



VIRAL DISEASES

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MOLECULAR CHARACTERIZATION OF THE SPIKE GENE OF THE PORCINE EPIDEMIC DIARRHEA VIRUS IN MEXICO

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Introduction

In Mexico, the first suggestive outbreaks of the circulation of the porcine epidemic diarrhea virus (PEDV) were identified at the beginning of July 2013. The Spike protein is the most antigenic protein of the virus and the main target for developing a vaccine or diagnostic system.

Material & Methods

To identify the molecular characteristics of the PEDV Spike (S) gene in Mexico, 116 samples of the intestine and diarrhea of piglets with clinical signs of porcine epidemic diarrhea (PED) were obtained. Samples were collected from six states of Mexico (Jalisco, Puebla, Sonora, Veracruz, Guanajuato, and Michoacán) from 2013 to 2016. After amplification of the S gene by RT-PCR, the obtained products were sequenced and assembled.

Results

The complete amino acid sequences of the spike protein were used to perform an epitopes analysis, which was used to determine null mutations in regions SS2, SS6, and 2C10 compared to the sequences of G2. A phylogenetic analysis determined the circulation of G2b and INDEL strains in Mexico. However, several mutations were recorded in the collagenase equivalent (COE) region that were related to the change in polarity and charge of the amino acid residues.

Discussion & conclusion

The PEDV strain circulating in Jalisco in 2016 has an insertion of three amino acids (²³²LGL²³⁴) and one change in the antigenic site of the COE region, and strains from the years 2015 and 2016 changed the index of the surface probability, which could be related to the re-emergence of disease outbreaks. In conclusion, in this work, 10 PEDV strains were identified from outbreaks in six regions of Mexico from 2013 to 2016. Of the four analyzed neutralizing epitopes, the Mexican strains presented mutations only in the COE region. Funded by PDCPN2014-1, 249177, RF 13592932977.