

Abstract

Full Genomic Sequencing of Vesicular Stomatitis Virus Isolates from the 2004–2006 US Outbreaks Reveals Associations of Viral Genetics to Environmental Variables [†]

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Abstract: Vesicular stomatitis (VS) outbreaks in the western USA occur cyclically, approximately every 8–10 years. Phylogenetic evidence based on a 450 nt region of the P coding sequences suggests that the initial introduction was a single viral lineage closely related to those circulating in endemic areas of Mexico. In 2004, a VS outbreak was initiated in southern NM and TX, and spread as far north as northern CO. Subsequently, in 2005, VS cases appeared in nine states (AZ, CO, ID, MT, NE, NM, TX, UT and WY), and in 2006, VS reappeared only in WY. Phylogenetic analysis suggested that a single VS virus of New Jersey (VSNJV) lineage caused the 2004 outbreak, and re-emerged in 2005 and 2006. The mechanisms of VS emergence and re-emergence remain unclear. Here, we used near full-length genomic sequences of 60 viral strains isolated from 2004–2006 in the US and Mexico to determine the phylogeographic relationships and environmental variables associated with the outbreak dynamics. The results confirmed that a single VSNJV lineage caused the 2004–2006 US outbreaks, and that its closest ancestor was a virus circulating in Colima, Mexico in 2004. We also present evidence that the virus lineage overwintered in 2005 and 2006. Furthermore, rather than a simple geographic relationship, specific viral sublineages or patristic groups were associated to environmental variables, particularly precipitation and temperature. The results confirm the role of environmental factors in the evolution and spread of VSNJV in the USA.

Keywords: vesicular stomatitis virus; molecular ecology; phylogeography



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