Genotyping and pathogenic characterization of canine distemper virus based on mutations in the hemagglutinin gene in Chinese domestic dogs

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Abstract

Canine distemper virus (CDV) infects wild and domestic Canidae worldwide. The hemagglutinin (H) gene has the highest genetic variation in the genome of this virus. Thus, the H gene is commonly used for lineage identification and genetic analyses. In order to study the genetic characteristics and pathogenicity of CDV strains prevalent in China, 132 samples were collected from domestic dogs with suspected CDV infection, 58 samples were confirmed to be positive, and the H gene was successfully amplified from 15 samples. The epidemic strain was identified as type Asia-1 and the novel mutations, A51T, V58I, R179K and D262N, were detected in this strain. Isolated strains, BJ16B53, BJ16B14, and BJ17B8, were used for an animal infection experiment in raccoon dogs. BJ16B53 and BJ16B14 were found to cause clinical symptoms, death, and extensive lesions in various organs. These results are expected to facilitate the development of effective strategies to monitor and control CDV infection in China.

Key words: canine distemper virus, hemagglutinin, phylogenetic analysis, animal infection

Introduction

Canine distemper (CD) is a highly contagious viral disease caused by the CD virus (CDV), and results in high morbidity and mortality in both wild and domestic carnivores. The hemagglutinin (H) gene has the highest genetic variation in the CDV genome, and is used for lineage identification and genetic analysis of CDV strains (Iwatsuki et al. 2000). Strains in the same clade that share >95% amino acid similarity in the H protein are considered the same genotype. Based on this criterion, the America-1 and -2, Asia-1 and -2, Asia-3 and -4,