




Review

Evolution and Interspecies Transmission of Canine Distemper Virus—An Outlook of the Diverse Evolutionary Landscapes of a Multi-Host Virus

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Abstract: Canine distemper virus (CDV) is a worldwide distributed virus which belongs to the genus *Morbillivirus* within the *Paramyxoviridae* family. CDV spreads through the lymphatic, epithelial, and nervous systems of domestic dogs and wildlife, in at least six orders and over 20 families of mammals. Due to the high morbidity and mortality rates and broad host range, understanding the epidemiology of CDV is not only important for its control in domestic animals, but also for the development of reliable wildlife conservation strategies. The present review aims to give an outlook of the multiple evolutionary landscapes and factors involved in the transmission of CDV by including epidemiological data from multiple species in urban, wild and peri-urban settings, not only in domestic animal populations but at the wildlife interface. It is clear that different epidemiological scenarios can lead to the presence of CDV in wildlife even in the absence of infection in domestic populations, highlighting the role of CDV in different domestic or wild species without clinical signs of disease mainly acting as reservoirs (peridomestic and mesocarnivores) that are often found in peridomestic habits triggering CDV epidemics. Another scenario is driven by mutations, which generate genetic variation on which random drift and natural selection can act, shaping the genetic structure of CDV populations leading to some fitness compensations between hosts and driving the evolution of specialist and generalist traits in CDV populations. In this scenario, the highly variable protein hemagglutinin (H) determines the cellular and host tropism by binding to signaling lymphocytic activation molecule (SLAM) and nectin-4 receptors of the host; however, the multiple evolutionary events that may have facilitated CDV adaptation to different hosts must be evaluated by complete genome sequencing. This review is focused on the study of CDV interspecies transmission by examining molecular and epidemiological reports based on sequences of the hemagglutinin gene and the growing body of studies of the complete genome; emphasizing the importance of long-term multidisciplinary research that tracks CDV in the presence or absence of clinical signs in wild species, and helping to implement strategies to mitigate the infection. Integrated research incorporating the experience of wildlife managers, behavioral and conservation biologists, veterinarians, virologists, and immunologists (among other scientific areas) and the inclusion of several wild and domestic species is essential for understanding the intricate epidemiological dynamics of CDV in its multiple host infections.

Keywords: genome evolution; canine distemper virus; hemagglutinin gene; genotype