

عنوان مقاله:

Phylogenetic analysis of canine parvovirus isolates from west Mediterranean region of Türkiye

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خلاصه مقاله:

Canine parvovirus type 2 (CPV-2) causes hemorrhagic enteritis, and is one of the most important and contagious pathogens of dogs. In this study, we aimed to determine the prevalence and antigenic variants of CPV enteritis in dogs. Fecal samples were collected from 35 dogs with mucoid to hemorrhagic diarrhea in the Western Mediterranean region of Türkiye between October 2019 and March 2021. DNA was isolated from the samples and examined using PCR analysis. Twenty-eight out of 35 dogs (80.00%) were detected to be positive for CPV. Of these, three had already been vaccinated. The partial VP2 genes of 15 CPV positive samples producing strong bands in agarose gels were sequenced. All strains were identified as CPV-2b, and the amino acid changes were identified. Discriminative amino acid changes were detected for different amino acid positions clearly defining new CPV-2b variants. Of the 15 isolates, three had previously unreported synonymous mutations. Phylogenetic analysis indicated that the strains obtained in this study were closely related to isolates from the Mersin province of Türkiye, except for three isolates that had synonymous mutations and were located in a separate branch from the other CPV-2b genetic variants previously detected in Mersin Province and Urfa Province in Türkiye. This study demonstrates the increase in the prevalence rates for CPV-2b circulating in vaccinated and nonvaccinated dogs. Taking into account the data from phylogenetic trees which highlights differences between the vaccine strains and the isolates, re-designing immunization strategies .needs necessary

کلمات کلیدی:

Canine, Parvovirus, Strain, VP2 gene

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