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Genetic variability of human pegivirus type 1 (HPgV-1) among Congolese co-infected with hepatitis C virus in Brazzaville, Congo ☆

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ABSTRACT

The aim of this study was to determine the rate of human pegivirus type 1 (HPgV-1) and hepatitis C virus (HCV) co-infection, and the genotype distribution of HPgV-1 among patients with chronic hepatitis C and blood donors in Brazzaville. Two groups of patients in Brazzaville were recruited: blood donors ($n = 35$) and individuals with chronic hepatitis C ($n = 73$). The overall positivity rate of HPgV-1 was 4.63%: 2.86% in blood donors and 5.48% in chronic hepatitis C patients. Phylogenetic analysis showed that all samples were genotype 1. However, studies with a larger sample size are needed to estimate the true burden of HPgV-1 infection in the country and to confirm the distribution of genotypes in the general population.

Human pegivirus type 1 (HPgV-1) is frequently found in carriers of blood-borne viruses such as hepatitis C virus (HCV). Unlike HCV, HPgV-1 is lymphotropic, and it appears to influence the course of the disease in patients co-infected with HCV or hepatitis B virus (HBV). HPgV-1 is mainly transmitted parenterally, sexually, or perinatally. In addition, this virus is prevalent in high-risk groups, such as people undergoing hemodialysis, those with hemophilia, HIV- or HBV-infected patients, intravenous drug users, and carriers of HCV markers [1]. In developed countries, 1–5% of healthy blood donors are viremic at the time of blood donation [2]. In developing countries, the prevalence of HPgV-1 is higher, sometimes reaching 20% [3], particularly among HCV-positive individuals and those living with HIV (20–40%) [4]. These data, combined with studies of blood donors, suggest that at least a quarter of the world's population carries HPgV-1 [5].

Phylogenetic analyses of HPgV-1 strains have identified seven genotypes whose prevalence varies according to the geographical area. Genotype 1 is more prevalent in sub-Saharan Africa, genotype 2 in the United States and Europe, genotypes 3 and 5 in Asia and Africa [3,6,7,8], genotype 4 in Asia, and genotype 6 in Indonesia. The available data show the predominant circulating genotype to be genotype 1.

HCV prevalence rates of up to 6% have been documented in the Republic of Congo [9], suggesting active HPgV-1 circulation. Thus, the main objective of this study was to determine the rate of HPgV-1 and HCV co-infection, as well as the distribution of HPgV-1 genotypes among chronic HCV-infected patients and blood donors in Brazzaville.

HCV-positive samples from blood donors and chronic hepatitis C patients were collected at the National Public Health Laboratory between April and September 2021. After RNA extraction using the QIAamp RNA Kit (Qiagen, Germany), HPgV-1 RNA was amplified by nested RT-PCR following the protocol developed by Katayama et al. [10]. A fragment of the 5′ untranslated region (UTR) of 158 bp was generated, sequenced, and phylogenetically analyzed using the maximum likelihood method [1–10].

A total of 108 samples were collected, 35 from blood donors and 73 from patients with chronic hepatitis C. Of the 108 samples, 58 were from females (53.7%) and 50 from males (46.3%) . The most represented age group in the study population was 18–30 years (45.4%), followed by 33–47 years (22.4%), 48–62 years (20.6%), and >62 years (11.6%). The mean age of this population was 40.76 ± 16.43 years.

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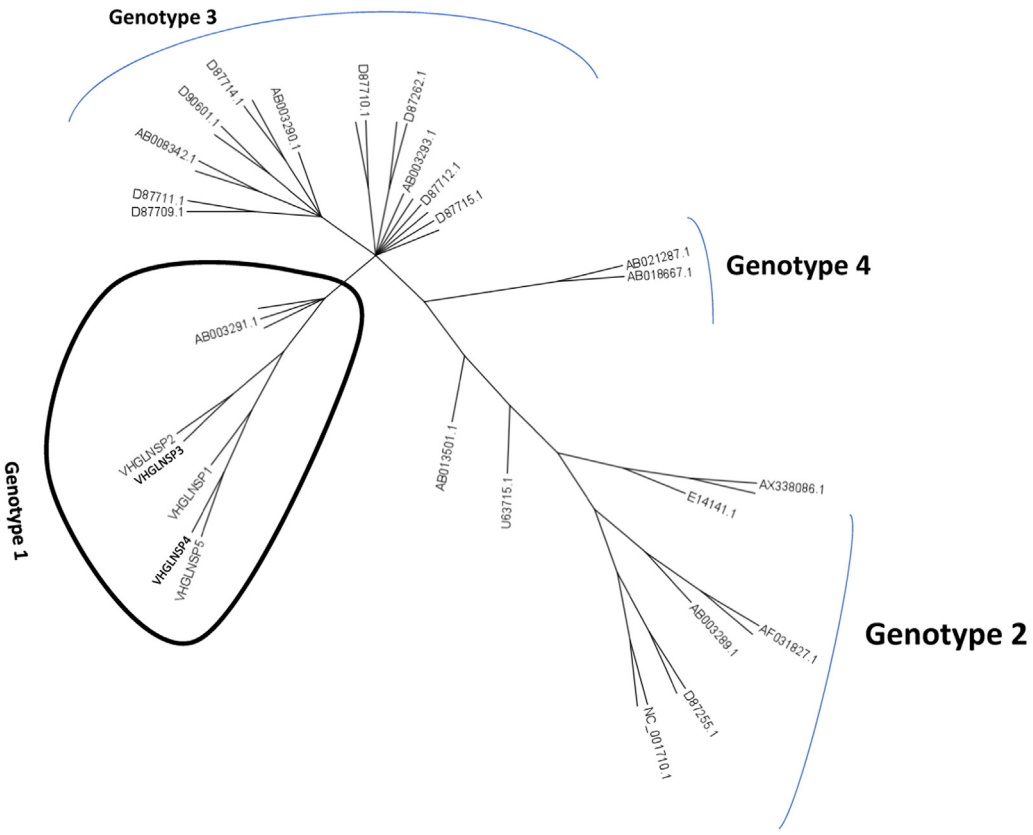

Figure 1. Phylogenetic tree of the 5′UTR region sequences of pegivirus type 1.

The overall positivity rate of HPgV-1 was 4.63% (5/108), with one blood donor (1/35, 2.86%) and four chronic hepatitis C patients (4/73, 5.48%) being positive . Out of the five HPgV-1-positive samples, three were from females and two were from males. The most affected age group was 33–47 years (three of the positives). Phylogenetic analyses of the study strains showed them to be genotype 1, as shown in Figure 1.

This study found a positivity rate of 4.63% in blood donors and chronic hepatitis C patients, comparable to the rates reported in various study populations in some African countries, which have shown prevalence rates generally between 1% and 17% [3]. Although no statistical significance was found in the current study, factors such as age and sex may be associated with a predisposition to infection or co-infection [8].

One genotype of HPgV-1 was found in the current study, i.e. genotype 1, confirming the data available in the literature. However, taking into account the limited study site and number of samples, as well as the size of the fragment analyzed, it is important to extend this study to the national level to increase the sample size and also to analyze the complete genome of these strains, in order to identify points of recombination and evolution of these strains.

Conflict of interest

The authors declare no conflict of interest.

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Ethical approval

The study was conducted after obtaining ethical clearance from the Comité d'Ethique pour la Recherche en Sciences de la Santé (CERSSA) of the Ministère de la Recherche et de l'Innovation Technologique (N°343/MRSIT/IRSSA/CERSSA). Interviews were conducted in private to ensure the confidentiality of the information collected in accordance with the Declaration of Helsinki (WMA, World Medical Association).

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