Detection and Genotyping of Canine Parvovirus in Enteritic Dogs by PCR and RFLP

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Canine Parvovirus (CPV), a member of the genus Autonomous Parvovirus, is a non-enveloped, single-stranded DNA virus of approximately 5 kb. The virus was first described in 1978, with the original isolate being termed CPV type 2 (CPV-2). In 1979, a variant CPV strain designated CPV type 2a (CPV-2a) started to become widespread, followed by a further antigenic variant designated CPV type 2b (CPV-2b), which emerged in 1984. In due course, CPV-2b replaced CPV-2a. The vaccines presently in use are CPV-2 strain specific. Hence, the objective of the present study was to detect and genotype CPV by polymerase chain reaction (PCR), using primer sequences derived from the conserved VP2 region of the genome, and to subsequent restriction fragment length polymorphism (RFLP) analysis of the PCR product. The RFLP analysis employed the endonucleases Rsa I and Hph I in order to differentiate the CPV-2 antigenic variants and establish their distribution in Thailand. We investigated 55 fecal samples from dogs with signs of enteritis, 55 samples from healthy dogs and CPV-2 strain genotype vaccine. Thirty-four out of the 55 specimens (61.8%) from dogs with enteritis were found to be CPV DNA positive. None of the specimens from healthy dogs provided evidence of CPV NDA. After establishing the difference between wild and vaccine strains using RFLP, we found that all virus strains in our study were either CPV-2a or CPV-2b type, which differed from the vaccine strain (CPV-2). Molecular characterization and CPV typing are crucial in epidemiological studies for future prevention and control of the disease.