

Spatial And Phylogenetic Analysis Of The Vesicular Stomatitis Virus Epidemic In The Southwestern United States in 2004-2006

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ABSTRACT

The southwestern United States has been incidentally affected by vesicular stomatitis virus (VSV) epidemics during the last 100 years. By the time when this manuscript was written, the last episodes were reported in 2004-2006. Results of space clustering and phylogenetic analysis techniques used here suggest that the 2005 and 2006 VSV outbreaks may have been associated with virus over-wintering in certain regions of the country. This knowledge will help to develop effective prevention and control strategies for the disease in the United States.

KEYWORDS: Vesicular stomatitis virus, over-wintering, United States

INTRODUCTION

Vesicular stomatitis (VS) is a viral disease of cattle, pigs, horses, small ruminants, and some wild life species, that is endemic in certain regions of The Americas. There are two *vesicular stomatitis virus* (VSV) serotypes, which have been referred to as New Jersey (VSNJ) and Indiana.

The U.S.A. is sporadically affected by VS epidemics and from 2004 through 2006, 751 outbreaks caused by the VSNJV were reported in nine Southwestern states. Outbreaks occurred during late spring and summer and it has been hypothesized that over-wintering VSNJV strains were responsible for the outbreaks that took place in 2005 and 2006.

The objective of this paper was to assess whether the spatial distribution and phylogenetic relations of VSNJV outbreaks reported in nine Southwestern states in 2004-2006 were compatible with over-wintering of the virus in the United States. Findings were displayed using a publicly-accessible web-based system referred to as the FMD BioPortal (<https://fmdbiportal.ucdavis.edu/>).

TEXT

Space clustering and phylogenetic techniques were used in a web-based system, referred to as the FMD BioPortal, with the objective of assessing whether the 2005 and 2006 VS outbreaks were likely to be associated with VSNJV over-wintering in 2004 and 2005, respectively.

Distance (km) to the nearest VSV outbreak reported at the previous or posterior year (d), whichever was shorter, was recorded for each of the 751 VSV outbreaks. The normal model of the time-space scan statistic was used to identify clusters of VS outbreaks for which the value of d was shorter than the background value of d observed from 2004 through 2006 in the study region.

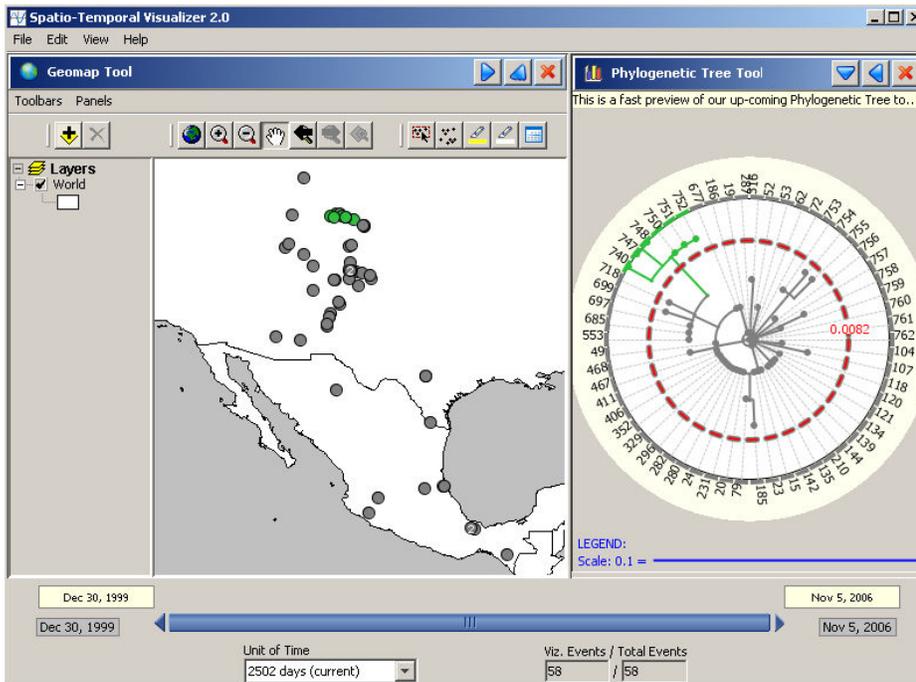
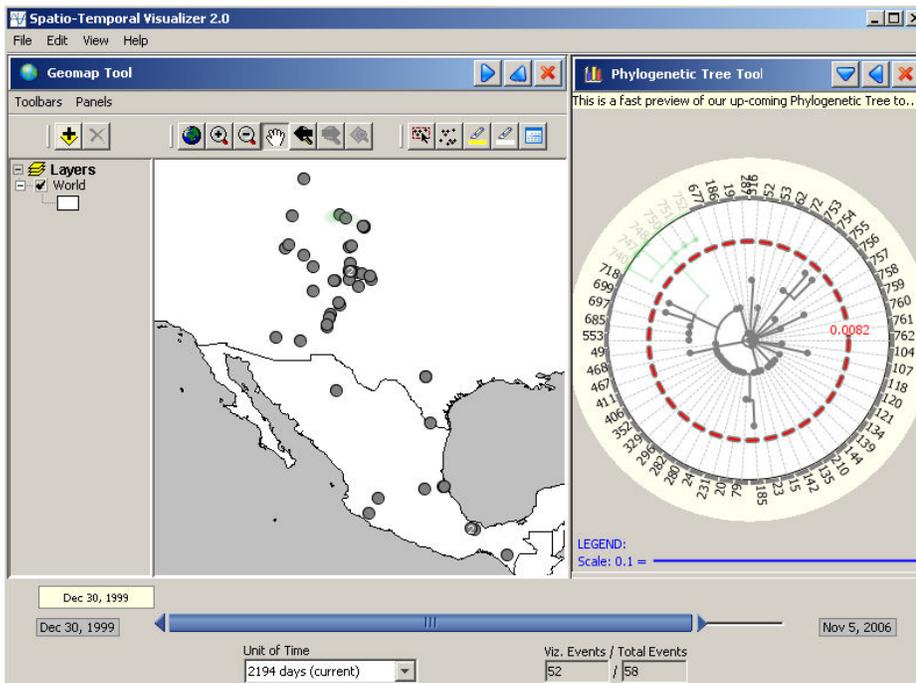


Figure 1: Screenshot of a video demonstration of the genetic (right panel), geographical (left panel), and temporal relation (bottom tab) of vesicular stomatitis virus isolates from Mexico, 2000-2004, and from the United States, 2004-2006, using a web-based system referred to as the FMD BioPortal. The video is publicly accessible at (<http://fmdbiportal.ucdavis.edu/vsv/demo.avi>). Top figure: VSV isolated from Mexico and from the United States through 2005. Bottom figure: VSV isolated from Mexico and

from the United States through 2006. Green dots (geographical and phylogenetic displays) indicate the group of distinct viruses that emerged from Wyoming in 2006.

Two clusters of VS outbreaks with values of d significantly ($P < 0.01$) smaller than the country's background value were identified. The average value of d was 3.9 times smaller than the average value observed throughout the study region in a cluster of 375 outbreaks reported in Colorado and New Mexico. A cluster centered in Wyoming included 21 outbreaks for which the value of d was 11.7 times smaller than the background value of the VS-affected region.

The phylogenetic analysis of 49 VSV samples collected from 2004 through 2006 in the United States and of 10 VSV samples originated from Mexico indicated that the Colorado and Wyoming clusters were caused by two different sublineages of VSNJV, derived from the lineage identified at early stages of the epidemic and distinct from other viral genetic lineages circulating in endemic areas of Mexico.

CONCLUSIONS

Results presented here support the hypothesis that specific sub-lineages of VSNJV overwintered in a limited geographical region of the United States affected by VS in 2005 and 2006. These finds will help to identify areas in which the virus is most likely to over-winter in the event of a VS epidemic and, ultimately, to design and implement prevention and control strategies to prevent or limit the impact of future VS epidemics in the United States.

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