

## Hepatitis viruses: prevalence of equine parvovirus-hepatitis virus and equine hepacivirus in France and Australia

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► **To cite this version:**

Christine Fortier, Charlie El-Hage, Erika Hue, Gabrielle Sutton, Christel Marcillaud Pitel, et al.. Hepatitis viruses: prevalence of equine parvovirus-hepatitis virus and equine hepacivirus in France and Australia. 11th International Equine Infectious Diseases Conference, Sep 2021, On line, France. pp.68-0103, 10.1111/evj.103\_13495 . hal-03362318

**HAL Id: hal-03362318**

**<https://hal-normandie-univ.archives-ouvertes.fr/hal-03362318>**

Submitted on 13 Oct 2021

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### 103 | Hepatitis viruses: prevalence of equine parvovirus-hepatitis virus and equine hepacivirus in France and Australia

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**Background:** Recent identification of viruses considered responsible for Theiler's disease (acute hepatitis) in horses include equine parvovirus-hepatitis (EqPV-H) and the most likely of several flaviviruses, equine hepacivirus (EqHV). Both of these viruses have now been detected in North America, Asia, and Europe.

**Objectives:** To determine the prevalence of EqPV-H and EqHV in French and Australian horses and to analyse their respective phylogenetic relationships.

**Study design:** Cross-sectional.

**Methods:** Clinically documented sera from 188 Australian horses and 259 French horses collected between 2016-2019 were analysed. qPCRs validated according to the NF47-600 standard were used to detect EqPV-H and EqHV in sera. Sequencing for phylogenetic analysis was performed on two NS1 fragments (516 nt and 587 nt) for EqPV-H and one NS5B fragment (308 nt) for EqHV. A phylogenetic network was built using a Median Joining Network algorithm.

**Results:** 1) EqPV-H: 12/259 (4.6%) and 6/188 (3.2%) samples from French and Australian horses were positive, respectively. Viral loads ranged from 2.3e05 to 6.5e05 copies genome/ml. 2) EqHV: 5/259 (1.9%) and 21/188 (11.2%) samples from French and Australian horses were positive, respectively. Viral loads ranged from 6.1e04 to 1.4e08 copies genome/ml. Both EqPV-H (587 nt fragment) and EqHV phylogenetic analyses showed that Australian strains were clustered, while overall distribution was more heterogenous in French horses.

**Main limitations:** The study population is built by accessing laboratory submissions and potentially biased. The 516 nt NS1 fragment could not be sequenced.

**Conclusions:** This is the first report of EqPV-H detection in both Australian and French horses. The EqPV-H prevalence was similar between the two countries (p-value=0.6) although phylogenetic differences were observed between the two populations. This is also the first reported detection of EqHV in Australian horses, with a higher prevalence when compared with French horses.

**Ethical animal research:** Research ethics committee oversight not currently required by this journal: the study was performed on archived material collected previously during clinical procedures.

**Informed consent:** Explicit study consent was not stated but owners were aware that samples could be used for research activities.

**Competing interests:** None declared.

**Source of funding:** RESPE programme 2018\_pegRESPE.

### 104 | Equine parvovirus-hepatitis screening in equines with histopathological liver abnormalities

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**Background:** There is strong evidence that equine parvovirus-hepatitis (EqPV-H) is associated with the onset of Theiler's disease, a potentially life-threatening fulminant hepatic necrosis. The virus has been detected in serum and liver tissues of affected horses. Recently, hepatotropism and persistence of viral nucleic acids in different tissues were reported. The relationship of EqPV-H to other hepatopathies beside Theiler's disease is still unknown.

**Objective:** The aim of this study was to evaluate the prevalence and to quantify the viral load of EqPV-H in equine livers with histopathologic abnormalities.

**Study design:** Retrospective case series.

**Methods:** Equine livers were retrospectively selected from archived, formalin-fixed, paraffin-embedded tissue samples, assigned to different groups according to their histopathologic abnormalities and screened for the presence of EqPV-H. EqPV-H was monitored by quantitative PCR. Positive samples were subjected to viral load determination by digital PCR.

**Results:** In total, 92 livers were included in the study and assigned to the following groups: hepatitis/cholangitis (n = 24), cirrhosis (n = 5), primary or secondary neoplasia (n = 20), metabolic/toxic disease (n = 14), congestion (n = 4), mixed abnormalities (n = 17) and normal livers (n = 8). Two out of 92 livers tested positive for EqPV-H nucleic acid and contained 3,000 and 7,000 genome equivalents per million cells according to digital PCR. Both samples originated from horses diagnosed with abdominal neoplasia and liver metastasis.

**Main limitations:** Due to the retrospective design of the study, numbers of included livers were only moderate and sizes of the histopathologic groups not identical.

**Conclusion:** EqPV-H could be detected in two livers originating from horses with abdominal neoplasia. The amount of viral nucleic acids counted would indicate rather a chronic infection or persistence of EqPV-H. In summary, this study did not provide evidence for EqPV-H being involved in other hepatopathies than Theiler's disease.