zuernii* was dominant in others. This result might reflect differences of their pathogenicity.