

Establishment of a method for estimating the location of infection and drug discovery for parasites that cause calf diarrhea

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Cattle are major hosts of *Cryptosporidium parvum*. Cryptosporidiosis in neonatal calves is associated with retarded growth, weight loss and calf mortality, and zoonotic infections in humans. Nitazoxanide is the only agent currently approved by the FDA, but its efficacy is limited. Nevertheless, molecular epidemiological studies, development of subtyping tools, and drug discovery studies of *C. parvum* are lacking.

This study shows that that bovines and wild animals in Japan are infected with a variety of *Cryptosporidium* species¹⁾. Furthermore, a virus that persistently infects the parasite was shown to be a new subtyping tool for *C. parvum*.

Cryptosporidium parvum virus 1 (CSpV1), a member of the family *Partitiviridae*, genus *Cryspovirus* that can infect *C. parvum*, is a new candidate for high-resolution tool for tracing *C. parvum*. CSpV1 was detected in all *C. parvum*-positive samples tested. Phylogenetic analysis of dsRNA1 sequence from CSpV1 can distinguish infected areas of *C. parvum* on the national level. This system can differentiate the samples from Hokkaido and south part of Japan. Samples from Iwate, Tanegashima, and Okinawa belonged to a single subclade, respectively. Therefore, the CSpV1 dsRNA sequences reflect the regional distribution of their host and have potential as a high-resolution tool to trace *C. parvum* IIAA15G2R1 subtype²⁾.

Furthermore, epigenetic compounds that inhibit the growth of *C. parvum* were screened in this study. Nullscript was identified as a compound with an inhibitory effect on *C. parvum* growth, and was less toxic to host cells. Nullscript was also able to significantly decrease oocyst excretion in *C. parvum*-infected SCID mice³⁾.

Thus, a very unique tool has been developed to use viruses that persistently infect parasites in this study to estimate the location of infection. Furthermore, epigenetic inhibitors with specific effects on *C. parvum* were found. These findings will be useful in controlling *C. parvum* infections in the future.

References

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