

Analysis of VP2 gene sequences of canine parvovirus strains from diarrheal feces of dogs in Korea

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Canine parvovirus (CPV) is a non-enveloped virus with a single-stranded DNA genome and causes infectious enteritis in dogs. A few amino acid differences in the viral protein VP2 account for important antigenic and biological changes among canine parvovirus (CPV-2) and CPV-2 variants 2a and 2b.

We amplified VP2 gene by polymerase chain reaction (PCR) using 35 strains from diarrheal feces of dogs in Kangwon, Kyunggi, Gyeongbuk, and Seoul areas from June, 2003 to May, 2006. The PCR products were sequenced by direct sequencing method and the phylogenetic analysis on PCR fragments of VP2 gene was conducted.

Sequence alignment analyses showed that there were different silent mutations and a number of coding changes in the VP2 gene. Among 35 field strains, 31 strains were classified as type 2a of CPV and 3 strains were type 2b. And 1 strain was classified in CPV type 2. Members of the type 2a were classified into five subclusters (2a-I, II, III, IV, and V). and the type 2b were classified into two subclusters (2b-I and II) by the amino acid sequences of their VP2 regions. The strains in 2a-I, II and III were authentic strains of Korea. The strains in 2a-IV and V had similar amino acid sequences to the type 2a recent isolates from the world. The strains in 2b-I and II had similar amino acid sequences to the 2b recent isolates from Asia, Italy and USA. Alignment with the amino acids sequences of type 2a exhibited 97.1-100% similarity to the type 2a (virulent) reference strains and type 2b exhibited 92.0-100% similarity to the type 2b reference strains. Whereas type 2 had 100% homology to the type 2 vaccine strain.

The molecular analysis of VP2 gene of CPV provided the useful information for the identification of CPV types and the understanding of their relationship.

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