All horse "hepatitis viruses" are detected in Brazil: search for the novel equine parvovirus-hepatitis (EqPV-H)

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The horse "hepatitis viruses" have been studied in Brazil since 2013, with the description of infections by equine hepacivirus (*Hepacivirus A*, EqHV), equine pegivirus (*Pegivirus E*, EPgV) and the Theiler's disease associated-virus (*Pegivirus D*, TDAV). The equine parvovirus-hepatitis (*Ungulate copiparvovirus 6*, EqPV-H), recently identified in association with serum hepatitis in horses (also known as Theiler's disease), has been so far described in horses from North America, Asia, and Europe. The aim of this study was to investigate the presence of the EqPV-H in horses grouped according to previous status of infection: known to be positive for one or more horse "hepatitis viruses" and known to be negative. Viral DNA was screened by a nested-PCR directed to the NS1 gene, serum biochemical parameters (AST, GGT and GLDH) were evaluated in positive horses and molecular characteristics of the isolates were analyzed by DNA sequencing and phylogenetic analysis. The population studied was composed of 96 horses from 15 farms in Rio de Janeiro state, Brazil. Fifty-seven horses (group i) were known to be positive for at least one of the following viruses: EqHV, EPgV and TDAV, while the remaining 39 were negative (group ii). EqPV-H DNA was detected in 12.5% (12/96) of horses from 46.6% (7/15) of the farms. Detection rates were similar in both groups, i and ii, respectively: 12.3% (7/57) and 12.8% (5/39). Coinfection with EPgV was the most frequent (5/7). Both EqHV-positive (3/21) and EPgV-positive (5/35) horses presented 14.3% EqPV-H DNA. Means of AST (± 307.5 UI/L) and GLDH (± 4.7 U/L) activity levels were within the reference range. However, three animals presented a mild (± 1.2-fold) increase of the AST levels, with concomitant increased GGT levels. The nucleotide identity range between Brazilian isolates and the EqPV-H isolates from China, the USA, and Austria was 94.6% – 99.7%. The nucleotide identity range between Brazilian isolates was 95.7% – 99.7%. The phylogenetic tree constructed with all EqPV-H available sequences in the GenBank database (354 bp) showed two clades (posterior probability, pp = 1), one composed of Brazilian isolates and the other composed of interspersed isolates described here, and those from China, the USA, and Austria. In conclusion, this is the first report of EqPV-H in Brazil; infection rates were similar to those found in other countries and between horses previously tested positive for another "horse hepatitis" virus and horses known to be negative. Altered serum biochemical parameters suggested a subclinical hepatopathy in

some animals, but the majority presented no clinical or laboratory signs of infection. Molecular evaluation demonstrated low genetic diversity. This study encourages more research on virus distribution and genome analysis. More importantly, a broad investigation of virus-associated hepatitis cases in Brazil must be conducted.

Financial support: CNPq (IC), CIEE-Fiocruz (IC), IOC-Fiocruz.

Acknowledgments: Plataforma Genômica – Sequenciamento de DNA-RPT01A-PDTIS/FIOCRUZ.