





Origin and spreading of canine morbillivirus in South America

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Highlights

- South America lineages arose from independent migration from North America and Europe.
- The circulating South America lineages spreading by intra-continental migration routes.
- South American lineages have amino acids under signatures of evolutionary relevance.

Abstract

Canine distemper virus (CDV) is a *Morbillivirus* (*Canine morbillivirus*) that greatly impacts domestic and wildlife carnivores worldwide. The CDV RNA genome has high genetic variability, evidenced by several lineages that follow a global geographic pattern. The evolutionary trajectories and population dynamics of CDV lineages are still unclear and debatable, particularly in South America, where relatively few sequences are available. We performed phylogenetic and Bayesian analyses using an updated dataset of the highly variable hemagglutinin (H) gene, including seven South American countries. The time to the most recent common ancestor (tMRCA) of the current CDV lineages was dated to the early 1900s in North America. Maximum likelihood and Bayesian maximum clade credibility phylogenies showed similar topologies with two main branches (L1 and L2) corresponding to the NA1 lineage (L1) and the remaining lineages worldwide (L2). The four circulating lineages in South America (EU1/SA1, SA2, SA3, NA4/SA4) arose from independent

migration events from North America and Europe. North American strains colonized most northern South American countries via Ecuador and then Colombia and Peru, originating the SA3 and NA4/SA4 lineages during their spread. The entry and expansion in the southern part of South America (Argentina, Brazil, Chile, and Uruguay) occurred through three independent migration events and gave rise to the EU1/SA1 and SA2 lineages. South American lineages have specific combinations of amino acids under positive selection that constitute signatures of taxonomic and evolutionary relevance. Our findings provide a comprehensive scenario for the origin and migration routes of *Canine morbillivirus* in South America and highlight the importance of phylodynamics in understanding the geographic patterns of modern genetic variability.

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Keywords

Canine morbillivirus (CDV); Hemagglutinin, South America; Phylogenetic

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