

Phylogenetic Characterization of Canine Distemper Viruses Isolated from the Domestic Dogs and Wild Raccoon Dogs in South Korea

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Purpose: The canine distemper (CD) is one of serious diseases in several susceptible animals including domestic and wild Canidae. The purpose of this study is to examine the similarity of canine distemper virus (CDV) between domestic dogs and wild raccoon dogs.

Materials and Methods: We sequenced full-length hemagglutinin (H) genes sequence of CDV isolated from the six domestic dogs and twelve wild raccoon dogs, which were diagnosed as CDV infection by clinical signs and a serological diagnostic kit. The primers specific to H gene were designed based on the canine distemper virus strain CDV3 sequence (GenBank accession number EU726268).

Results: The sequencing and phylogenetic analysis revealed that all new isolated CDV strains are included in ASIA group. The nucleotide identity of H gene between domestic dogs and wild raccoon dogs was 99 %. Identities of nucleotide and predicted amino acid sequence between the isolates and vaccine strains were 89-91% and 87-88 %, respectively.

Conclusion: The findings of this study suggest that domestic dogs and wild raccoon dogs share endemic virus strains in South Korea, and that new vaccine based on the endemic virus should be vaccinated.

Key words: CDV, domestic dog, wild raccoon dog, H gene, phylogenetic analysis

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