



LETTER TO THE EDITOR

New virus discovered in blood supply: *Human hepegivirus-1* (HHpgV-1)



Nuevo virus descubierto en los bancos de sangre: *Hepegivirus humano-1* (HHpgV-1)

Dear Editor,

I wish to provide some perspective from the viral community with regard to a recent article published by the American Society for Microbiology in the medical journal *mBio*. The research group led by Amit Kapoor discovered a virus that shares features with hepatitis C virus (HCV) and human pegivirus (HPgV; formerly known as GB virus C or hepatitis G virus)¹; both of them, members of the family *Flaviviridae*. The new virus, named human hepegivirus-1 (HHpgV-1) is a blood-borne virus that was found in serum samples from two blood transfusion recipients and two hemophilia patients that received blood-derived products.

Since HPgV, Torque teno virus (or transfusion-transmitted virus, TTV), TTV-like minivirus (TLMV) and SEN virus (SENV) were discovered in the years 1995, 1997 and 2000 respectively, no more transfusion-associated virus has been described so far. Furthermore, many cases of post-transfusion hepatitis of unknown etiology still occur among blood recipients. If HHpgV-1 is going to be a significant cause of human hepatitis, nobody knows. What it is known is that most HPgV infections are asymptomatic, transient and self-limiting². In contrast, chronic infection by HCV is a problem of health concern of extraordinary magnitude, that represents the most common cause of many costly and morbid complications including liver cirrhosis, end-stage liver disease and liver transplantation^{3,4}.

I would like to shed some more light on the implications associated with the new blood-borne virus discovered. Blood transfusions have been and continue to be a valuable way to save lives and improve health. Only in the United States, more than 300 million blood components are transfused every year. However, a myriad of agents

can potentially be transmitted by this way. HHPgV-1 should be added to the list of virus that may be studied at Hemotherapy Services. Therefore, epidemiological research works from different parts of the world are really essential for gaining insight into the prevalence and characteristics of this novel blood-borne virus. Once available, such information will be extremely valuable both for designing new assays for its detection as well as for avoiding false negative results when screening its presence in blood donors. Surveillance of the different agents that may potentially be transmitted by blood is mandatory to ensure the safety of this valuable resource for medicine and public health.

Finally, as the field of molecular biology advances, the discovery of new viruses raises the need for a valid set of criteria to verify that exists a causal relationship between the presence of certain viruses and a specific disease, or even if its presence is associated to poorer prognosis of liver disease in those patients co-infected with hepatotropic viruses such as hepatitis B virus (HBV) or HCV or between the presence of this newly identified virus and its pathogenic evolution in human immunodeficiency virus (HIV)-infected patients, just to mentioned some examples. The investigation of the prevalence and impact of coinfections with HHpgV-1 and known hepatitis viruses or HIV would provide additional information for the assessment of the relationship between this novel virus and disease.

So far, the two most relevant findings with potential medical impact were the persistent long-term HHpgV-1 viremia in two hemophilia patients and, the genetic similarity among HHpgV1 with both highly pathogenic HCV and the apparently nonpathogenic HPgV¹.

References

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