

Public Abstract

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M.S.

Veterinary Pathobiology

Phylogenetic Characterization of Canine Distemper Viruses Detected in Naturally Infected North American Dogs

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In 2004, dogs with clinical signs suggestive of viral disease known as canine distemper virus (CD) were referred to the University of Missouri Veterinary Diagnostic Laboratory for testing. From eleven such cases, a diagnosis of CD was confirmed in seven dogs (six puppies and one adult) by a combination of both general and specific tests. To further characterize the Canine distemper virus (CDV) strains causing disease in these seven dogs, complete gene sequences were determined for the viral genes coding for hemagglutinin (H) and fusion (F) proteins, while partial gene sequencing was performed for the viral phosphoprotein (P). A total of 4,508 bases were sequenced for the CDV strains detected. Two strains were found to have identical sequences except for 2 bases in the intergenic region of the F and H genes. Analysis of the gene sequences strongly suggested that two of the CDV strains were likely to be related to phocine distemper virus 2 and two other strains of CDV not previously detected in the United States of America. Clear phylogenetic relationships were not established for viruses detected in the two additional cases. However, one strain showed similarity to CDV strains detected in a panda from China. Importantly, the CDV strains detected in this research were demonstrated to be genetically distant from known vaccine strains and strains previously reported in the continental United States. Future research is required to determine if the currently available commercial vaccines adequately protect dogs from infection with the divergent CDV strains detected in this study.