

SUMMARY

Viral hepatitis recently gained relevance in the veterinary medicine because of the variety of new viruses discovered. Equine Hepacivirus (EqHV) is an RNA virus of the *Flaviviridae* family which can cause subclinical hepatitis in horses and, occasionally, evolves in a chronic disease. EqHV was identified worldwide, therefore it is highly important to study its characteristics, especially in function of the wide use of blood products and transfusions carried out in veterinary practices.

The goal of this study is to evaluate the presence of the virus in Italy estimating the prevalence of the infection and conduct a molecular characterization of the detected viruses. A sample of 1801 horses was collected, stratified per region and production category (Equestrian, Competition, Reproduction, Production/Meat/Work) based on the total number of equids premises registered in the National Data Base. Among the 77 samples positive to the Real Time PCR, those with a $CT \leq 30$ were selected and subjected to an RT-PCR. The eligible samples (35) were then analysed by Sanger sequencing and the sequences obtained were used for the phylogenetic analyses. The sequences obtained belonged to the 3 subtypes described previously in literature and homogeneously distributed both geographically and within production categories. This study demonstrates that this virus is evenly distributed on a national level, due to the uncontrolled movement of equidae. Furthermore, it is recommended that it should be included in laboratory diagnostic protocols for hepatic diseases. The data obtained also confirms the need to include this virus in the sanitary protocols for the control of equids that are used as blood donors or employed for the production of

haemoderivatives. The polymorphisms detected also confirm EqHV as being the Hepacivirus closest to the Hepatitis C virus (HCV) of humans.

Key words: Hepacivirus; equids; virological prevalence, phylogenesis