



Complete Genome Sequences of Two Vesicular Stomatitis New Jersey Viruses Representing the 2012 U.S. Epidemic Strain and Its Closest Relative Endemic Strain from Southern Mexico

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ABSTRACT We report here the complete genome sequences of two vesicular stomatitis New Jersey virus (VSNJV) field strains isolated from epithelial lesions from naturally infected animals in Mexico and the United States. The close phylogenetic relationship of these isolates makes them an ideal model for assessing potential genetic factors linked with the emergence of VSNJV in the United States.

Vesicular stomatitis virus (VSV) affects horses, pigs, and cattle throughout the Americas, causing a disease known as vesicular stomatitis (VS), which results in vesicular epithelial lesions. In cattle and swine, the clinical signs resemble those caused by foot-and-mouth disease virus (1).

VSV is the prototype virus for the *Rhabdoviridae* family and the genus *Vesiculovirus*, for which two main serotypes have been described, vesicular stomatitis New Jersey virus (VSNJV) and vesicular stomatitis Indiana virus (VSIV) (2). VSV has an ~11-kb negative-sense single-strand genome which codes for five structural proteins (the nucleoprotein [N], phosphoprotein [P], matrix protein [M], glycoprotein [G], and polymerase [L]) and two nonstructural proteins (C and C') that are encoded in a second open reading frame within the P gene (2, 3).

Important gaps remain in our understanding of the epidemiological and virulence factors mediating cyclical disease emergence in the United States. Previous studies have shown that there is a close ancestral genetic relationship between viral strains causing outbreaks in the United States and viruses circulating in regions of endemicity in southern Mexico (4, 5). However, the genetic determinants of virulence associated with the emergence of epidemic strains remains unclear. In this context, it is essential to have well-characterized viral strains and reliable animal models to associate *in vivo* phenotype with genotype characteristics associated with disease emergence.

In this announcement, we report two full-length genome sequences of VSNJV, one isolated from southern Mexico in 2006 (NJ0806VCB) and the other isolated from the southwestern United States in 2012 (NJ0612NME6).

Viral strain NJ0806VCB was isolated in 2006 from a cow naturally infected in the state of Veracruz, Mexico, where the virus is endemic, and viral strain NJ0612NME6 was recovered from epithelial lesions collected from a horse in New Mexico during an outbreak of VSNJV in 2012. Phylogenetic analysis indicated that viral strain NJ0612NME6 belongs to the epidemic lineage 1.1 and viral strain NJ0806VCB belongs to the endemic lineage 1.2, the latest common endemic ancestor of lineage 1.1 responsible for the outbreaks in the United States in 2012 (5).

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Viral sequences were obtained as previously described (6). Viral RNA was extracted from cell culture (one passage in Vero cells) supernatants using the RNeasy minikit (Qiagen). The full-length genome sequence of each viral isolate was amplified in 19 overlapping fragments (~600 to 700 bp) by reverse transcription-PCR (RT-PCR) using a specific set of primers. RT-PCRs were conducted using the SuperScript III one-step RT-PCR Platinum *Taq* high-fidelity kit (Invitrogen). RT-PCR products were analyzed on a 1.5% agarose gel stained with SYBR safe DNA gel stain (Thermo Fisher) and visualized by UV transillumination and then purified using QIAquick PCR purification columns (Qiagen) and sequenced using the dideoxy termination method with a Big Dye terminator (Life Technologies). To assemble consensus sequences of each virus, chromatograms were analyzed using Sequencher v4.8 (Gene Codes, Ann Arbor, MI, USA). The genomic termini were obtained as previously described (7).

These two viral sequences are useful for identifying genetic determinants and possibly distinctive biological characteristics between endemic and epidemic VSNJV strains as well as for the construction of infectious clones to study genetic factors linked to virulence.

Accession number(s). The complete genome sequences of NJ0806VCB and NJ0612NME6 described herein have been deposited in GenBank under the accession no. [MG552608](#) and [MG552609](#), respectively.

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