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Genetic characteristics of the capsid protein (VP2) in canine parvovirus circulating in Korea

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Canine parvovirus 2 (CPV2) is an etiological agent that causes acute hemorrhagic enteritis and fatal myocarditis in carnivore species. CPV2 evolved from feline parvovirus by host transmission and has continuously been replaced by the genetic variants of capsid protein (VP2). In this study, it was investigated that the genetic diversity and phylogenetic relatedness of the VP2 gene encoding capsid protein in CPV2 obtained from symptomatic domestic dogs obtained ranging from 2011 to 2017 in Korea. Positively selected sites on VP2 of CPV2 variants during a decade were identified and the multiple proteins were evaluated with the theoretical homology modeling using SWISS-MODEL and PyMOL. To investigate the subtype of CPV circulating in Korea, a total of 28 partial VP2 sequences were analyzed. Both CPV2a (15/28, 53.6%), and CPV2b (12/28, 42.9%) were dominant subtypes and Korea CPV2c in 2017 was first detected in this study. Of them, eighteen complete VP2 nucleotide sequences (1755bp) and the amino acid were constructed with phylogenetic tree. A clustering of our variants was closely related to China and Vietnam strains, but in different groups from US, Europe and vaccine strains. Non-synonymous mutations, Phe267Ala, Tyr324Ile and Thr440Ala have been increased during last decade and minor 10 mutations have been also observed. A codon-based maximum likelihood analysis of dN/dS (ω) revealed that specific amino acid 324 (ω=3.518), 426 (ω=3.517) and 440 (ω=3.459) in VP2 gene was under strong positive selection of Korea CPV2. These results support that dynamic process of CPV2 in Korea results in the locally adaptation.

Biography

Boyoun Moon has completed her PhD thesis in College of Veterinary Medicine of Seoul National University. She is in charge of the diagnosis and prevention of companion animal viral diseases in Animal Disease Diagnostic Division (ADDD), Animal and Plant Quarantine Agency (APQA) in South Korea.

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