



Complete Genome Sequences of Two Vesicular Stomatitis Virus Isolates Collected in Mexico

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ABSTRACT We report two full-genome sequences of vesicular stomatitis New Jersey virus (VSNJV) obtained by Illumina next-generation sequencing of RNA isolated from epithelial suspensions of cattle naturally infected in Mexico. These genomes represent the first full-genome sequences of vesicular stomatitis New Jersey viruses circulating in Mexico deposited in the GenBank database.

Vesicular stomatitis virus (VSV) is the prototype of 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). The ~11-kb negative-sense single-stranded genome encodes five structural proteins, nucleoprotein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), and polymerase (L), along with two nonstructural proteins encoded in a second reading frame of the P gene and termed C and C' (1, 2).

VSV affects cows, horses, and pigs and is considered endemic from northern South America to southern Mexico. VSNJV accounts for roughly 80% of the clinical cases reported annually in the Americas (3). In the United States, VSV outbreaks occur cyclically at 8- to 10-year intervals and cause disruption and economic losses associated with animal quarantines (4). Phylogenetic studies have shown that viruses causing outbreaks in the United States originate in regions of endemicity in southern Mexico (5, 6); however, the mechanisms mediating the emergence and reemergence of VSV in North America remain poorly understood and are the subject of ongoing investigations. Here, we report two full-length genome sequences of VSNJV circulating in Mexico between 2007 and 2008 that have been deposited in GenBank, as well as the methodology used to obtain these sequences. One of these sequences (NJ1008JAB), which was isolated in 2008 in central Mexico, belongs to the viral lineage 1.1, which was recently associated with the most recent VSNJV outbreak in the United States, which occurred between 2012 and 2015. This strain represents one of the latest common ancestors from Mexico of previous full-length genomic viral sequences associated with lineage 1.1 isolated from the United States. Conversely, sequence NJ1007CPB was isolated in 2007 from the state of Chiapas, Mexico, where it is endemic, and is not directly associated with the viral lineage that caused outbreaks in the United States in 2012 to 2015.

Both viral isolates were recovered from epithelial lesions of naturally infected cows in Mexico after one passage in Vero cells. Viral RNA was extracted from cell culture supernatants using Trizol and precipitated with isopropanol. Whole-genome viral sequencing was performed at the next-generation sequencing core facility of the National University of Mexico located at the Instituto de Biotecnología in Cuernavaca, Morelos, as previously described (7). Two hundred base-pair-sized libraries, prepared

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using Illumina's mRNA-Seq 8 sample preparation kit as suggested by the manufacturer, were loaded in separate lanes of a flow cell on a Genome Analyzer IIX (Illumina, San Diego, CA). Sequencing was performed through 36 cycles of single-base-pair extensions. Image analysis was conducted using Genome Analyzer Pipeline version 1.4. Assembly of viral reads was carried out with Mapping and Assembly with Qualities (MAQ) (8) version 0.7.1, using the VSNJV isolate NJ95COB as the assembly reference genome (GenBank accession no. JX121112). In total, 99.85% of each viral genome was sequenced in both strains. The missing nucleotides are located in noncoding regions at the 3' and 5' ends of the genome. Compared with previously reported full-length VSNJV genome sequences, both samples showed comparable genomic organization.

Accession number(s). The complete genome sequences of the NJ1008JAB and NJ1007CPB viral strains described herein have been deposited in GenBank under the accession no. [MF196237](https://doi.org/10.1093/genome/10.1016/j.genome.2013.10.025) and [MF196238](https://doi.org/10.1093/genome/10.1016/j.genome.2013.10.025).

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