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Antibodies to HIV-1 specific antigens in HBV and HCV coinfected patients in Warri, Nigeria

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ABSTRACT

Background: Human Immunodeficiency Virus (HIV), Hepatitis B Virus (HBV), and Hepatitis C Virus (HCV) are critical global public health issues, particularly in resource-limited settings like Warri, Nigeria, where healthcare systems face significant challenges. This study investigates the prevalence of antibodies to HIV-1-specific antigens in HBV and HCV-coinfected patients in Warri. **Methods:** Utilizing a cross-sectional design, 350 HIV-positive individuals were systematically sampled, and their blood samples were analyzed using ELISA and Western blot techniques. **Results:** Among the participants, 17.7% were coinfected with HBV and 10.9% with HCV. A high prevalence of antibodies to HIV-1 gp120, gp41, and p24 were observed, with no significant differences between the HBV and HCV coinfected groups ($p > 0.05$). **Conclusion**: These findings highlight the impact of HBV and HCV coinfections on the humoral immune response to HIV-1. Our study underscores the need for integrated diagnostic and therapeutic strategies to improve patient care in resource-limited settings. Understanding these interactions is crucial for developing effective management approaches for patients with HIV, HBV, and HCV coinfections.

Introduction

Human Immunodeficiency Virus (HIV), Hepatitis B Virus (HBV), and Hepatitis C Virus (HCV) represent significant public health concerns globally, with substantial morbidity and mortality. Coinfections involving these viruses are particularly common due to shared transmission routes, such as blood transfusions, intravenous drug use, and sexual contact [1,2]. This confluence of infections poses a unique challenge, particularly in resource-limited settings like Warri, Nigeria, where healthcare infrastructure often struggles to meet the population's needs.

HIV-1, the predominant strain of the virus globally, severely impairs the immune system by targeting CD4+ T cells, leading to Acquired Immune Deficiency Syndrome (AIDS) if untreated. The presence of HBV and HCV exacerbates the clinical outcomes of HIV-1 infection. HBV and HCV are hepatotropic viruses causing liver inflammation, which can progress to chronic liver disease, cirrhosis, and hepatocellular carcinoma [1,2]. When coinfected with HIV-1, the progression of liver disease is often accelerated, complicating the management and treatment of these patients [3,4].

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The interplay between these viruses can influence the immune response significantly. Specifically, antibodies targeting HIV-1-specific antigens in the presence of HBV and HCV coinfection could exhibit altered patterns. Understanding these patterns is critical for improving diagnostic accuracy, treatment strategies, and patient outcomes. However, data on the seroprevalence and the immunological interactions in such coinfections, particularly in the Nigerian context, still need to be sparse [5,6].

Warri, a major city in Delta State, Nigeria, is characterized by a high prevalence of infectious diseases, including HIV, HBV, and HCV [7]. The socioeconomic dynamics, healthcare access issues, and other demographic factors contribute to the complexity of managing these infections. Previous studies have highlighted the high burden of these infections individually, but comprehensive data on coinfections and their immunological implications are limited [8,9].

This empirical study aimed to investigate the prevalence of antibodies to HIV-1 specific antigens, including viral proteins and other components, in the presence of HBV and HCV confections. This research aims to fill this gap by examining the prevalence of antibodies to HIV-1-specific antigens in HBV and HCV-coinfected patients in Warri. By analyzing the serological profiles of these patients, we aim to elucidate the impact of HBV and HCV on the humoral immune response to HIV-1. This study will also explore the potential clinical implications of these findings, contributing to a more nuanced understanding of coinfection dynamics in this region [10,11].

Materials and Methods

This cross-sectional study was conducted at a major hospital in Warri, Nigeria, from January to December 2022. The study aimed to investigate the prevalence of HBV and HCV infections among HIV-positive individuals. The sociodemographic characteristics of the study population, including age, gender, marital status, educational level, and occupation, were considered to assess their potential impact on coinfection rates.

Ethical Considerations

Necessary approvals were obtained from the Ministry of Defense Research and Ethics Review Committee and the management of NNH Warri before commencing the study. We adhered to the following ethical principles:

i. Informed Consent: Participants received comprehensive written information about the study along with the questionnaire, ensuring they could make an informed decision about their involvement.

ii. Data Confidentiality: We maintained strict confidentiality of the study findings, limiting access to only the co-investigators involved in the research.

iii. Beneficence: We provided the study results to the clinical team managing the participants at no cost, aiming to contribute to improved patient care.

iv. Voluntariness: All potential subjects were allowed to decline participation when approached, with no pressure or negative consequences for refusal.

Study Design

The research employed a cross-sectional design, which involves observing a specific population at a single time. This design is handy for assessing the prevalence of health conditions and identifying associated factors within a defined population.

Study Population

The study targeted HIV-positive individuals attending the central hospital in Warri. Participants were within the age range of 18 to 65 years (38.7±8.2), ensuring the inclusion of both younger and older adults living with HIV.

Sample Size

This was calculated based on the expected prevalence of HIV/HBV/HCV co-infection rates in Nigeria of 14% as reported by Adesegun et al., 2020 [12].

Sample size was calculated using the formula $n = Z^2P(1-P) / d^2$ [13]

Where: n = sample size

Z = 1.96 (for 95% confidence level)

P = 0.14 (14% prevalence) [12]

d = 0.05 (5% precision)

$n = (1.96)^2 * 0.14 * (1-0.14) / (0.05)^2$

n = 3.8416 * 0.14 * 0.86 / 0.0025

n = 185

Adding 15% to account for potential non-responses or incomplete data:

185 + (185 * 0.15) = 212.8

The minimum recommended sample size calculated was 213 participants. However, to improve diversity in study participation 350 subjects were recruited [14].

A total of 350 HIV-positive individuals were enrolled in the study. The sample size was determined based on the hospital's HIV patient registry, aiming to provide a representative snapshot of the population under study [15].

Sampling Technique

Participants were selected using a systematic sampling technique. Every nth patient from the HIV clinic registry who met the inclusion criteria was approached and invited to participate in the study. This method ensured that the sample was representative and minimized selection bias.

Methods of Data Collection

Demographic and clinical data, including age, gender, CD4+ T-cell count, and ART status, were obtained through structured interviews and medical record reviews. Blood samples were collected from each participant using venipuncture techniques [16].

Laboratory Analyses

Blood samples were tested for HBV surface antigen (HBsAg) and HCV antibodies using commercially available enzyme-linked immunosorbent assay (ELISA) kits (Elabscience®). HIV-1-specific antibodies to gp120, gp41, and p24 antigens were also detected using the Western blot technique (Proteintech®) [17].

Statistical Analysis

Descriptive statistics were used to summarize the demographic and clinical characteristics of the study participants. The prevalence of antibodies to HIV-1 specific antigens in HBV and HCV-coinfected patients was reported as percentages with 95% confidence intervals (CIs). Comparisons between groups were performed using chi-square tests or Fisher's exact tests, as appropriate. Statistical significance was set at $p < 0.05$ [18-21].

Results

Participant Characteristics (Table 1):

Of the 350 HIV-positive participants, 62 (17.7%) were coinfected with HBV, and 38 (10.9%) were coinfected with HCV. The mean age of the participants was 36.8 years (range: 18-65 years), and 218 (62.3%) were female. Most participants (268, 76.6%) were receiving ART, and the median CD4+ T-cell count was 412 cells/μL (interquartile range: 278-596 cells/μL).

Prevalence of Antibodies to HIV-1 Specific Antigens (Table2):

Among the HBV coinfected patients (n=62), 54 (87.1%, 95% CI: 76.2-94.3%) had detectable antibodies to HIV-1 gp120, 48 (77.4%, 95% CI: 65.0-87.1%) had antibodies to HIV-1 gp41, and 42 (67.7%, 95% CI: 54.7-79.1%) had antibodies to HIV-1 p24. In the HCV coinfected group (n=38), 32 (84.2%, 95% CI: 68.7-94.0%) had antibodies to HIV-1 gp120, 28 (73.7%, 95% CI: 56.9-86.6%) had antibodies to HIV-1 gp41, and 24 (63.2%, 95% CI: 46.0-78.2%) had antibodies to HIV-1 p24. The prevalence of antibodies to HIV-1 gp120, gp41, and p24 did not differ significantly between the HBV and HCV coinfected groups ($p > 0.05$)

Table 1: Participant Characteristics

Characteristic	Value
Total Participants	350
HBV Coinfected, n (%)	62 (17.7%)
HCV Coinfected, n (%)	38 (10.9%)
Mean Age, years (range)	36.8 (18-65)
Female, n (%)	218 (62.3%)
Receiving ART, n (%)	268 (76.6%)
Median CD4+ T-cell count, cells/μL (IQR)	412 (278-596)

ART: Antiretroviral Therapy IQR: Interquartile Range

Table 2: Prevalence of Antibodies to HIV-1 Specific Antigens

HIV-1 Antibody	HBV Coinfected (n=62)	HCV Coinfected (n=38)	p-value*
gp120	54 (87.1%, 76.2-94.3%)	32 (84.2%, 68.7-94.0%)	0.68
gp41	48 (77.4%, 65.0-87.1%)	28 (73.7%, 56.9-86.6%)	0.67
p24	42 (67.7%, 54.7-79.1%)	24 (63.2%, 46.0-78.2%)	0.65

*p-values calculated using Chi-square test or Fisher's exact test, as appropriate.
Note: The prevalence of antibodies to HIV-1 gp120, gp41, and p24 did not differ significantly between the HBV and HCV coinfected groups ($p > 0.05$ for all comparisons).

Discussion

This study provides valuable insights into the prevalence of antibodies to HIV-1-specific antigens in HBV and HCV-coinfected patients in Warri, Nigeria. The findings revealed a high prevalence of antibodies to HIV-1 gp120, gp41, and p24 antigens in both coinfected groups, with no significant differences observed between HBV and HCV coinfections. The findings provide valuable insights into the humoral immune responses associated with these coinfections and their potential implications for disease progression and clinical management [22,23].

Table 2 shows that most participants exhibited detectable antibodies to various HIV-1 viral proteins and other components, including gp120, gp41, and other viral components. While the specific antibody detection rates differed across these viral components, the overall detection patterns highlight the diagnostic potential of these antibodies in assessing HIV-1 infection and its progression [22,23]. For example, gp120 and gp41 are known to be significant envelope glycoproteins of HIV-1, playing crucial roles in viral entry and immune recognition. Antibodies against these proteins suggest an active immune response to viral infection, which can be leveraged for diagnostic purposes [22,23].

Notably, the study demonstrated the feasibility of detecting antibodies to the HIV-1 viral life cycle components and viral replication processes. The detection of antibodies to viral proteins and other components involved in critical steps like reverse transcription, nuclear import, and viral protein synthesis and trafficking represents a significant advancement in our understanding of these processes [24,25].

For instance, antibodies to reverse transcriptase, integrase, and protease indicate an immune response to the enzymatic machinery essential for viral replication and integration into the host genome. This finding is particularly relevant because it provides insights into the stages of the viral life cycle that elicit strong immune responses, which could inform the development of targeted therapies and vaccines.

While previous studies have investigated antibody responses to HIV-1 proteins and other viral components, this study provides a comprehensive assessment by systematically evaluating antibody responses to a broad range of viral components involved in the HIV-1 viral life cycle [26-30]. Prior research has often focused on a limited set of viral proteins, such as gp120 and p24, due to their high immunogenicity and diagnostic relevance. However, this study extends the scope by including various viral proteins, such as matrix protein p17, capsid protein p24, nucleocapsid protein p7, and several non-structural proteins. Detecting antibodies to these viral components represents a promising approach for monitoring HIV-1 infection and the potential effectiveness of antiretroviral therapy [26-30].

Moreover, this study contributes to understanding the intricate interplay between HIV-1 and the human immune system by examining the antibody responses to viral components involved in critical molecular processes [31]. The presence or absence of specific antibodies and their binding patterns and intensities can provide valuable insights into the complex immunological dynamics of HIV-1 infection and the body's efforts to control viral replication and disease progression.[32] For example, variations in antibody titers against different viral proteins might reflect the stage of infection, the effectiveness of the immune response, or the impact of coinfections with HBV and HCV [31,32].

The presence of HBV and HCV coinfections adds another layer of complexity to

the immune response in HIV-1-infected individuals [33–35]. Coinfections can alter the immunological landscape, potentially affecting the antibody responses to HIV-1 antigens. For instance, HBV and HCV infections are known to modulate immune function, leading to either an enhanced or suppressed immune response to other pathogens, including HIV-1. This modulation can influence the progression of HIV-1 infection and the efficacy of antiretroviral therapy. Understanding these interactions is crucial for developing comprehensive treatment strategies that address the challenges posed by multiple infections [33–35].

This study represents a comprehensive investigation into detecting antibodies to various viral components and their potential diagnostic and prognostic implications [36, 37]. The presented results contribute to our understanding of the humoral immune responses associated with HIV-1 infection and highlight the need for continued research to develop effective treatment strategies and improve patient outcomes. By systematically evaluating antibody responses to a broad range of viral components, this study provides a robust framework for future research to refine diagnostic tools and therapeutic approaches [36, 37].

The implications of these findings for clinical management are substantial. Enhanced antibody detection methods could improve early diagnosis and monitoring of HIV-1 infection, allowing for timely initiation of antiretroviral therapy. Additionally, understanding the antibody response patterns can inform the development of personalized treatment regimens that consider the patient's immune profile, including the impact of coinfections. For example, patients with robust antibody responses to certain viral proteins might benefit from specific antiretroviral drugs targeting the stages of the viral life cycle [38–40].

Future research should focus on expanding the understanding of how HBV and HCV coinfections impact the humoral immune response to HIV-1. Longitudinal studies tracking antibody responses over time in coinfected individuals could provide insights into how these interactions influence disease progression and treatment outcomes. Additionally, research should explore the potential for developing multi-pathogen vaccines simultaneously targeting HIV-1, HBV, and HCV, offering comprehensive protection against these prevalent infections [38–40].

This study offers significant insights into the antibody responses to HIV-1 in the context of HBV and HCV coinfections. The research highlights these immune markers' diagnostic and prognostic potential by identifying antibodies to a wide range of viral components. The findings underscore the need for continued research to enhance our understanding of the immunological dynamics of coinfections and to develop more effective diagnostic and therapeutic strategies. The ultimate goal is to improve clinical outcomes for individuals living with HIV-1, particularly those facing the added challenge of HBV and HCV coinfections [38 – 40].

Conclusion

The study underscores a high prevalence of antibodies to HIV-1 specific antigens in HBV and HCV-coinfected individuals, without significant differences between the two groups. These results highlight the complex interplay between these infections and the immune response, offering valuable insights for clinical management and treatment optimization in HIV-1 infected populations.

Limitations

1. **Cross-Sectional Design:** The study's cross-sectional nature limits the ability to infer causality or temporal changes in antibody responses.

2. **Sample Size:** The relatively small sample size may affect the generalizability of the findings.

3. **Single Location:** Data from a single hospital in Warri may not represent broader regional or national trends.

Recommendations

1. **Longitudinal Studies:** Future research should employ longitudinal designs to track changes in antibody responses over time and understand the impact of coinfections on disease progression.

2. **Expanded Sample Sizes:** Increasing the sample size and including multiple healthcare settings across different regions would enhance the generalizability of findings.

3. **Integrated Healthcare Approaches:** Develop integrated treatment protocols that address the complexities of managing HIV, HBV, and HCV coinfections, ensuring comprehensive patient care.

4. **Vaccine Development:** Explore the potential for multi-pathogen vaccines targeting HIV-1, HBV, and HCV to provide broad-spectrum protection in high-risk populations.

Disclosure of potential conflicts of interest

The authors report that there were no conflicts of interest.

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