Co-Infection Of HPgV And HIV In A Nigerian Population: An Epidemiological Analysis

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ABSTRACT
PLWHIV in Northeast Nigeria were investigated for the prevalence of infection and to identify risk factors associated with HPgV infection, given the potential impact of HPgV on HIV disease progression. In Northeast Nigeria, we conducted a cross-sectional study of 249 PLWHIV. We used bivariate and multivariate logistic regression models to assess the association between HPgV infection and sociodemographic characteristics, risk behaviors, and healthcare access. 23.3% of the study population had HPgV infection. In the multivariate analysis, inhaled drug use was associated with HPgV infection. In Northeast Nigeria, there is a concerning prevalence of HPgV infection among PLWHIV. A potential transmission route beyond traditional routes is suggested by the identification of inhaled drug use as a risk factor. To address this significant public health concern, targeted interventions and harm reduction strategies are necessary.

KEYWORDS: HIV; Human Pegivirus 1; HPgV; Co-Infection; Prevalence; Public Health.

ABBREVIATIONS: PLWHIV: People Living with HIV; PLWHA: People Living with HIV/AIDS; HPgV: Human Pegivirus 1; HIV: Human Immunodeficiency Virus.

1. INTRODUCTION

An RNA virus belonging to the Flaviviridae family, HPgV-1 has a genome of approximately 9400 nucleotides [1,2]. While HPgV isn't associated with specific diseases, research indicates that CD4+ lymphocyte count is correlated with HIV infection, which may influence HIV infection progression. HPgV's viral influence on lymphocyte counts in co-infected individuals has been linked to a slower progression of HIV infection [3,4], and co-infected patients have been shown to experience a decrease in morbidity and mortality [3,5]. Moreover, prior HPgV infection of lymphocytes can inhibit HIV replication, which may contribute to the observed slower progression of HIV infection [1].

Several studies [6-8] have examined HPgV prevalence among PLWHA and found that it varies by region. It has been observed that regional development and prevalence are inversely related [9-11]. According to studies, HPgV-1 monoinfection is common in parts of North America and Europe, with a prevalence of 1% to 4%, while it is common in parts of Africa, Asia, and South America, with a prevalence of 5% to 19% [12]. In some regions of Nigeria, researchers have reported high HIV/HPgV prevalence rates, ranging from 17% in the North to 34% in the South [13, 14].

This study was conducted in order to estimate the prevalence of HIV/HPgV co-infection and identify the associated risk factors. A specific goal of our study was to examine the influence of HPgV infection on HIV disease progression, as well as the demographics and clinical characteristics of co-infected individuals. To enhance future research and contribute to the development of more effective prevention and treatment strategies for HIV/HPgV co-infection, we examined these factors to provide a comprehensive understanding of the epidemiology of HIV/HPgV co-infections in a Nigerian Northeastern state.

2. METHOD(S)

The study recruited 249 HIV-positive individuals aged 18 and over who received care at the University of Maiduguri Teaching Hospital. Our study was conducted during routine outpatient visits with these patients. An informed consent questionnaire was used to collect comprehensive information about sociodemographic characteristics, sexual behavior, and potential transmission routes from those who provided informed consent.

Blood samples were collected from participants during routine laboratory examinations. Upon receipt of these samples, we immediately transported them to the Virology Laboratory at the University of Maiduguri Teaching Hospital. We separated the plasma and serum and stored them at -80°C for future analysis.

At the University of Maiduguri Teaching Hospital's Clinical Virology Laboratory, we conducted HPgV research. Axygen Miniprep Kit was used to extract RNA from plasma samples, strictly following the manufacturer's instructions. According to Sousa *et al*. [15], we used the AgPath-IDTM One-Step RT-PCR Kit to perform reverse transcription real-time polymerase chain reaction assays. It contained a 5 µL sample, 0.4 µM forward and reverse primers, and 0.15 µM probe. In the PCR cycle, the initial cycle was conducted at 50°C for 10 minutes and the second cycle at 95°C for 10 minutes, followed

by 45 cycles of 15 seconds at 95°C and 40 seconds at 60°C.

HPgV infection is associated with HIV infection based on odds ratios and confidence intervals, chi-square tests, and Fisher's exact tests. Our first step was to conduct a bivariate analysis to pinpoint potential variables associated with HPgV infection. Based on a bivariate analysis, various demographic, behavioral, and clinical factors were evaluated in relation to the presence of HPgV infection. Following the bivariate analysis, variables with p-values less than 0.2 were included in the multivariate analysis. Using the forward stepwise logistic regression method, we developed a predictive model for the presence of HPgV, allowing us to assess the independent effects of each variable while controlling for potential confounding factors. All statistics were generated using Jamovi software version 2.3.28.

3. RESULTS

PLWHIV were reported to have 23.3% HPgV RNA in their blood. This population's sociodemographic factors, sexual behavior variables, blood transmission and HPgV infection were examined in a univariate analysis.

Using bivariate analysis, we included age, with a p-value of 0.039, in the initial logistic regression model. Our next step was to add the remaining variables to the model in ascending order of their p-values, ensuring that the age variable remained statistically significant throughout the entire model-building process.

Nine variables were identified as predictors of HPgV presence in the forward stepwise logistic regression analysis: age, piercing, inhaled drug use, income, and history of surgery. Model fit was acceptable ($\chi2=24.7$, df=9, p=0.003) and explained 14.3% of the variance in HPgV presence (Nagelkerke R2=0.143). It was found that omnibus likelihood ratio tests showed significant correlations between HPgV presence and age ($\chi2=7.51$, df=3, p=0.057), piercing ($\chi2=8.45$, df=1, p=0.004) and inhaled drug use ($\chi2=6.56$, df=1, p=0.010). A multivariable model did not find an association between surgery history and HPgV presence ($\chi2=2.41$, df=2, p=300).

For each variable, the estimated coefficients, standard errors, odds ratios and 95% confidence intervals were calculated. HPgV was significantly more prevalent in older age groups compared to the youngest. However, HPgV was substantially more likely to be present among individuals with piercings than among those without piercings.

4. DISCUSSION

The HPgV virus is a globally prevalent virus with a quiescent nature that persistently attempts to occupy ecological niches conducive to its survival. The fact that HPgV interacts complexly with HIV in co-infected individuals indicates that the virus has a multifaceted function.

Our study found that 23.3% of PLWHIV were infected with HPgV RNA, similar to studies that reported prevalence rates of 23.4% in Yunnan province in China [9], 33% in Mexico [6], 19.6% in Cape Verde, Africa [15] and 27.3% in Turkey [8]. PLWHIV prevalence was reported at 32% in the extreme south of Nigeria by Mota *et al*., which is higher than the prevalence found in our study [12]. In contrast, Miranda *et al*. found a 17% prevalence in the North region of their study [13]. As a result of these comparisons, it becomes apparent that HIV/HPgV co-infection is endemic across a broad range of geographical regions and countries with differing prevalence rates of infection. Several sociodemographic characteristics, risk behaviors, and healthcare access factors may contribute to the epidemiology of this co-infection across diverse geographical contexts, according to these findings.

HIV/HPgV coinfection was more likely among individuals over 50, suggesting that exposure increases with age. There have been other studies that have found the rate of co-infection to be higher among young patients [9,15] or that age is not associated with co-infection [8]. Different study populations, sampling methods, analytical approaches, and even geographical and cultural factors may influence transmission dynamics and disease progression among diverse settings, resulting in inconsistencies.

We found that individuals with piercings had a lower likelihood of contracting HPgV. Although this is true, piercings don't guarantee protection. In addition, HPgV exposure could also be influenced by other factors, such as differences in health behaviors or social networks [16,17]. Furthermore, it is possible that those with piercings engage in risk-taking behavior, possibly increasing their exposure to HPgV [18,19]. Additionally, research has shown that body piercings can contribute to the transmission of HBV and HCV [16,17]. The complex relationship between piercings and health needs further research, so we should be cautious before assuming that they provide a protective effect.

Co-infection with HIV and HPgV and the use of inhaled medications were associated with our data. It is not uncommon for users to share these drugs, which can come into contact with blood and other bodily fluids in the nose and/or mouth, thus serving as potential sources of contamination [20,21].

Of the PLWHA who started their sexual activity under 18 years of age, 23.8% (44/185) tested positive for HPgV, as compared to 21.9% (14/64) of those who started their sexual activity after that. Although the age of onset of sexual activity was significantly associated with HPgV positivity, despite the difference in rates, there was no statistically significant association between HPgV positivity rates and age of onset. There may be other factors influencing the prevalence of the virus, despite an apparent disparity in infection rates between the two groups.

The results of the study regarding variables related to condom use were not in line with expectations and differed from other studies. Furthermore, no information is available regarding the use of contraceptives during serological

conversion. The variables related to homosexuals having multiple partners found no statistically significant association with HPgV infection. In contrast to studies that found an association [22,23], this study found no such association.

5. CONCLUSION

Among the significant risk factors identified are being over 50 years of age and inhalation of drugs. These findings suggest that transmission routes go beyond traditional modes of transmission. Consequently, current strategies for reducing harm and preventing addiction need to be reevaluated and expanded. Identifying the complex interaction between HPgV and HIV will lead to effective evidence-based policies and programs for the mitigation of the burden of these intertwined viral diseases across a range of populations through further research.

In our study, we face some limitations as a result of a cross-sectional design, which does not allow us to verify the temporal sequence, thus limiting the interpretation of our results. The presence of HPgV RNA indicates a current infection, but it does not provide information about virus clearance. There is a possibility that some individuals considered negative for HPgV may have been infected in the past. Additionally, not all patients had CD4+ lymphocyte counts to evaluate HPgV's possible beneficial effect on HIV infection because they were on Antiretroviral Therapy. Aside from that, we were not able to determine the phase of HIV infection, which has an effect on the CD4+ count. Researchers in Northeast Nigeria confirmed a 23.3% HPgV prevalence among people with HIV in this innovative investigation, emphasizing the potential burden of this co-infection throughout the Americas.

ETHICAL APPROVAL

This project was approved by the Institutional Ethics Committee for Human Health at the University of Maiduguri.

AUTHOR CONTRIBUTIONS

All authors contributed equally to this study.

CONFLICT OF INTEREST

None.

ORCID

PI – not available.
SO – not available.
DU – not available.

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