

## Phylogenetic comparison of the whole genome of rabies virus strains from San Luis Potosi and Queretaro, Mexico

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### INTRODUCTION

In Mexico, the main transmitter of rabies virus (RABV) in cattle is the vampire *D. rotundus* and the 89.1% of rabies cases in animals occur in cattle, this disease is known as Bovine Paralytic Rabies<sup>1</sup> (BPR). The fluctuation in the number of BPR cases, as well as its appearance in regions previously considered free, including areas in the state of Querétaro<sup>2</sup> (Qro.), has been of interest to explain the epidemiological phenomenon of this disease based on molecular methods of whole genome sequencing (WGS). Currently, it is not known whether the infection occurring in Qro. is caused by strains from neighboring states or if it is the same strain, which indicates its origin. Therefore, genotyping several RABV isolates and complementing it with epidemiological information is necessary to support decision making based on a more robust identification of the strains circulating in this endemic area.

### METHODS

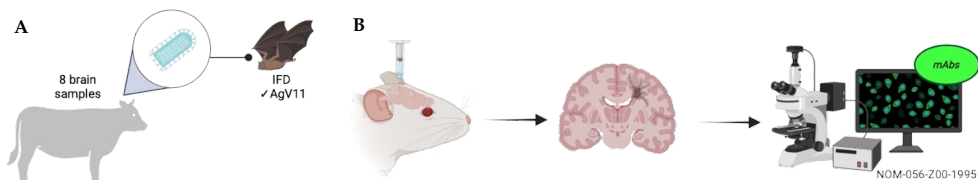


Fig.1. RABV isolation. A. Eight cattle brain samples positive for rabies by IFD, characterized as AgV11, antigenic variant associated with *D. rotundus*, genotype 1, provided by the CEFPP-SLP. B. Encephalic tissue samples from cattle were processed for inoculation into weanling albino mice using 30  $\mu$ L intracerebrally (IC). Brains with lesions suggestive of RABV were diagnosed according to NOM-056-ZOO-1995.<sup>3</sup>

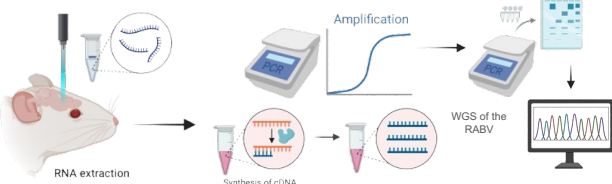


Fig.2. RT-PCR and Whole Genome Sequencing of the RABV. Total RNA was extracted directly from brain. RT-PCR was performed for amplification of the products and cDNA was examined by agar-gel electrophoresis. For whole genome sequencing the Illumina platform was used and the sequence JQ685936.1 (extracted from GenBank) was used as reference sequence for bioinformatics analysis.

### RESULTS

From the WGS obtained, it was observed that the sequence IB1VR25S01 (ibr.1) has 98% identity with the complete reference genomic sequence reported in GenBank (JQ685936.1). The strain ibr.1 corresponds to a bovine from the municipality of Cd. Valles in the state of SLP. We obtained a phylogenetic tree performed to compare the sequence ibr.1 and four other sequences from the municipalities of Colon, Jalpan and Ezequiel Montes (Qro) and one from Acatlan, Hidalgo (Hgo), obtained previously, this is showed at Figure.3.

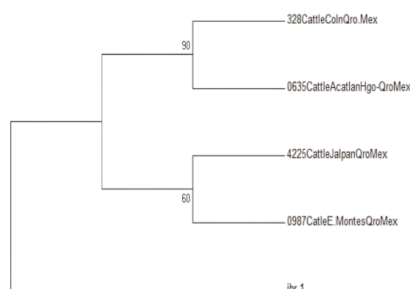


Fig.3. Dendrogram of the relationship between four previously obtained strains and the ibr.1 sequence. ibr.1 and the strains from Colon (Qro) and Acatlan (Hgo) are more similar to each other by obtaining a bootstrap value in the clade of 90%, while the strains from Jalpan and Ezequiel Montes (Qro) obtained a value of 60%. The evolutionary history was inferred using the Neighbor-Joining method.

### CONCLUSION

The comparison of the whole genome sequence ibr.1 with those previously obtained, allowed observing that the strains of rabies virus in Queretaro are very similar to each other, indicating possible genetic stability of the strains. While the RABV strain distributed in the central valleys of Queretaro is another source of infection.

### REFERENCES

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