Title: FIRST DETECTION AND MOLECULAR CHARACTERIZATION OF NEBOVIRUS IN BRAZIL

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Abstract:

Enteric diseases associated with diarrhea, dehydration and weight loss are one of the major problems of cattle worldwide, contributing to significant morbidity and mortality, especially among newborns. In this context, demands for improving the laboratory diagnosis of infectious enteric diseases, became constant, given the economic losses involved. Nebovirus (NeV) is a new genus of viruses belonging to the Caliciviridae family recently characterized in cattle, and is associated with gastroenteric disorders, such as diarrhea, anorexia and intestinal lesions particularly in calves. Due to lack of data concerning the occurrence of this virus in South America, the present study was aimed at molecular detection and characterization of NeV strains in fecal samples from cattle with and without diarrhea of different ages. The study was conducted on 62 animals from different states of Brazil; the fecal samples were tested by RT-PCR with primers specific for the 3' end polymerase region of neboviruses. Of the samples collected, three (4.8%) were positive for NeV. All positive animals were aged less than 20-days-old and had diarrhea, two positive calves were female, and two positive samples were from beef cattle. Two animals were from the state of Goiás and one from the state of São Paulo. The samples sequenced in this study shared >93.0% nt (>96.3% aa) sequence identity when compared each other and when compared to reference samples of each NeV genogroup these samples shared 86.0%-89.5% nt (91.4%-94.4% aa) identity with Newbury1/UK, 78.8%-80.9% nt (85.2%-87.7% aa) identity with Nebraska/US, and 78.4%-81.1% nt (84.4%-86.4% aa) identity with DijonA216/FR. Phylogenetic analysis clustered our sequences into Newbury1 clade. Our results indicate, for the first time, the occurrence of NeV in Brazil as well as in South America, and the first Newbury1-like NeVs found outside the United Kingdom.

Keywords: Caliciviridae, Bovine Nebovirus, diarrhea, cattle, molecular epidemiology

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