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Human Pegivirus (HGV) Prevalence among Blood Donors in Burkina Faso: New Data after 2013

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Abstract

Introduction: Human pegivirus (HPgV), initially identified as hepatitis G virus in the 1990s, predominantly causes acute hepatitis and may persist particularly in individuals with compromised immune systems or those co-infected with HIV, HBV, or HCV. Despite its potential public health implications, particularly in transfusion contexts, comprehensive epidemiological data on HPgV in Burkina Faso remains scarce. **Objectives:** This study aimed to determine 1) the prevalence of human pegivirus infection among blood donors at the Regional Blood Transfusion Centre (Koudougou, Burkina Faso), and 2) the rates of co-infection between human pegivirus with HIV, HBV, HCV and *Treponema pallidum*. **Material and Methods:** Between 9 and 27 August 2022, 100 blood samples were collected and analyzed at the Regional Blood Transfusion Centre. Screening for HIV, HBV, HCV, and Treponema pallidum was conducted using the Cobas e 601 system (Roche Diagnostics). A 100 µL volume of each donor's plasma was utilized for viral RNA extraction with the DNA/RNA Prep Kit (Sacace Biotechnologies) following the manufacturer's instructions. HPgV RNA detection was conducted using the HGV Real-TM amplification kit (Sacace Biotechnologies). **Results:** The study was comprised of 100 blood donors, identifying HPgV RNA in 14 individuals (14% prevalence),

with one noted co-infection with HBV. None of the participants were HIV positive. The prevalence rates for HBV and HCV were each found to be 5%, and syphilis also presented a prevalence of 5%. **Conclusion:** Our findings indicate a significant prevalence of HPgV among blood donors in Burkina Faso, underscoring the need for heightened surveillance and preventive measures in blood transfusion services and the broader population to enhance transfusion safety and public health.

Keywords

HPgV/VHG, RT-PCR, Transfusion Safety, Burkina Faso

1. Introduction

Human pegivirus (HPgV), previously known as hepatitis G virus (HGV), was identified in the 1990s and recognized as a causative agent of hepatitis. Viral hepatitis remains a substantial public health challenge in sub-Saharan Africa, especially in Burkina Faso, where blood transfusion serves as a major transmission route for key hepatitis viruses. Although these viruses are routinely tested for during the biological qualification of blood donations in Burkina Faso, HPgV is not currently included in screening protocols, potentially posing significant risks to public health and transfusion safety because the virus has been associated with several diseases beyond hepatitis. It has been linked to pathologies such as Sjogren's syndrome, hepatocellular carcinoma, cryoglobulinemia, and various hematologic diseases [1] [2].

The discovery of HPgV is part of ongoing research into acute idiopathic hepatitis. In 1966, Deinhardt *et al.* initiated studies using South American primates, Saguinus labiatus, to test their susceptibility to human pathogens [3]. Subsequent research efforts culminated in the mid-1990s with the formal identification of this virus as Hepatitis G Virus (HGV) [4] [5]. HPgV, an enveloped virus measuring between 60 and 70 nm and containing single-stranded RNA of positive polarity, belongs to the Flaviviridae family and the Pegivirus genus [6]. It has been referred to by various names, including GBV-C and VHG, until the International Committee on Taxonomy of Viruses (ICTV) officially renamed it "Human Pegivirus (HPgV)" [7] [8].

A new taxonomy proposed in 2016 categorized eleven pegivirus species, ranging from A to K, and specifically noted HPgV type 1 (HPgV-1), differentiating it from other types such as HPgV-2 [9]. HPgV is known to be present in Hepatitis Associated with Aplastic Anemia [10]. An interesting correlation has also been observed where infection with this virus is associated with better survival outcomes in HIV-infected patients [11] [12].

Globally, HPgV affects around 750 million people, with a general prevalence of about 4% in developed nations and higher rates in developing countries [13]. In Burkina Faso, while pre-transfusion screening currently includes tests for HBV,

HCV, HIV, and Treponema pallidum (syphilis), studies in Africa, such as those conducted in Ghana and Cameroon, report HPgV prevalences of 10% among HIV-negative individuals and 9% among HCV-positive individuals, respectively [14] [15]. In Burkina Faso, a study by Tao *et al.* at the Regional Center of Blood Transfusion in Ouagadougou reported an HPgV prevalence of 7.4% among blood donors [16]. The absence of routine screening for HGV underscores the potential for uncontrolled spread within the population and represents a significant risk to transfusion safety. This study aims to describe the prevalence trend and the risk factors associated with HPgV infection among blood donors in Koudougou after that of 2013 at the Regional Blood Transfusion Center of Ouagadougou, elaborating on both the general prevalence and specific rates of co-infection with viruses such as HIV, HBV, HCV, and *Treponema pallidum*.

2. Materials and Methods

2.1. Study Design and Location

This descriptive cross-sectional study was conducted from August 2022 to March 2023. Plasma samples for virus identification were collected at the Regional Blood Transfusion Centre (RBTC), a decentralized unit of the National Blood Transfusion Centre. Viral serological data were obtained from the RBTC, while molecular analyses were performed at the Molecular Biology and Genetics Laboratory of Joseph KI-ZERBO University and the Pietro Anigoni Biomolecular Research Center in Ouagadougou.

2.2. Study Population and Sampling

The sample size was calculated using Schwartz's formula: $n = (t^2 \times p\,(1 - p))/(e^2)$, where "t" is the confidence level (1.96 for 95% confidence), p is the estimated prevalence of infection (7.4% from [16]), and e is the margin of error (5%). This calculation suggested a sample size of 105. Sampling involved the systematic collection of blood from volunteer donors at the RBTC in Koudougou, along with socio-demographic data such as age, gender, occupation, and donation frequency.

2.3. Sample Collection and Storage

Blood samples were collected in EDTA tubes and centrifuged at 800 - 1600 g for 20 minutes to obtain plasma aliquots, which were stored at −32˚C. After collection, these were transported to the Pietro Anigoni Biomolecular Research Center in a medical refrigerated cooler and stored at −70˚C for five months prior to analysis.

2.4. Serological and Molecular Diagnostics

Serological tests for HIV-1 p24 antigen, anti-HIV 1 and 2 antibodies, hepatitis B virus surface antigen (HBsAg), anti-HCV antibodies, and anti-treponemal antibodies were conducted using electrochemiluminescence on the cobas e 601 (Roche Diagnostics) at the RBTC. Molecular diagnosis for HGV was performed at the Pietro Anigoni Center. Viral RNA was extracted using the DNA/RNA Prep

Kit (Sacace Biotechnologies, Ref K-2-9) according to the manufacturer's protocol. RT-PCR for HGV detection was conducted using the HGV Real-TM kit (Sacace Biotechnologies). The PCR setup included specific volumes of reaction mixes and controls, with amplification over 45 cycles at specified temperatures. Results were interpreted using real-time PCR v7.9 software, identifying HGV cDNA by fluorochrome HEX and internal control by FAM.

2.5. Ethical Considerations and Data Analysis

The study received approval from the CERBA/LABIOGENE and the National Center for Blood Transfusion ethics committees. Confidentiality and anonymity were maintained by coding patient data. Collected data were processed using Microsoft Excel 2019, and statistical analysis was performed using Stata version 14 and Epi Info version 7.0.

3. Results

3.1. Socio-Demographic Characteristics

The participant cohort comprised 93 men and 7 women, reflecting a sex ratio of 13.28:1. The average age was 29.81 years (SD = 8.59), with the majority aged between 24 and 44 years, representing 57% of the sample. A large proportion of the donors were pupils and students (40%) (Figure 1).

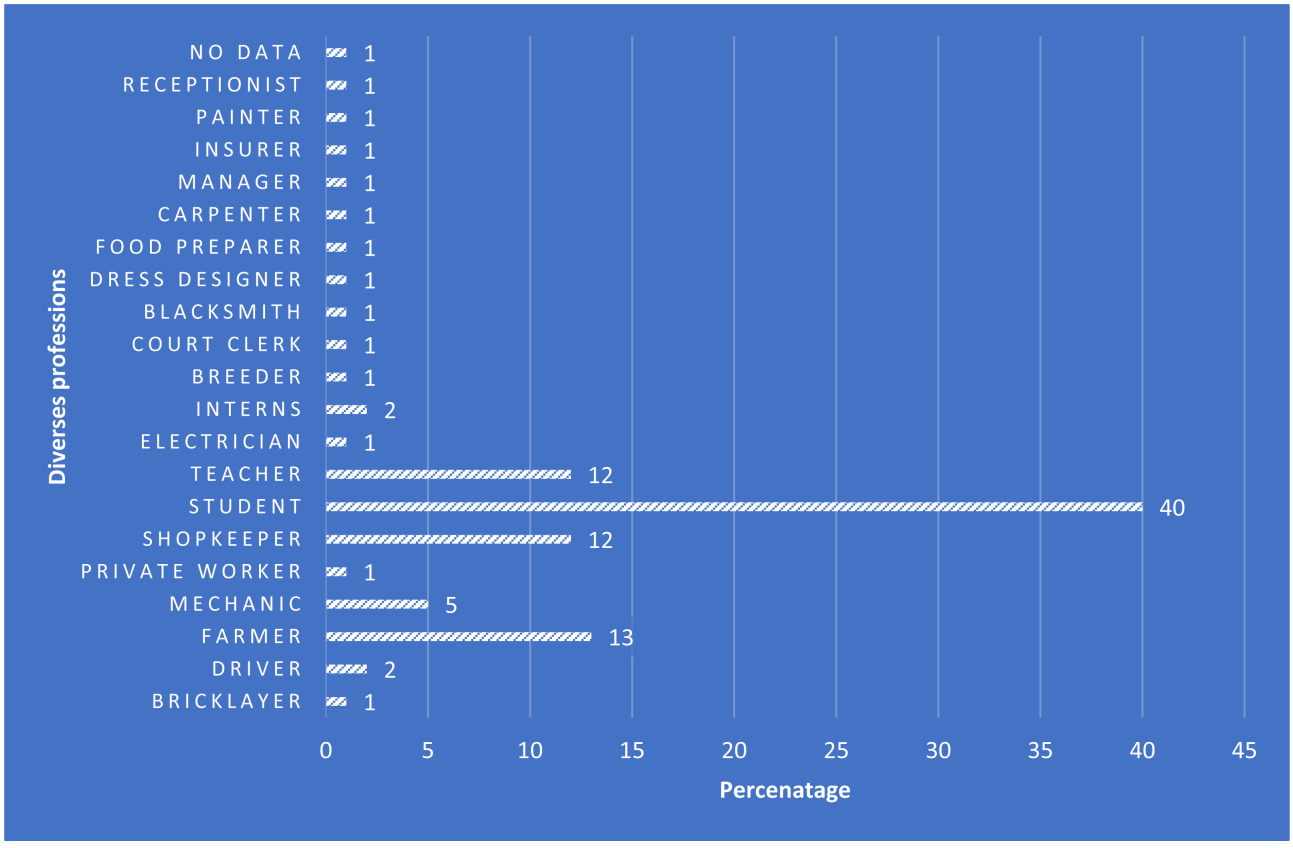

Figure 1. Breakdown of the study population by occupation.

3.2. Identification of Infectious Agents

Table 1 summarizes the results of the serological and molecular testing for HIV, Hepatitis B Virus (HBV), Hepatitis C Virus (HCV), Treponema pallidum (syphilis), and human pegivirus (HPgV, formerly HGV). The tests reveal that none of the blood donors tested positive for HIV. However, HBV and HCV both exhibited positivity rates of 5%. Syphilis showed a slightly higher prevalence at 9%. Notably, PCR testing for HPgV indicated a 14% prevalence rate of viral RNA among the samples.

Table 1. Positivity rates for tested agents.

RESULTS	HIV	HBV	HCV	SYPHILIS	RNA HGV
Positive	0	5	5	9	14
Negative	100	95	95	91	86
Total	100	100	100	100	100
% Positive	0%	5%	5%	9%	14%

3.3. Occupational Breakdown of HGV-Positive Cases

Figure 2 details the occupational breakdown of those testing positive for HGV. Among the 14 HGV-positive cases, the most frequently represented group were pupils and students, reflecting the high exposure or risk behaviors prevalent within this demographic group. This insight into occupational risk factors is critical for targeting educational and preventive measures in blood safety and public health initiatives.

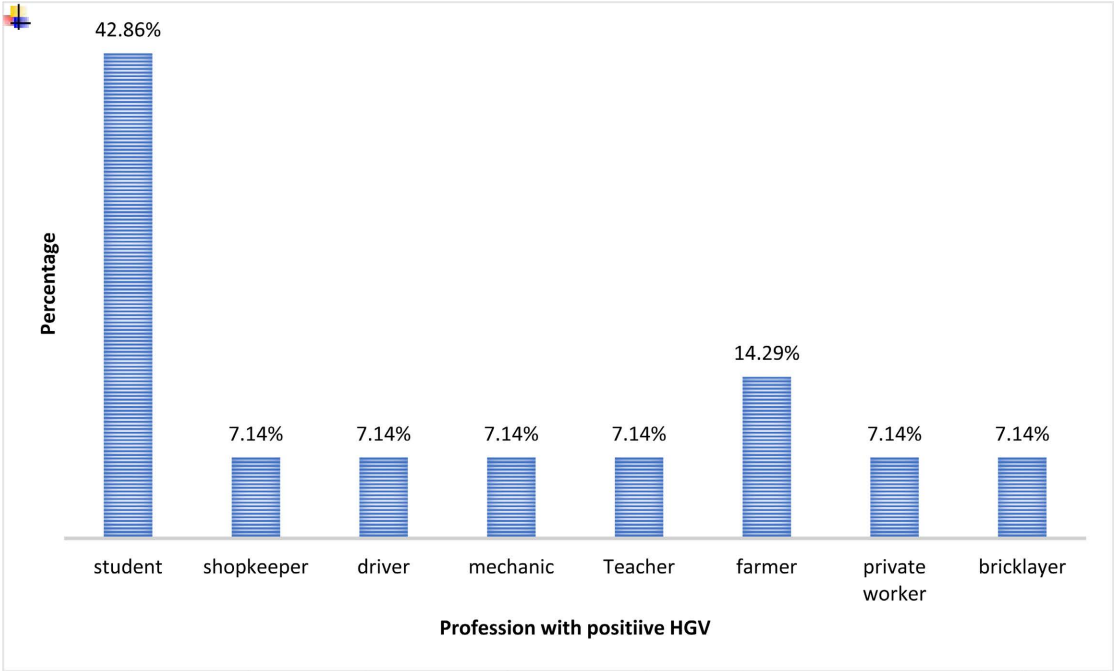

Figure 2. Representation of positive HGVs by occupation.

3.4. Co-Infection Between HPgV and Other Pathogens

The investigation into co-infections between human pegivirus (HPgV, formerly known as HGV) and other pathogens commonly screened in blood donation—HIV, Hepatitis B Virus (HBV), Hepatitis C Virus (HCV), and Treponema pallidum (syphilis)—revealed a generally low rate of co-infection. Notably, there was only one recorded case of co-infection between HPgV and HBV, which constitutes 7.14% of the HPgV-positive cases (Table 2).

Table 2. Co-infection between human pegivirus and HIV, HBV, HCV, Syphilis.

	HIV (+)	HBV (+)	HCV (+)	SYPHILIS (+)
HGV positive (n = 14)	0	1	0	0
%	0.00%	7.14%	0.00%	0.00%

4. Discussion

The primary objectives of this study were to assess the prevalence of human pegivirus (HPgV) in a cohort of blood donors in Burkina Faso and to estimate the rates of co-infection with HIV, HBV, HCV, and syphilis. Our findings contribute significant insights into the epidemiology of HPgV in this region, where blood transfusion represents a major transmission route.

The study population was predominantly male (93%), with a sex ratio of 13.28, consistent with other local studies [17]. This male predominance may be attributed to cultural and medical restrictions that limit female participation in blood donation, such as guidelines regarding menstruation, pregnancy, and breastfeeding [17]. The most represented age group was 24 - 44 years, encompassing 57% of our sample, slightly older than the 18 - 24 age group which is the largest in national reports [18].

Most literature reports HPgV prevalence rates below 5% among blood donors, with variability depending on the geographic and demographic context [19]. Our study found a relatively high prevalence of 14%, comparable to findings from other nations where prevalence can range up to 46.6% in certain high-risk groups [20] [21]. Such high prevalence underscores the potential public health implications of HPgV, particularly in settings lacking systematic screening for this virus. Co-infections between HPgV and other viruses such as HBV, HCV, and HIV are well-documented, with varying prevalence rates depending on the population and regional health dynamics [19] [22]. In our study, co-infection rates were notably low, with only one instance of HPgV/HBV co-infection detected. This could be due to the low overall prevalence of HBV within the study sample (5%). The absence of HPgV in routine blood screening protocols poses a significant risk, particularly given its high prevalence and potential for causing or exacerbating liver diseases. The study also highlights the necessity for better surveillance and possibly incorporating HPgV screening in blood donation practices.

5. Conclusion

Our results indicate a notable prevalence of HPgV among blood donors in Burkina Faso, emphasizing the need for enhanced epidemiological monitoring and potential adjustments in blood safety policies. Further studies are required to explore the genotypes of HPgV circulating locally and their specific clinical impacts. Although statistically valid, the size of the study population may constitute a limit, also, a larger cohort studies could elucidate the potential protective effects of HPgV co-infection in HIV-positive individuals, as suggested by previous research and strengthen epidemiological knowledge of the virus.

6. Recommendations

To address the gaps in current knowledge and improve transfusion safety, it is advisable to undertake comprehensive studies with larger sample sizes and extended demographic representations. Genotyping of HPgV should also be considered to tailor prevention and treatment strategies more effectively.

This discussion integrates our findings with broader epidemiological data and suggests pathways for future research, reflecting the global and local importance of understanding HPgV in the context of transfusion medicine and public health.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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