Título: Detection of *Norovirus* genogroup II in free-living jaguars (*Panthera onca*) in protected areas of northern pantanal, Cáceres, Brazil.

Autores: Silveira M.M[1], Oliveira J.T.[1], Chitarra C.S. [1], Candido S.L.[1], Dutra V.[1], Onuma S.S.M.[2] Kantek D.L.Z.[2], Nakazato L.[1]

Instituição:[1] Universidade Federal de Mato Grosso (Av. Fernando Corrêa, 2367, Boa Esperança, Cuiabá, MT, 78060-900), [2] Instituto Chico Mendes de Conservação da Biodiversidade (Estação Ecológica de Taiamã, ICMBio, Cáceres, MT, Brasil)

Resumo: The Norovirus (NoV) are regarded as the major cause of nonbacterial gastroenteritis worldwide in humans and animals. Human NoVs are classified into genogroups I, II, and IV, and NoVs classified in genogroups II and III have been detected in pigs and cows. The aim of this study was to assess occurrence of NoV in free-living jaguars. The studied areas comprised two federal conservation units: Taiamã Ecological Station (16° 50' 34.31" S, 57° 35' 03.70" W) and Pantanal Matogrossense National Park (17° 50'47. 33" S, 57° 24'12.67" W) at Pantanal of Mato Grosso. We used nine samples of rectal swab of free-living jaguars (Panthera onca) for subsequent RNA extraction. Reverse transcription were performed followed by polymerase chain reaction (RT-PCR) with NoV primers SWNV1 (CGTACCAGAGGTCAACAAT) and SWNV2 (AATCTAACAAAATCTCACCTG) that amplify partial capsid gene. Six jaguars (66.6%) were positives in the RT-PCR with the expected size of 181 bp when analyzed by 2% agarose gel electrophoresis. Two positive samples were purified with PCR kit GFX^{TM} PCR DNA & Gel Band Purification Kit (GE Healthcare), and subjected to DNA sequencing with the respective primers, using BigDye Terminator sequencing kit (Applied Biosystems) on ABI 3500 sequencer Genetic Analyzer (Applied Biosistems). The sequences obtained were compared with BLAST with best hit result to *Norovirus* GII (gene nucleotide sequence 98% identity). A phylogenic tree was constructed by using clustalX and the neighbor-joining algorithm, with 1000 replicate based on the capsid protein of all genogroup of human and animal NoVs (GI to GV). The phylogenetic analysis allowed grouping two strains in genogroup II, along with other already characterized. This genogroup is associated to human and swine host, and recently was detected as contaminant in groundwater. In conclusion, this study demonstrates the occurrence of NoV to infect free-living jaguars, suggesting the presence of NoV in the wild environment.

Palavras-chaves: RNA Virus, wild animal, RT-PCR, Felidae

Agencia de Fomento: CAPES