

# Relationships between the severity of disease and infected *Eimeria* species in bovine coccidiosis

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## SUMMARY

The genus *Eimeria* are protozoan parasites that belong to the phylum Apicomplexa and are responsible for a bloody-stool diarrheal disease known as coccidiosis. In this study, to elucidate the relationship between disease severity and the infecting *Eimeria* species in bovine coccidiosis, we collected oocysts shed in feces from calves showing symptoms of coccidiosis, and determined the number of oocysts, their species, and the frequency of blood in feces. Our data suggest that heavy *Eimeria zuernii* infection increases the occurrence of bloody-stool diarrhea, but the possibility that *E. bovis* possesses high pathogenicity was not rejected. To identify the genotypes of detected oocysts that were morphologically similar to *E. zuernii*, we sequenced the 18S rRNA genes. DNA from a fecal sample containing oocysts identified morphologically as *E. zuernii* was used for PCR, and the sequences determined using a cloning procedure. Interestingly, oocysts in the sample were morphologically determined as *E. zuernii*, but the sequence was not identical to that of *E. zuernii* in GenBank (AY876932). Moreover, molecular phylogenetic analysis suggested that the identified sequence was closer to *E. bovis* than *E. zuernii*. Thus, accumulation of further molecular data is necessary to clarify the phylogenetic relationships among bovine *Eimeria* species.