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## **Molecular Epidemiological Survey for Zoonotic Parasite Infection in Livestock in the Tuul Basin in Mongolia**

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### ***Introduction***

Mongolia, a landlocked country of the central Asian plateau, has undergone significant modifications in herding systems, and the number of reared livestock has been increasing. Livestock sometimes act as reservoirs for pathogenic parasites, therefore shed feces have brought water pollutions by waterborne parasites such as *Cryptosporidium*, *Giardia*, and diarrheagenic *Escherichia coli* (DEC) that cause self-threatening diarrhea and that sometimes lead severe symptoms in young, older and immunocompromised hosts. Therefore, epidemiological information in those livestock is necessary to control parasite. In this study, we analyzed parasite infection in fecal specimens and assessed the prevalence of enteric pathogen in livestock in the Tuul River basin.

### ***Materials and Methods***

Three sites for sampling were selected from upstream or downstream regions of the Tuul River. Another three sites for sampling, including ponds and groundwater, were selected as study area. Fecal samples of cattle, horse, goat, and sheep were collected in those sites. To detect parasite infection, we used molecular biological techniques. In brief, fecal DNA was extracted by using commercial kit, and infection was evaluated by PCR amplification with following marker genes. For *Cryptosporidium*, 18S rRNA gene was used, and 18S rRNA gene and *gdh* were targeted for detection of *Giardia*. The DEC was evaluated with 10 genes (*eaeA*, *bfpA*, *stx1*, *stx2*, *estA1*, *estA2-4*, *eltB1*, and *ipaH*). In order to identify parasite species detected in feces, amplified PCR products were sequenced and applied to the BLAST search.

### ***Results***

In total, 59 fecal samples were collected in 6 designed sites, and fecal DNA extraction was performed in obtained samples. In *Cryptosporidium* detection, PCR product showing expected length was amplified in three samples. However, no sample was identified as *Cryptosporidium* sp. from nucleotide sequencing. After analyses for *Giardia* detection, five samples were pseudo positive. These results suggested that livestock were not likely to reserve zoonotic parasites.