



Complete Genome Sequence of a Representative New Jersey Vesiculovirus Strain, NJ03CPB, from a Region of Endemicity in Southern Mexico

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ABSTRACT We report the full-genome sequence of a New Jersey vesiculovirus strain, commonly referred to as vesicular stomatitis New Jersey virus (VSNJV), obtained from an epithelial lesion of a naturally infected cow in Chiapas, Mexico. This genome is a representative from the zone of endemicity in Mexico, a region of high genetic diversity.

Vesicular stomatitis (VS) is caused by vesicular stomatitis virus (VSV), an infectious agent belonging to the *Rhabdoviridae* family and the genus *Vesiculovirus*, of which Indiana vesiculovirus and New Jersey vesiculovirus are the two main serotypes. The negative-sense single-stranded RNA genome of VSV is about 11 kb and encodes five structural proteins, nucleoprotein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), and polymerase (L) (1).

VS is confined to the Americas, where vesicular stomatitis New Jersey virus (VSNJV) is the serotype responsible for the majority of the clinical cases reported annually in livestock (2). In Mexico, VSV is endemic in the southern states of Chiapas, Tabasco, and Veracruz, where multiple phylogenetic analyses have shown the great genetic diversity associated with the concurrent circulation of multiple lineages (3–5). A relevant aspect of these endemic lineages is that some of them may become the precursors of the epidemic lineages responsible for sporadic outbreaks in the United States (3, 5). Understanding the molecular and biological bases leading to the evolution of these epidemic lineages is vital to decipher the viral factors favoring the emergence of VS in the United States. Recent reports showing different virulence levels between endemic and epidemic VSNJV strains suggest that intrinsic viral factors might influence in part the emergence of these outbreaks (6). However, many questions remain regarding the specific sites in the genome that play a role in the emergence of epidemic phenotypes. In this context, the availability of the VSNJV endemic strain NJ03CPB constitutes the fourth complete viral sequence from Mexico in public databases (7, 8) and will support future genetic analyses.

Viral isolate NJ03CPB was recovered from an epithelial lesion of a naturally infected cow in Chiapas (southern Mexico) after one passage in Vero cells. Viral RNA was extracted from cell culture supernatants using the RNeasy minikit (Qiagen). Viral sequencing was performed at the Plum Island Animal Disease Center by the Sanger method using specific sets of primers to generate overlapping fragments (~600 bp) covering the whole VSV genome, as previously described (9). Additional genomic terminal sequences were obtained as previously published (10). Briefly, a poly(A) tail was added to the 3' end of the viral genome using poly(A) polymerase (USB), and the 5' and 3' rapid amplification of cDNA ends (RACE) systems (Invitrogen) were used to sequence the viral 5' and 3' termini, respectively. The final consensus sequence was generated using Sequencher v4.8 (Gene Codes, Ann Arbor, MI, USA).

The genome of NJ03CPB showed an organization, size (11,123 bp), and GC compo-

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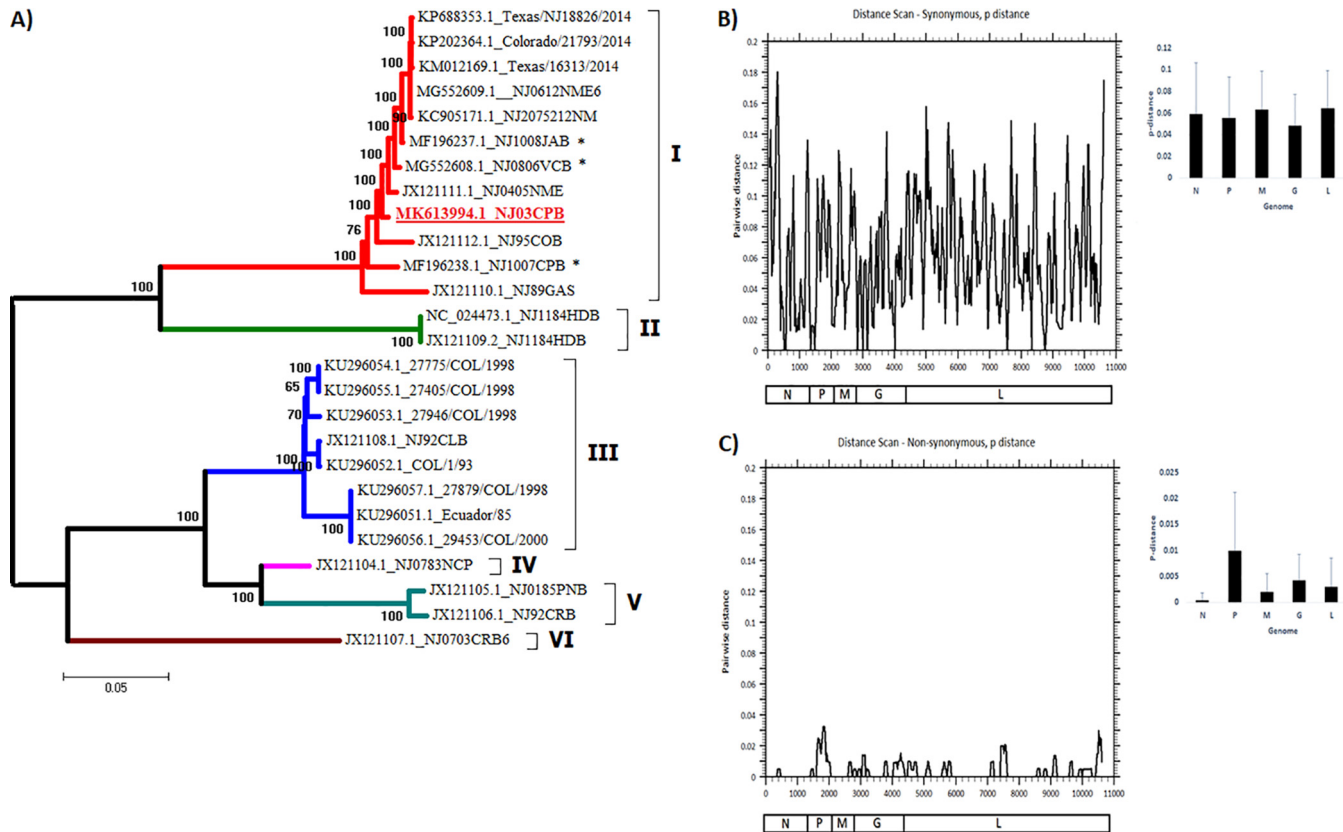


FIG 1 Genetic relationship of strain NJ03CPB with other New Jersey vesiculoviruses. (A) The phylogenetic analysis, conducted by maximum likelihood, using full-length genome sequences representing the six main clades of New Jersey vesiculovirus. NJ03CPB (red) grouped within clade I. (B and C) Pairwise distance comparisons using 100-nucleotide windows showed differences in synonymous (B) and nonsynonymous (C) sites at various coding regions between NJ03CPB and previously reported New Jersey vesiculoviruses reported from Mexico (*). Phylogenetic analysis was conducted using the MEGA 7 software package (12), while pairwise distance analysis was conducted using the program Sequence Distances in the SSE software version 1.3 (13).

sition (40.1%) that were comparable to those of previously published VSNJV genomes. Phylogenetically, NJ03CPB appears to be associated with VSNJV clade I, a group of viral lineages circulating in North America (9) (Fig. 1). Currently, the biological characteristics of NJ03CPB are being studied using a well-established natural host model in pigs (6, 11).

Data availability. The complete genome sequence of the NJ03CPB viral strain described here has been deposited in GenBank under the accession no. [MK613994](#).

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