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著者	SHEHATA Ayman Ahmed, BANDO Hironori, FUKUDA Yasuhiro, KABIR Mohammad Hazzaz Bin, MURAKOSHI Fumi, ITOH Megumi, FUJIKURA Atsushi, OKAWA Hiroaki, ENDO Takuto, GOTO Akira, KACHI Masayuki, NAKAYAMA Toshie, KANO Yuto, OISHI Shoko, OTOMARU Konosuke, KAZAMA Kei, ESSA Mohamed Ibrahim, KATO Kentaro
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P-2. Development of a Highly Sensitive Method for the Detection of *Cryptosporidium parvum* Virus Type 1 (CSpV1)

Ayman Ahmed SHEHATA^{1,2}, Hironori BANDO¹, Yasuhiro FUKUDA¹, Mohammad Hazzaz Bin KABIR^{3,4}, Fumi MURAKOSHI⁵, Megumi ITOH⁶, Atsushi FUJIKURA⁷, Hiroaki OKAWA⁷, Takuto ENDO⁸, Akira GOTO⁹, Masayuki KACHI¹⁰, Toshie NAKAYAMA¹¹, Yuto KANO¹², Shoko OISHI¹³, Konosuke OTOMARU¹³, Kei KAZAMA¹⁴, Mohamed Ibrahim ESSA² and Kentaro KATO^{1,3}

¹Graduate School of Agricultural Science, Tohoku University

²Department of Animal Medicine, Infectious Diseases, Faculty of Veterinary Medicine, Zagazig University

³National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine

⁴Department of Microbiology and Parasitology, Sher-e-Bangla Agricultural University

⁵Department of Infectious Diseases, Kyoto Prefectural University of Medicine

⁶Department of Veterinary Medicine, Obihiro University of Agriculture and Veterinary Medicine

⁷Fukuoka Dairy Cattle Artificial Insemination Clinic, Fukuoka Prefecture Dairy Farming Cooperative

⁸Kurume Dairy Cattle Artificial Insemination Clinic, Fukuoka Prefecture Dairy Farming Cooperative

⁹Veterinary Medical Center, Obihiro University of Agriculture and Veterinary Medicine

¹⁰Dairy Research Department, Gifu Prefectural Livestock Research Institute

¹¹Miyazaki Agricultural mutual aid association

¹²Soo Agricultural mutual aid association

¹³Joint Faculty of Veterinary Medicine, Kagoshima University

¹⁴School of Veterinary Medicine, Azabu University.

Cryptosporidium is one of the most important zoonotic parasites that causes cryptosporidiosis. Although, infection occurs throughout the world in high prevalence rates, none completely effective drugs are available. Therefore, the development of a rapid and accurate diagnostic method and genetic surveillance of *Cryptosporidium* are critically required to predict and prevent the spread of infection. Recently, some studies have been focused on *Cryptosporidium parvum* virus type 1 (CSpV1), the first member within Partitiviridae family to infect protozoan host, as a new tool for detection and genetic surveillance of *Cryptosporidium*. However, these studies followed different molecular detection methods, therefore the relationship between PCR-based CSpV1 detection, the target site of the virus genome, and detection sensitivity remains unclear. In this study, we show that the second half of the coding region of dsRNA2 is effectively detected from various types of clinical samples without the need for oocyst purification by using a nested PCR technique. Importantly, our method showed higher sensitivity in field fecal samples compared with *Cryptosporidium* 18S rRNA-based detection method. Moreover, this targeted short sequence reveals a high level of genetic polymorphism compared with the *Cryptosporidium* GP60 gene. Taken together, these results suggest that our method might be good strategy for *Cryptosporidium* and/or CSpV1 analysis.