MOLECULAR CHARACTERIZATION OF CANINE DISTEMPER VIRUS IN AN OUTBREAK IN GIANT ANTEATERS (MYRMECOPHAGA TRIDACTYLA) KEPT IN A RESCUE CAPTIVITY FACILITY

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RESUMO

Between October and November 2019, the Centro de Triagem de Animais Silvestres do IBAMA in Belo Horizonte (CETAS/BH) send samples from 4 giant anteaters (Myrmecophaga tridactyla) to the UFMG Animal Virology Research Laboratory (LPVA) to diagnosis of canine distemper virus (CDV). The animals, in the CETAS/BH, showed nonspecific signs such as dehydration, diarrhea, abdominal dilation, weight loss, hyporexia, prostation, hematochezia and dyspnea in different intensities and distinct periods. Even though the animals had veterinary assistance, due to complications of the signs the animals ended up dying and all the samples tested were collected during necropsy. The samples from intestine, lung, liver, kidney, lymph node, spleen from each animal were macerated and diluted 10-fold in phosphate-buffered saline and Trizol was used for RNA extraction according to the manufacturer's instructions. The total RNA was submitted to a semi-nested RT-PCR that amplifies part of the conserved CDV Nucleoprotein gene (NP). The CDV RT-PCR was positive for three of the four giant anteaters. To identify the genetic lineages and characterize the tested strains, positive samples were performed using primers that amplify a variable region of the CDV, that encodes the signal peptide of the F protein (Fsp). The amplicons were purified and sequenced using the ABI3730 DNA Analyzer. The nucleotide sequence data were analyzed and assembled using SeqMan Software 7.1.0 and sequences were compared by BLAST and the consensus sequences were aligned, using MUSCLE multiple alignment with sequences available from GenBank. A phylogenetic tree was constructed using the maximum composite likelihood method with 1,000 bootstrap replicates using MEGA X software. Phylogenetic analysis showed that of the Giant anteaters' sequences clustered into the Europe 1/South America 1 (EU1/SA1) clade and separeted of the other representative genotypes. These CDV sequences were closely related to each other, showed high nucleotide identity among themselves (99-100%). The close phylogenetic relationship was observed among others strains identified in Brazil, closely related to crab-eating-fox (Cerdocyon thous) (MH4267739), domestic dog (Canis lupus familiaris) (KY057352) and unknown host (MH362795; KX434626), with higher degree of nucleotide identity (98%). This report configures a possible CDV outbreak in the CETAS/BH, that was spread inside the institution. The animals from this institution comes, mostly, from free ranging wild animals that were apprehended by the authorities, and the animals from this study were free ranging animals. This study shows a serious threat to

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the conservation of wild animals, because of the major impacts that CDV can have in animals, especially in wild animals, as showed by other studies. These results show the importance of diagnosing infectious diseases animals in this kind of institution because, if an sick animal was release back in the wild it could infect many more animals and cause a huge impact in many more species.

PALAVRAS-CHAVE: Canine Distemper Virus, Diagnostic, Myrmecophaga tridactyla, Phylogeny

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