First detection and molecular characterization of bovine viral diarrhea virus (BVDV) in serum, semen and aborted fetuses samples from Paraguay.

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INTRODUCTION

Bovine viral diarrhea virus (BVDV) is the most prevalent pathogen in cattle and causes significant economic losses due to its variety of severe clinical manifestations (1). It belongs to the *Flaviviridae* family and is distributed in species *A, B* and *H* within the genus *Pestivirus*. The BVDV is endemic around the world, the prevalence of the different genotypes varies according to geographic regions (2). Currently in Paraguay, this disease is diagnosed only by serological methods, and no data from molecular methods are obtained until today. The objective of this work was to detect and characterize BVDV in Paraguay through molecular techniques, in different types of samples like; serum, semen and naturally aborted fetuses from different departments.

MATERIALS AND METHODS

100 pools of bovine sera (1 pool = 5 serum samples), 73 fresh semen bulls samples and 8 naturally aborted fetuses, received from different livestock establishments from different departments of Paraguay. RNA from serum and semen samples were obtained using the silica guanidine method, and from fetus samples RNA were obtained using a commercial kit Tiangen®. Molecular detection was carried out through conventional PCR amplification of the 5'UTR region to detect three genotypes (*A, B and H*) of BVDV (3). To confirm the target gene, sequencing was performed using the Sanger method (comercial platform) of some representative samples (serum, semen and organs of bovine fetuses).

RESULTS

The results obtained from pools of serum samples were: 67% (67/100) for *Pestivirus A*, 6% (6/100) for *Pestivirus B* and 2% (2/100) for *Pestivirus H* (Figure 1). *Pestivirus A* were detected in 54.7% (40/73) in semen samples. The presence of *Pestivirus A* and *H* was detected in 2/8 spontaneously aborted fetuses organs (lung, heart, liver, ear cartilage, and brain) (Figure 2). The genotype was confirmed by partial sequencing of the 5'UTR region of 8 individual samples of type *A* (2 sera, 2 semen, lung, heart, brain and ear cartilage). Sera of 5 samples of type *B* and 6 samples of type *H* (2 sera, heart, ear cartilage, liver and brain).

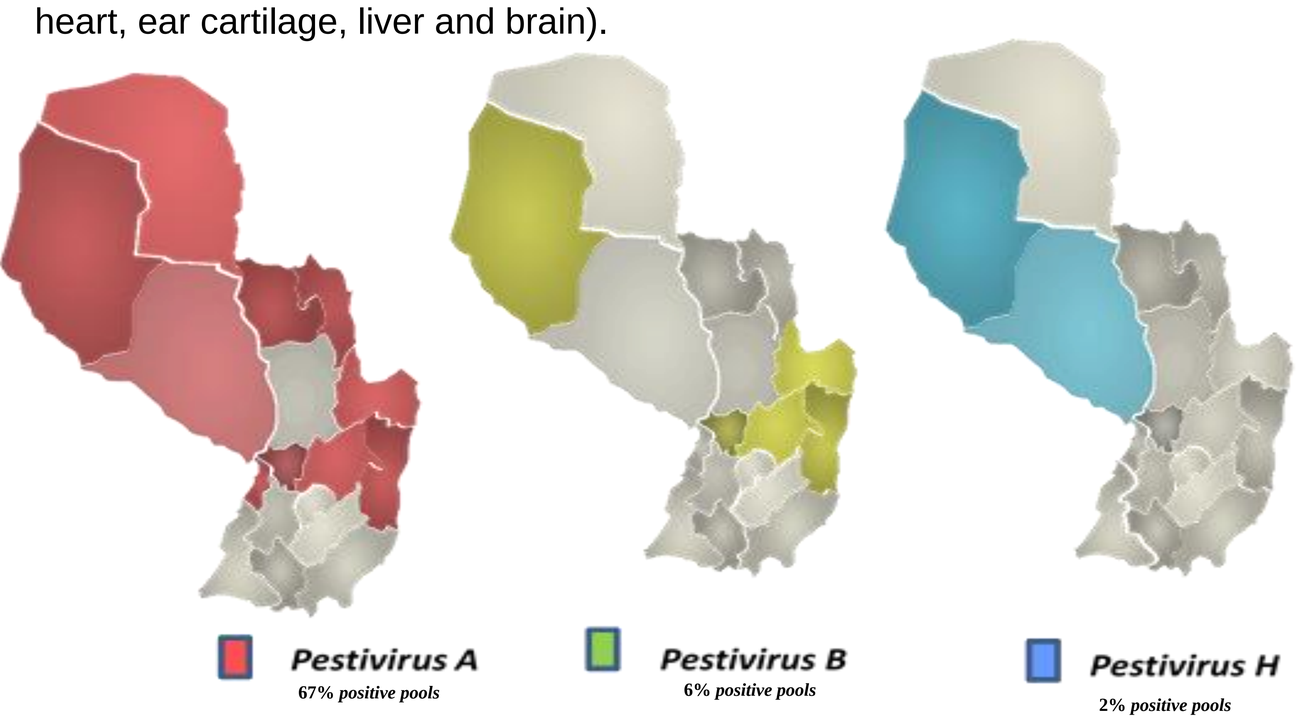

Figure 1: Geographic distribution of BVDV in pool serum samples detected by RT-PCR from diferents livestock establishment.

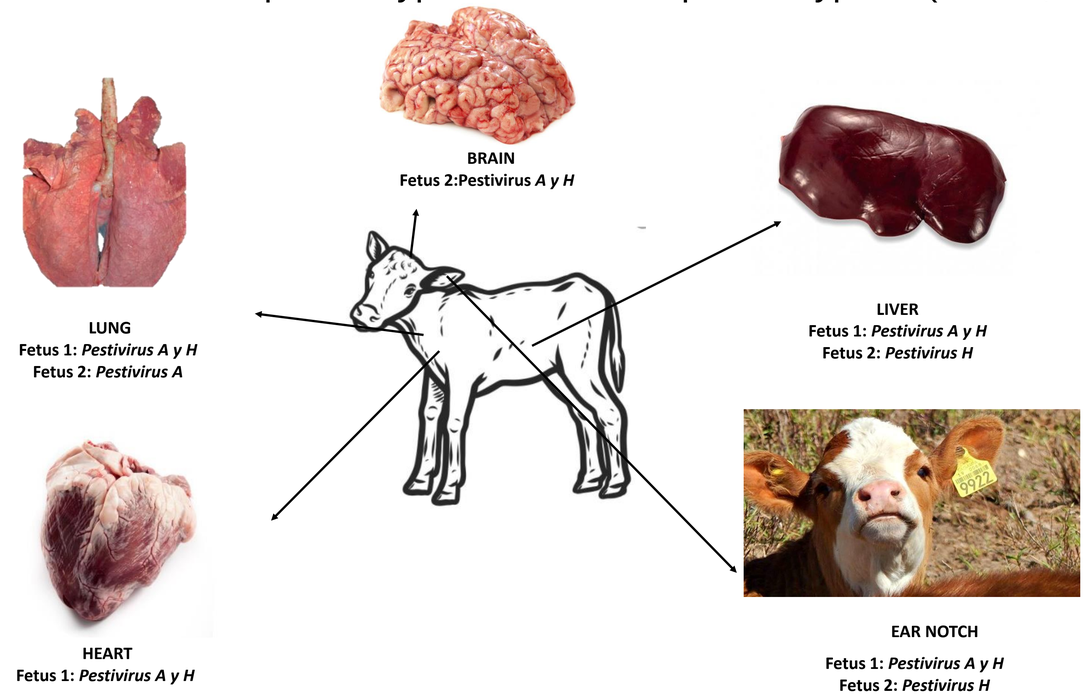

Figure 2: Tisular distribution of BVDV in organs of aborted fetuses and differents genotypes detected by RT-PCR.

CONCLUSION

The presence of BVDV was confirmed by molecular techniques for the first time in Paraguay, through its detection in different types of samples, as well as the presence of the three genotypes. This suggests that the virus is widespread around the country and can cause significant losses in Paraguayan bovine livestock production.

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