

# Global Distribution of Equine Herpesvirus Type 1: A Systematic Review

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## INTRODUCTION & AIM

Equine herpesvirus type 1 (EHV-1) is a widely distributed alphaherpesvirus that causes respiratory disease, abortion, neonatal death, and myeloencephalopathy in horses, with significant economic impact. Outbreaks such as Ogden (USA, 2011) and the international 2021 outbreak originating in Valencia (Spain) have demonstrated the virus's potential for rapid dissemination.

## METHOD

This study aimed to compile and compare molecular surveillance publications from 2020 to 2025 to identify, by region, the main circulating EHV-1 strains, lineages, and genotypes. Searches were conducted in PubMed, ScienceDirect, Scopus, Web of Science, and EBSCO databases using terms related to equine herpesvirus 1, genotyping, and molecular characterization, covering the period from January 2020 to October 2025. The quality of observational studies was assessed using the Joanna Briggs Institute (JBI) checklist, and data were organized and described in Microsoft Excel.

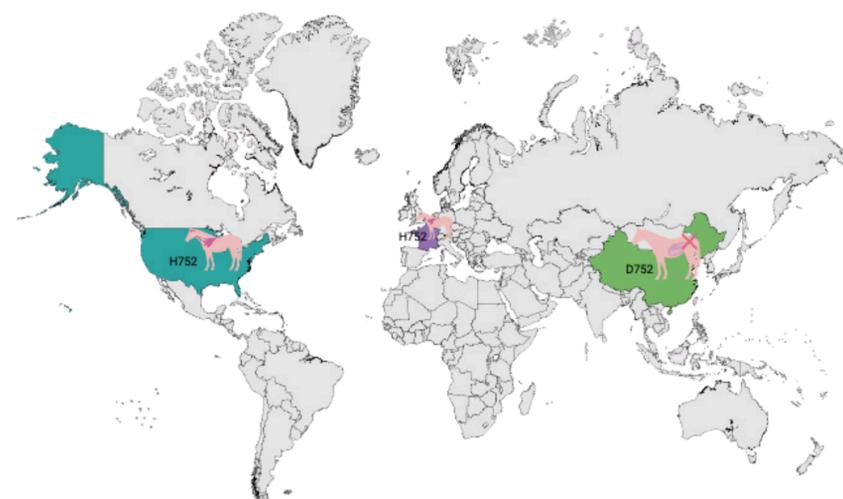
## RESULTS & DISCUSSION

The review showed that EHV-1 circulation is global, intense, and genetically heterogeneous. Classical genotypes N752 (A2254) and D752 (G2254) remain predominant, but an emerging genotype, H752 (C2254), was identified in outbreaks in France (2020) and the USA (2021), associated with respiratory and neurological signs and potentially undetected by assays that only distinguish between N/D752. Regional variation was observed: in China, abortion cases were 100% D752; in Europe, the 2021 Valencia outbreak occurred without the classical neuropathogenic marker; and Swedish series revealed multiple genovariants, reflecting international horse movement. In South American and North African countries, high prevalence and co-circulation with EHV-4, EHV-2, and EHV-5 were reported, including in environmental samples.

High-prevalence regions and co-circulation of EHV-4, EHV-2, and EHV-5



Regional EHV-1 variations



## CONCLUSION

Thus, it is evident that the D752 marker alone is insufficient to define neuropathogenicity, and the emergence of H752 requires the sequencing of multiple ORFs or complete genomes, confirming the globalized circulation of EHV-1 facilitated by equine movement.

## ACKNOWLEDGMENTS