

TITLE: DETECTION AND MOLECULAR CHARACTERIZATION OF BOVINE *ENTEROVIRUS* IN BRAZIL: FOUR DECADES OF THE FIRST REPORT

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ABSTRACT:

Enteric diseases associated with diarrhea, dehydration, and weight loss are one of the major problems for the cattle-raising business worldwide, contributing to significant morbidity and mortality rates, especially among newborns. In this context, demands for improving the laboratory diagnosis of infectious enteric diseases are frequent, given the economic losses involved. The bovine *Enterovirus* (BEV) belong to the family *Picornaviridae*. They infect a wide range of mammals, exhibiting very high genetic variability like other RNA viruses. BEV infects the gastrointestinal tract, causing asymptomatic or mild infections; however, diarrhea and abortions have also been associated with BEV infections. Enteroviruses are shed in large numbers in the feces and transmitted by the fecal-oral route. The virus particles are very stable under a wide range of environmental conditions, such as pH, temperature, and salinity. The first report of these viruses in cattle in Brazil was carried out over four decades ago in the states of São Paulo and Pernambuco through serological screening, and since then no reports have been published. Due to lack of new data regarding the occurrence of this virus in Brazil, the present study was aimed the detection and molecular characterization of BEV in fecal samples from cattle with and without diarrhea of different ages. The study was conducted on 103 animals from different states of Brazil. Fecal samples were tested by RT-PCR with primers specific for 5'-UTR region of BEV. The results showed that fifteen (15.4%) of the samples collected were positive for BEV including both calves and adult animals; 5 animals had diarrhea, 11 were females and the majority of the positive samples were from dairy cattle (n=13). Ten animals were from the state of São Paulo, 4 were from the state of Minas Gerais and 1 was from the state of Goiás. Out of all positive samples, 4 were sequenced and shared >91.1% nt (>77.9% aa) sequence identity when compared each other and shared 88.3%-95.0% nt (74.5%-91.6% aa) identity when compared to reference samples of BEV. Phylogenetic analysis clustered our sequences into *Enterovirus* clade F. Our results indicate, after four decades, the occurrence of BEV in Brazil and present the first phylogenetic characterization of this virus in Brazilian cattle herds.

Keywords: Bovine *Enterovirus*, RT-PCR detection, cattle diseases, molecular epidemiology

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