



9th EUROPEAN CONGRESS OF **VIROLOGY 2025**

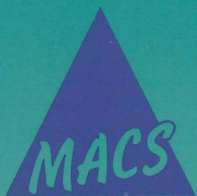


ABSTRACTS

27–30 APRIL

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Investigating canine distemper virus genomic diversity through comprehensive genomic sequencing

Z. Lanszki^{1,2}, Á. Ábrahám¹, D. Szieber^{1,2}, T. Görföl¹, G. Kemenesi^{1,2}

¹University of Pécs, Szentágothai Research Centre, National Laboratory of Virology, Pécs, Hungary

²University of Pécs, Faculty of Sciences, Institute of Biology, Pécs, Hungary

Canine Distemper Virus (CDV), a highly contagious paramyxovirus, poses a significant threat to domestic and wild animals worldwide. The Hemagglutinin gene is widely used to differentiate several lineages, however, complete genome sequencing is crucial for resolving genome-wide evolutionary patterns. Comprehensive genomic data are essential to uncover recombination events, adaptive mutations, and host-specific interactions, which are critical for accurate risk assessment, vaccine development, and conservation efforts. These investigations advance our understanding of CDV evolutionary dynamics and cross-species adaptability. We aimed to advance CDV genomic research by applying a pan-genotype, amplicon-based next-generation sequencing (NGS) approach, using Oxford Nanopore technology. The objective is to generate complete genome data, explore evolutionary dynamics, and identify recombination events across a diverse range of CDV lineages. We developed an efficient amplicon-based sequencing protocol that enables direct genome sequencing from clinical and archival samples. To date, 54 complete CDV genomes from multiple hosts and geographic regions have been sequenced. Phylogenetic and recombination analyses were conducted to investigate genetic diversity and recombination. The sequencing method demonstrated high sensitivity and robustness, successfully generating complete genome data from challenging sample types. Phylogenetic analyses revealed significant inter- and intra-lineage recombination events, suggesting dynamic viral evolution and highlighting the need for broader genomic surveillance. It is a novel and field-adaptable sequencing method that provides new insight into CDV's genomic diversity and evolutionary mechanisms. Expanding the global genomic dataset is imperative for refining phylogenetic frameworks, improving vaccine design, and informing conservation strategies. The methodology and findings offer a useful model for addressing similar challenges in other emerging infectious diseases.