

This text provides a comprehensive overview of a study conducted to understand the complex dynamics underlying the occurrence of Vesicular Stomatitis (VS) in the Western United States. The study aimed to address two primary objectives: first, to identify the key factors influencing the spatial variability of VS occurrence at landscape-to-regional scales, and second, to assess the local-scale environmental conditions associated with years of VS infection compared to non-infection years, distinguishing between incursion and expansion phases.

To achieve these objectives, the study utilized a multi-disciplinary approach, involving experts in VS disease, ecology, and ecoinformatics, alongside individuals with expertise in big data analytics and machine learning. They employed a multi-scale framework, focusing on both landscape-to-regional and local scales, and selected a range of environmental variables believed to influence disease ecology systems, including pedology, hydrology, topography, climate, livestock density, and vegetation.

The approach involved careful variable selection based on expert knowledge and comprehensive data harmonization to facilitate integration and synthesis across diverse data sources. Normalization of environmental variables was performed to limit sensitivity to differences in magnitude, ensuring robust analysis. Spatial distribution models were constructed using machine learning techniques, such as Maxent, to identify the most important drivers of VS occurrence.

Results from the analysis revealed that hydrology, vegetation, and climate were significant drivers of VS occurrence, with differences observed between incursion and expansion years. Specifically, high horse density, proximity to streams with water, and high green vegetation during the summer emerged as important factors associated with VS occurrence. Moreover, differences in environmental conditions between incursion and expansion years suggested a shift in vector populations and their interactions with the environment.

Furthermore, the study examined the influence of viral genetic lineage on VS occurrence patterns, finding that environmental factors played a more substantial role than viral phylogeny in driving disease occurrence. This finding underscores the importance of understanding vector-environment interactions in disease dynamics.

The study's findings have significant implications for the development of early warning strategies for VS and other vector-borne diseases. By identifying key indicators associated with disease occurrence, veterinarians and livestock owners can proactively implement measures to mitigate disease spread, such as reducing exposure to vectors.

In conclusion, the study highlights the importance of a multi-disciplinary, multi-scale approach to understanding disease dynamics and developing effective management strategies. It underscores the potential of leveraging big data analytics and machine learning to improve our understanding of emerging diseases and enhance animal and human welfare.