

Hepatitis G virus RNA positivity among the voluntary blood donors: a summary

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Abstract

Hepatitis virus infection is an increasing problem. Millions of humans all over the world are infected. Viral hepatitis is accepted as a significant public health problem with several life altering complications. Recently, new viruses have been identified for their association with hepatitis. Hepatitis G virus (HGV) is a single stranded RNA virus which represents a newly discovered virus belonging to the flavivirus family. Epidemiological data indicate that the virus is transmitted via blood/blood products, sexually and vertically from infected mothers to children. There are some previous reports on the prevalence of HGV infection among the blood/blood products. The purpose of this study is to summarize the prevalence of HGV infection, defined as HGV RNA positivity, among the voluntary blood donors in the previous reports. Due to this study, there have been at least 30 reports. Of 13,610 documented voluntary donors, there are 649 cases with HGV RNA positivity. The summative percentage for HGV RNA positivity is 4.8%: 4.5% in Caucasian, 3.4 % in Asian and 17.2% in Negroid. There is no significant association between ethnicity of donors and prevalence of HGV RNA positivity ($p > 0.05$). The HGV infection seems to distribute in all ethnicities all over the world, implying the global importance of this hepatitis virus infection. Screening for HGV RNA might be an important test in blood bank process in the future.

Key words: HGV, prevalence, blood donor.

Introduction

Hepatitis virus infection is an increasing problem. Millions of humans all over the world are infected. It is accepted as a significant public health problem with several life altering complications. Five viruses are usually associated with hepatitis in humans: hepatitis A virus, hepatitis B virus, hepatitis C virus, hepatitis D virus and hepatitis E virus.¹ In addition to these viruses, Sehgal and Sharma said that there remained a number of patients with hepatitis in whom no virus could be identified and it was therefore postulated that there might be other agents, which might cause hepatitis.¹ Recently, new viruses have been identified for their association with hepatitis. Hepatitis G virus (HGV) is a single stranded RNA virus which represents a newly discovered virus belonging to the flavivirus family.¹ Firstly, hepatitis G virus (HGV) and GB virus type C (GBV-C) were independently discovered, however, it was later determined that they were two isolates of the same virus.²

HGV replicates in peripheral blood cells, while replication in liver cells has not been observed till date.¹⁻² Diagnosis of HGV viremia is mainly by polymerase chain reaction (PCR). Epidemiological data indicate that the virus is transmitted via blood/blood products, sexually and vertically from infected mothers to children.² There are some previous on the prevalence of HGV infection among the blood/blood products. The purpose of this study is to summarize the prevalence of HGV infection, defined as HGV RNA positivity, among the voluntary blood donors in the previous reports.

Materials and methods

This study was designed as a descriptive retrospective study. A literature review on the papers concerning HGV infection, given definition as positive for HGV RNA or viremia, among the voluntary blood donors was performed. The author performed the literature review from database of the published works cited in the Index Medicus and Science Citation Index. The literature review was focused till August 2004. The reports without complete data, those not focusing on the voluntary blood donor (such as paid and commercial donors) and those lacked for English text, were excluded.

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According to the literature review, 30 available reports³⁻³² were recruited for further study. The prevalence of HGV infection from each included reports was collected. Descriptive statistics, including range and percentage, were used in summative analysis. In meta-analysis, pooled prevalence from all reports was calculated. Pooled prevalence for each ethnic group (Caucasian, Asian and Negroid) was also determined. In addition, Chi Square test was performed to assess the association between ethnicity of the subjects and prevalence of infection. All the statistical analyses in this study were made using SPSS 7.0 for Windows Program.

Results

Due to this study, there have been at least 30 reports³⁻³² (Table I). Of 13,610 documented voluntary donors, there are 649 cases with HGV RNA positivity (Table I). The summative percentage for HGV RNA positivity is 4.8%: 4.5 % in Caucasian, 3.4% in Asian and 17.2% in Negroid (Figure 1). There is no significant association between ethnicity of donors and prevalence of HGV RNA positivity ($p > 0.05$).

Discussion

HGV is a newly discovered hepatitis virus.¹⁻² Infection with this virus is common and frequently persists in humans.¹⁻² Similar to many hepatitis viruses, transfusion of viremic blood/blood product can be the route of this viral infection. Luckily, HGV infection is not detected to associate with serious manifestation because this virus is not strongly associated with acute or chronic hepatitis.¹⁻³ Further researches for the possible diseases caused by this viral infection have been continuously performed.

Although it seems to be rather unlikely, it still remains unclear whether hepatitis G virus (HGV) is involved in post-transfusion hepatitis.³³ Hitzler and Runkel said that transmission of HGV by blood components did occur and persistence of HGV viremia was common.³³ Halarsz *et al* noted that recent data indicating that HGV infection might infect as well as replicate in hepatocytes and might lead to some presently unknown long-term complications.³⁴ Screening for HGV RNA in the donated blood can be a good tool to detect viremia and prevent for HGV transmission by blood transfusion.³⁵⁻³⁷ Although the HGV contamination in blood and blood products is already known

Table I. Reports on the prevalence of HGV infection among the voluntary blood donors.

| Author | Setting* | Number of donors | Rate of HGV RNA positive (%)** |
|---------------------------------------|---------------------------------|------------------|--------------------------------|
| Stark <i>et al</i> ³ | Germany ¹ | 90 | 2 |
| Orito <i>et al</i> ⁴ | Japan ² | 200 | 0.5 |
| Hwang <i>et al</i> ⁵ | Taiwan ² | 66 | 3 |
| Jongerius <i>et al</i> ⁶ | The Netherlands ¹ | 250 | 1.2 |
| Tacke <i>et al</i> ⁷ | Germany ¹ | 80 | 2.5 |
| Levi <i>et al</i> ⁸ | Brazil ¹ | 545 | 9.7 |
| Jeon <i>et al</i> ⁹ | Korea ² | 110 | 1.8 |
| Oliveira <i>et al</i> ¹⁰ | Brazil ¹ | 241 | 7.1 |
| Yan <i>et al</i> ¹¹ | China ² | 203 | 15.8 |
| Yu <i>et al</i> ¹² | Taiwan ² | 500 | 3.4 |
| Nordbo <i>et al</i> ¹³ | Norway ¹ | 1,001 | 2.5 |
| Al-Ahdal <i>et al</i> ¹⁴ | Saudi Arabia ² | 200 | 2 |
| Brojer <i>et al</i> ¹⁵ | Poland ¹ | 219 | 3.2 |
| Love <i>et al</i> ¹⁶ | Iceland ¹ | 370 | 3.8 |
| Oubina <i>et al</i> ¹⁷ | Argentina ¹ | 200 | 5.5 |
| Konomi <i>et al</i> ¹⁸ | Bolivia ¹ | 574 | 14.6 |
| Cesaire <i>et al</i> ¹⁹ | French West Indies ¹ | 221 | 4.1 |
| Sathar <i>et al</i> ²⁰ | South Africa ³ | 232 | 18.9 |
| El-Zayadi <i>et al</i> ²¹ | Egypt ³ | 354 | 16.1 |
| Sauleda <i>et al</i> ²² | Spain ¹ | 2,210 | 1.9 |
| Cantaloube <i>et al</i> ²³ | France ¹ | 1,660 | 2.6 |
| Minton <i>et al</i> ²⁴ | UK ¹ | 100 | 1 |
| Blair <i>et al</i> ²⁵ | UK ¹ | 1,020 | 2.25 |
| Hyland <i>et al</i> ²⁶ | Australia ¹ | 565 | 13.3 |
| Wang <i>et al</i> ²⁷ | Taiwan ² | 1,500 | 2.1 |
| Lampe <i>et al</i> ²⁸ | Brazil ¹ | 87 | 10 |
| Shev <i>et al</i> ²⁹ | Sweden ¹ | 62 | 22 |
| Prati <i>et al</i> ³⁰ | Italy ¹ | 200 | 1.5 |
| Loiseau <i>et al</i> ³¹ | France ¹ | 500 | 4.2 |
| Wu <i>et al</i> ³² | Japan ² | 50 | 2 |

*Ethnicity of the donor:¹ means Caucasian, ² means Asian and ³ means Negroid.

** In all studies, HGV infection was determined by reverse transcription polymerase chain reaction (RT-PCR) for RNA.

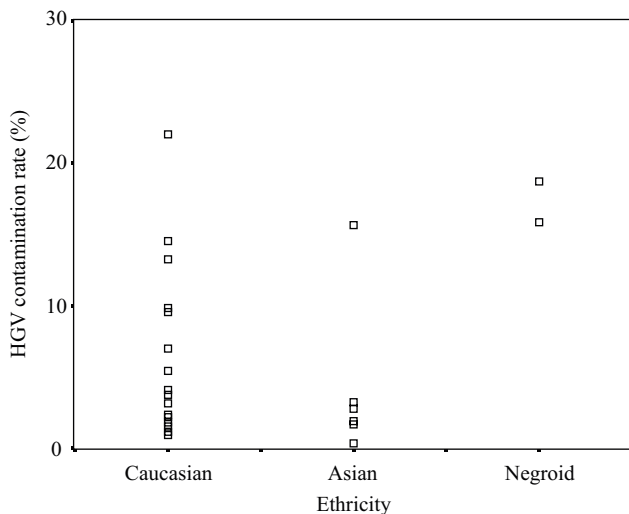


Figure 1. The prevalence of HGV RNA positivity in different ethnics.

there is no appraisal on its global distribution. No assessment for the pattern of HGV infection in donors from different ethnics is performed. Indeed, the ethnical predominance of viral hepatitis, very high prevalence of hepatitis B infection among Asian as an example, is mentioned.³⁸

Here, the author reports the summative prevalence of HGV RNA positivity from screening of voluntary blood donors. The prevalence of HGV viremia in this study is about 5%. Of interest, the rates of viremia are similar between the Caucasian and Asian, but the rate is higher among the Negroid. However, there is no significant association between ethnicity and positivity. The HGV infection seems to distribute in all ethnicities all over the world, implying the global importance of this hepatitis virus infection. Screening for HGV RNA might be an important test in blood bank process in the future.³⁵⁻³⁷

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