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Serum IgM Levels and Hepatitis D Virus Co-Infection in HBsAg-Positive Patients in Abakaliki, Nigeria

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Abstract

Hepatitis delta virus (HDV) is a defective RNA virus that relies on co-infection with *Hepatitis B virus* (HBV) for its replication. This study aimed to identify HBsAg-positive patients co-infected with HDV and quantify serum IgM levels in a hospital-based population in Abakaliki, Ebonyi State, Nigeria. A cross-sectional analytical study was conducted among 1,000 patients attending the Federal Teaching Hospital Abakaliki (FETHA) and Mile 4 Hospital Ishieke. HBsAg-positive individuals were identified using a rapid diagnostic kit, while HDV-IgM was detected using ELISA. Among the 1,000 participants, 89 (8.9%) tested positive for HBsAg, and of these, 5 (5.6%) were also positive for HDV-IgM, indicating active co-infection. HDV co-infection prevalence was higher among females (7.7%) compared to males (2.7%), and significantly higher among married individuals (6.9%) than singles (3.2%) ($p < 0.05$). Age-specific analysis revealed the highest co-infection rate (10%) among individuals aged 29–33 years, while no cases were recorded in the 34–45 years age group. Geographically, patients from Mile 4 Hospital had a higher co-infection rate (7.5%) than those from FETHA

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(2.8%). Educational status and occupation also influenced prevalence; tertiary-educated individuals had the highest rate (13.6%), while no cases were reported among those with only primary education. Students recorded a prevalence of 8.9%, with no co-infections detected among traders or housewives. Among clinical subgroups, pregnant women had a higher co-infection rate (9.5%) compared to blood donors (2.1%). These findings underscore the importance of routine HDV screening among HBsAg-positive patients, especially in high-risk groups, and the urgent need for targeted public health interventions to reduce the burden and severity of HBV/HDV co-infection in Nigeria. Further research is warranted to better understand the epidemiological dynamics and clinical implications of co-infection.

Keywords: Abakaliki; Co-Infection; *Hepatitis B Virus* (HBV); *Hepatitis Delta Virus* (HDV); IgM; Serum; Prevalence

INTRODUCTION

Hepatitis B virus (HBV) belongs to a family of viruses called hepadnavirus (Karim, 2008). The virus is made up of a superficial lipid packet and an icosahedral nucleocapsid core composed of protein (Imarenezor *et al.*, 2023). These virions are 30-42 nm in diameter. The nucleo-capsid encloses the viral DNA and a DNA polymerase that has reverse transcriptase movement (Imarenezor *et al.,* 2023). The outer wrapping has implanted proteins, useful in viral attachment of, entry into, susceptible cells. The virus is one of the smallest enveloped animal viruses, and the 42 nm virions, which are competent of infecting liver cells known as hepatocytes, are referred to as Dane particles (Hotta, 2008).

In totaling the Dane particles, filamentous and sphere-shaped bodies deficient of nucleus can be found in the serum of infected persons. These particles are not infectious and are serene of both lipid and protein that constitutes part of the outer covering of the virus particle, which is called the surface antigens (HBsAg), and is fashioned in excess during the life phase of the virus (Bruss, 2007). It consists of HBsAg, HBcAg (HBeAg is a splice variant),Hepatitis B virus DNA polymerase and HBx (Imarenezor *et al.,* 2016). The function of this protein is not yet well known, but evidence suggests it plays a part in the activation of the viral transcription process. Hepatitis D virus requires HBV envelope particles to become virulent (Bruss, 2007).

The hepatitis B virus is classified as the type species of the *Orthohepadnavirus*, which contains three other species: the *Ground squirrel hepatitis virus*, *Woodchuck hepatitis virus*, and the *Woolly monkey hepatitis B virus*. The genus is classified as part of the *Hepadnaviridae* family, which contains two other genera, the *Avihepadnavirus* and a second which has yet to be assigned. This family of viruses have not been assigned to a viral order. Viruses similar to hepatitis B have been found in all apes (orangutan, gibbons, gorillas and chimpanzees), in Old World monkeys and in a New World woolly monkeys suggesting an ancient origin for this virus in primates (Chang, 2007).

The virus is divided into four major serotypes (adr, adw, ayr, ayw) based on antigenic epitopes present on its envelope proteins, and into eight genotypes (A–H) according to overall nucleotide sequence variation of the genome (Imarenezor *et al*.,2024). The genotypes have a distinct geographical distribution and are used in tracing the evolution and transmission of the virus. Differences between genotypes affect the disease severity, course and likelihood of complications, and response to treatment and possibly vaccination (Chang, 2007).

Acute infection with hepatitis B virus is associated with acute viral hepatitis – an illness that begins with general ill-health, loss of appetite, nausea, vomiting, body aches, mild fever, and dark urine, and then progresses to development of jaundice. It has been noted that itchy skin has been an indication as a possible symptom of all hepatitis virus types. The illness lasts for a few weeks and then gradually improves in most affected persons. Few people may have more severe liver disease (fulminant hepatic failure), and may die as a result. The infection may be entirely asymptomatic and may go unrecognized (Neuveut *et al.,* 2013).

Chronic infection with hepatitis B virus either may be asymptomatic or may be associated with a chronic inflammation of the liver (chronic hepatitis), leading to cirrhosis over a period of several years. This type of infection dramatically increases the incidence of hepatocellular carcinoma (liver cancer) (Imarenezor *et al.,* 2016). Across Europe hepatitis B and C cause approximately 50 % of hepatocellular carcinomas. Chronic carriers are encouraged to avoid consuming alcohol as it increases their risk for cirrhosis and liver cancer. Hepatitis B virus has been linked to the development of membranous glomerulonephritis (MGN) (Lin and Anderson, 2000).

Symptoms outside of the liver are present in 1–10 % of HBV-infected people and include serum-sickness–like syndrome, acute necrotizing vasculitis (polyarteritis nodosa), membranous glomerulonephritis, and papular acrodermatitis of childhood (Gianotti–Crosti syndrome) (Zhou and Holmes, 2007).

The serum-sickness–like syndrome occurs in the setting of acute hepatitis B, often preceding the onset of jaundice (Hatzakis, 2013). The clinical features are fever, skin rash, and polyarteritis. The symptoms often subside shortly after the onset of jaundice, but can persist throughout the duration of acute hepatitis B. About 30–50 % of people with acute necrotizing vasculitis (polyarteritis nodosa) are HBV carriers (Kay and Zoulim, 2007).

HBV-associated nephropathy has been described in adults but is more common in children (Imarenezor and Benjamin, 2024). Membranous glomerulonephritis is the most common form (Kay and Zoulim, 2007). Other immune-mediated hematological disorders, such as essential mixed cryoglobulinemia and aplastic anemia (Kay and Zoulim, 2007).

The genome of HBV is made of circular DNA, but it is unusual because the DNA is not fully double-stranded. One end of the full-length strand is linked to the viral DNA polymerase. The genome is 3020–3320 nucleotides long (for the full-length strand) and 1700–2800 nucleotides long (for the short length-strand) GeneCards (Imarenezor et al., 2024).

The negative-sense (non-coding) is complementary to the viral mRNA. The viral DNA is found in the nucleus soon after infection of the cell. The partially double-stranded DNA is rendered fully double-stranded by completion of the (+) sense strand and removal of a protein molecule from the (−) sense strand and a short sequence of RNA from the (+) sense strand. Non-coding bases are removed from the ends of the (−) sense strand and the ends are rejoined. There are four known genes encoded by the genome, called C, X, P, and S. The core protein is coded for by gene C (HBcAg), and its start codon is preceded by an upstream in-frame AUG start codon from which the pre-core protein is produced. HBeAg is produced by proteolytic processing of the pre-core protein. (Imarenezor *et al.,* 2024). In some rare strains of the virus known as Hepatitis B virus precore mutants, no HBeAg is present. The DNA polymerase is encoded by gene P. Gene S is the gene that codes for the surface antigen (HBsAg). The HBsAg gene is one long open reading frame but contains three in frame "start" (ATG) codons that divide the gene into three sections, pre-S1, pre-S2, and S. Because of the multiple start codons, polypeptides of three different sizes called

large (the order from surface to the inside: pre-S1, pre-S2, and S), middle (pre-S2, S), and small (S) are produced (Bruss, 2007).

The function of the protein coded for by gene X is not fully understood but it is associated with the development of liver cancer. It stimulates genes that promote cell growth and inactivates growth regulating molecules (Bruss, 2007).

Acute hepatitis B infection does not usually require treatment and most adults clear the infection spontaneously. Early antiviral treatment may be required in fewer than 1% of people, whose infection takes a very aggressive course (fulminant hepatitis) or who are immuno-compromised. On the other hand, treatment of chronic infection may be necessary to reduce the risk of cirrhosis and liver cancer (Imarenezor and Benjamin, 2024). Chronically infected individuals with persistently elevated serum alanine aminotransferase, a marker of liver damage, and HBV DNA levels are candidates for therapy. Treatment lasts from six months to a year, depending on medication and genotype (Imarenezor *et al.*, 2023). Although none of the available drugs can clear the infection, they can stop the virus from replicating, thus minimizing liver damage. As of 2008, there are seven medications licensed for treatment of hepatitis B infection in the United States.

These include antiviral drugs lamivudine (Epivir), adefovir (Hepsera), tenofovir (Viread), telbivudine (Tyzeka) and entecavir (Baraclude), and the two immune system modulators interferon alpha-2a and PEGylated interferon alpha-2a (Pegasys).

The World Health Organization recommended a combination of tenofovir and entecavir as first line agents. Those with current cirrhosis are in most need of treatment (Imarenezor *et al.*, 2023). The use of interferon, which requires injections daily or thrice weekly, has been supplanted by long-acting PEGylated interferon, which is injected only once weekly. However, some individuals are much more likely to respond than others, and this might be because of the genotype of the infecting virus or the person's heredity.

The treatment reduces viral replication in the liver, thereby reducing the viral load (the amount of virus particles as measured in the blood). Response to treatment differs between the genotypes. Interferon treatment may produce an e antigen seroconversion rate of 37% in genotype A but only a 6% seroconversion in type D. Genotype B has similar seroconversion rates to type A while type C seroconverts only in 15% of cases. Sustained e antigen loss after treatment is ~45% in types A and B but only 25–30% in types C and D (Imarenezor *et al.,* 2023). This study is to investigate the serum IgM levels and Hepatitis D

Virus (HDV) co-infection in HBsAg-positive patients in Abakaliki, Nigeria. Specifically, the study seeks to:

- Determine the prevalence of HDV co-infection among HBsAg-positive patients
- Evaluate the levels of IgM antibodies against HDV in co-infected patients
- Explore the clinical implications of HDV co-infection on HBV infection

among individuals in Abakaliki in Ebonyi State, Nigeria.

MATERIALS AND METHODS

Study Area

The study was carried out in Ebonyi State in Nigeria. The State capital and largest town is Abakaliki which is the focus point of this study. The inhabitants are primarily members of Igbo Nations with farming as their pre-dominant occupation. The study area has a geographical population of about 134,102 with Geographic coordinates of Latitude: 6.32° N Longitude: 8.12° Elevation: 117 m.

Study Population

A prospective cross-sectional study was carried out among 1000 patients who visited the FETHA-11 Hospital and the Mile Four Maternity Hospital, Ebonyi State, Nigeria and were screened for the HBsAg. Further studies were then carried out to clearly ascertain cases of ongoing co-infection between HBsAg/ HDV-IgM. The age of subjects was 19-23, 24-28, 29-33, 34-39 and 40-45. The age group, 19–23 years constituted the largest population making up 35 % (n=350) while 40-45 years were the least making up 1 % (n=10). Gender, females constituted the largest population of 62 % (n=620) while the males were 38 % (n=380) of the total population. The singles were 65 % (n=650) whereas married made up 35 % (n=350). FETHA-II had 35.4 % (n=354), Mile 4 had 64.6 % (n=646).

Informed Consent Form

An informed consent form was first given to all who consented to enroll in the study through the patient's physician. All the patients gave their consent.

Ethical Considerations

Ethical approval was obtained from the management of FETHA-11 and Mile 4 Hospital all in Abakaliki before we proceeded with the study.

Sampling Technique for HBsAg

Blood samples were collected from all subjects for serological test first for HBsAg antibody. Five millitres (5mL) of venous blood was obtained from each participant under aseptic procedure into a properly labeled serial number-tagged clean EDTA. Sera extracted were then placed into a plain bottle and stored until the time of use for analysis.

Serological Analysis for the HBsAg

All 89 samples that tested positive for the HBsAg were then analyzed using ELISA assay technique to detect the presence of HDV-IgM antibodies. The kit used for the study was DIA.PRO Diagnostic Bioprobes Srl Via G. Carducci nº 27 20099 Sesto San Giovanni (Milano) – Italy. All tests were performed according to manufacturer's specifications as described briefly. Each kit contains the components described below and sufficient reagents to carry out 89 tests.

Negative Control for ELISA Analysis

The negative control was contained in a 1× 2.0 ml/vial with the following components; ready to use, human IgM antibodies positive to HDV, 3 % skimmed milk, 0.2M Tris buffer pH 6.0 +/- 0.1, 0.2 % Tween 20, 0.09 % Na azide and 0.1 % Kathon GC as preservatives. The negative control is pale yellow in colour. We ensured that the ready to use negative controls are thoroughly mixed on vortex before use.

Positive Control for ELISA Analysis

Positive control was in a 1× 2.0 ml/vial with the following components; ready to use, human IgM antibodies positive to HDV, 3 % skimmed milk, 0.2M Tris buffer PH 6.0 +/- 0.1, 0.2 % Tween 20, 0.09 % Na azide and 0.1 % Kathon GC as preservatives. The positive control is green yellow colour coded. Calibrator lyophilized reagent was then dissolved with EIA grade water as reported in the label and it contains fetal bovine serum human IgM antibodies to HDV, 0.2mg/ml gentamicine sulphate and 0.1 % kathon GC as preservatives.

HDV Antigen Diluent for ELISA Analysis

HDV diluents were in 1×16 ml/vial. The buffered solution for the dissolution of the lyophilized HDV antigen contained 0.2M Tris buffer ph 6.0+/-0.1 % kathon GC and 0.2 % Triton × 100. The component is red colour coded.

Specimen Diluent for ELISA Analysis (DILSPE)

Specimen diluent was in a 2 × 60.0 ml/vial. It's a buffered solution for the dilution of the samples; it contained 0.2M Tris buffer pH 6.0+/-0.1, 0.2 % Tween 20, 3 % skimmed milk, 0.1% kathon GC and 0.09 % sodium azide as preservatives. The component is blue colour coded.

Interpretation of Results for HBsAg

Negative: Result is negative when only one colour band appears on the control region. This indicates that there is no detectable HBsAg.

Positive: Results are positive when distinct colour bands appear on both the control and test region, this is an indication that the specimen contains detectable amount of HBsAg.

Invalid Results: Occurs when no visible band occurs at all or when only one colour band appears on the test region, this could be due to possible error in performing the test and such tests were repeated using a new device

Statistical Analysis for HBsAg/HDV-IgM

Data generated for HBsAg/HDV-IgM co-infection in this study was then analyzed using SPSS (statistical package for social sciences) software package, version 13.0 (USA).

RESULTS

Prevalence of HBsAg among Patients in FETHA-11 and Mile Four Hospital with Respect to Age

The highest prevalence rate of 20 % (n=2) was observed in the age group of 40-45 years while the lowest prevalence rate of 2.5 % (n=2) was observed in the age group of 34-39 years. However, the age groups of 19-23 years, 24-28 years and 29-33 years had prevalence rate of 9.4 %(n=33), 13.5 % (n=42) and 4 % (n=10) respectively as shown in Table 1 below.

Prevalence of HBsAg among Patients with Respect to Gender and Marital Status

The prevalence rate of 9.7 % (n=37) and 8.38 % (n=52) was found for the males and females. The total of 89 samples which tested seropositive for HBsAg infection was stratified into two groups; the singles and married based on their marital status. However, it was found that the married group had a higher prevalence rate of 16.6 % (n=58) wherein 4.8 % (n=31) was the prevalence rate of the single group as shown in Table 2 below.

Prevalence of HBsAg Infection in relation to Educational Status

Results of the analysis showed a higher prevalence rate of 20 % (n=22) in the study population who had attained tertiary level of education when compared to the primary level of education which showed the lowest prevalence rate of 4.8 % (n=14) as shown in Table 3 below.

Prevalence of HBsAg among Patients with Respect to Occupation

The occupational status was 48 % (n=480) for students, 4 % (n=40) for Housewife, 35 % (n=350) for civil servant, traders had 13 % (n=130). FETHA-II had 35.4 % (n=354) while Mile 4 had 64.6 % (n=646) on the basis of location (Table 4). In relation to occupational status, this study showed that HBsAg infection was higher among house wife 25.0 % (n=10), followed by traders 14.7 % (n=19), students with 9.4% (n=45) while civil servants had the lowest rate of 4.3 % (n=15) as shown in Table 4 below.

Prevalence of HBsAg Infection among Blood Donors in FETHA-11 and Pregnant Women in Mile Four Maternity Hospital.

On the bases of location blood donors from FETHA- II showed the highest prevalence rate of 10 % (n=36) compared to 8 % (n=53) observed among pregnant women attending the Mile Four Maternity Hospital as shown in Table 5 below.

Prevalence of HBsAg/HDV-IgM Co-infection among Study Population

A total of 89 samples that tested positive for HBsAg were investigated to ascertain the occurrence of HBsAg/HDV-IgM co-infection. A prevalence rate of 5.6 % (n=5) was recorded in this study.

Table 1: Prevalence of HBsAg among Patients with respect to Age

Age Bracket	No. Tested %	No. Positive (%)	No. Negative %
19-23	350 (35.0)	33 (9.4)	317 (31.7)
24-28	310 (31.0)	42 (13.5)	268 (26.2)
29-33	250 (25.0)	10 (4.0)	240 (24.0)
34 – 39	80 (8.0)	2 (2.5)	78 (7.8)
40 – 45	10 (1.0)	2 (20.0)	8 (0.8)
Total	1000	89	911

Table 2: Prevalence of HBsAg among Patients with Respect to Gender and Marital Status

Socio-Demographic Factor	Gender/ Marital status	No. Tested %	No. Positive (%)	No. Negative %
Gender	Male	380 (38.0)	37 (9.7)	343 (34.3)
	Female	620 (62.0)	52 (8.38)	568 (56.8)
Marital Status	Single	650 (65.0)	31 (4.8)	619 (61.9)
	Married	350 (35.0)	58 (16.6)	292 (29.2)

Table 3: Prevalence of HBsAg among Patients with Respect to Educational Status as Socio-demographic Factor

Level of Education	No. Tested %	No. Positive (%)	No. Negative %
Primary	290 (29.0)	14 (4.8)	276 (26.7)
Secondary	600 60.0()	44 (7.3)	556 (55.6)
Tertiary	110 (11.0)	22 (20.0)	88 (8.8)
Total	1000	89	920

Table 4: Prevalence of HBsAg among Patients with Respect to Occupation as a Socio-demographic Factor

Occupation	No. Tested %	No. Positive (%)	No. Negative %
Student	480 (48.0)	45 (9.4)	435 (43.5)
House Wife	40 (4.0)	10 (25)	30 (3.0)
Civil Servant	350 (35.0)	15 (4.3)	335 (33.5)
Trader	130 (13.0)	19 (14.6)	111 (11.1)

Table 5: Prevalence of HBsAg Infection among Blood Donors in FETHA-11 and Pregnant Women in Mile Four Maternity Hospital.

	Location	Number Tested	Number Positive	Number Negative
Blood Donors	FETHA-11	354 (35.4)	36 (10.1)	318 (31.8)
Pregnant Women	Mile Four Maternity Hospital	646 (64.6)	53 (8.2)	593 (59.3)
Total		1000	89	911

DISCUSSION

The prevalence rate for the male HBsAg/HDV-IgM co-infection was found to be 2.7 % which is lower when compared to the prevalence rate of HBsAg/HDV-IgM co-infection among the females which was 7.7 %. Our observation was not supported by the findings of a previously published epidemiological survey in Pakistan where the rate of HDV infection was reported higher (8.7 %) in young males compared to females (Mumtaz *et al.,* 2005). However, there was no significant difference between genders ($p > 0.31$). With regards to marital status, HBsAg/HDV-IgM coinfection was higher among the married, having a prevalence rate of 6.9 % which is much lower when compared to their single counterparts which have a prevalence rate of 3.2 %. The prevalence of 6.9 % obtained among the married in this study contradicts the higher rates (6 -27.6%) of HBsAg/HDV coinfection which have been reported from studies carried out in Nairobi by Noubiap *et al.* (2015). Variation in prevalence observed may be attributed to difference in geographical setting and study methodology adapted. There was a significant difference for marital status at ($p < 0.02$).

The age group of 29-33 years is shown to have the highest HBsAg/HBV-IgM co-infection prevalence rate of 10 % this was in sharp contrast with the 13.1 % HBsAg/HBV-IgM co-infection obtained from participants within the age of 36 in previous work done by Imarenezor *et al.* (2016) on the Prevalence of Hepatitis B virus and Hepatitis D virus coinfection in Western Burkina Faso and molecular characterization of the detected virus strains.

The age group 24-28 years had 7.1 %. A lower rate of HBsAg/HBV-IgM was detected in age group 20-24 years (4.3%) in Kenya by Mutuma *et al.* (2011).

This finding slightly disagrees with the 7.1 % prevalence obtained in this study and also differs with those obtained from Fomolu *et al.* (2013) study which reported higher positivity rate among age group 25-29 (15.4 %). This may have occurred due to the high vulnerability of subjects within this age bracket to risk factors that could possibly facilitate HBV and HDV transmission (Imarenezor *et al.*, 2023). However, the age groups of 34-39 years and 40-45 years showed the lowest HBsAg/HDV-IgM co-infection prevalence rate of HBsAg/HDV-IgM co-infection which is 0 % which was lower than the 13.1 % value obtained by Armel *et al.* (2018) from those within the age of 36. There is no significant difference between the various age groups at ($p > 0.88$).

Mile 4 had the highest HBsAg/HBV-IgM co-infection prevalence rate of 7.5 % as opposed to FETHA-II which had a much lower HBsAg/HBV-IgM co-infection prevalence rate of 2.8 % in relation to location. Since there are no previous data from our study area we are unable to compare for location. Our result could be due to the high influx of rural dwellers (who lack the basic information about some of the risk factors and other practices that could possibly make one vulnerable to such infection) at Mile Four Hospital compared to FETHA-11. There is no significant difference between the various locations studied at ($p > 0.33$).

Participants with the primary level of Education show no case of HBsAg/HDV-IgM co-infection which is closely followed by their secondary school counterparts having a prevalence rate of 4.5 %. The highest prevalence rate in this category is shown by participants in the tertiary level of education having a prevalence rate of 13.6 %. Contrarily, HBsAg/HDV positivity was reported by Pennap *et al.* (2011) to decrease with increase in education level. This did not tally with our findings. This may be due to limited /scarcity of focused HBV infection advocacy material and awareness within the community. There is no significant difference on the basis of education at ($p > 0.13$).

Participants who were pregnant women showed the highest HBsAg/HDV-IgM co-infection prevalence rate of 9.5 % while participants who were blood donors had the lowest prevalence rate of 2.1 %. Other studies conducted in Bobo-Dioulasso reported prevalences of 3.38 % and 2.50 % among blood donors and pregnant women, respectively (Andernach *et al.,* 2014; Sawadogo *et al.,* 2015). The prevalence rate of 9.5 % obtained in this study for pregnant women was higher than the 2.50 % reported by Andernach *et al.* (2014) and Sawadogo *et al.* (2015). However, the 2.1 % obtained in this study was lower

than the 3.38 % value recorded by Andernach *et al.* (2014) and Imarenezor *et al.* (2016). This could be attributed to the weak state of their immune system. However, no significant difference was observed among pregnant women and blood donors ($p > 0.13$).

Conclusively, HDV co-infection is a significant concern among HBsAg-positive patients in Abakaliki, Nigeria, potentially contributing to the severity of HBV infection. The study highlights the need for routine screening of HDV among HBsAg-positive patients and targeted public health interventions to prevent HDV co-infection and manage HBV infection severity. Further research is necessary to understand the epidemiological and clinical changes associated with HBV/HDV co-infection. Also, public awareness campaigns, complete immunization against viral hepatitis and well- equipped hospitals for intensive care will go a long way in the reduction of viral hepatitis among the population. We therefore recommend to various guideline committees to consider advocating for all patients with HBV to be screened for HDV co-infection. Screening all patients who are HBsAg-positive for HDV could result in earlier diagnosis and possible treatment intervention. Multiple studies have indicated that there is at least some benefit from interferon treatment,16 –19 with the most recent publication showing that treatment with peginterferon alfa-2a for 48 weeks resulted in sustained HDV-RNA clearance in about one quarter of HDV-infected patients. As new treatments for HDV such as prenylation inhibitors emerge, 21 higher rates of HDV viral clearance on treatment may become evident. In addition, universal screening of chronic hepatitis B (CHB) patients for HDV infection could support the important public health goal of reducing transmission. With universal screening, HDV-negative patients should be educated on the need for protection against super-infection. Also, HDV-infected patients should be educated on the need to protect themselves.

CONCLUSION

This study highlights the clinical and epidemiological significance of Hepatitis Delta Virus (HDV) co-infection among Hepatitis B surface antigen (HBsAg)-positive individuals in Abakaliki, Nigeria. Of the 1,000 participants screened, 8.9% were HBsAg-positive, and among them, 5.6% also tested positive for HDV-IgM, indicating active co-infection. The prevalence of HDV co-infection was notably higher among females, married individuals,

those aged 29–33 years, patients attending Mile 4 Hospital, individuals with tertiary education, students, and pregnant women.

Although many demographic and clinical subgroups showed varying prevalence rates, most differences were not statistically significant. Nevertheless, the findings underscore the need for heightened clinical vigilance and public health attention to HBV/HDV co-infection, particularly among high-risk populations.

Routine HDV screening for all HBsAg-positive individuals is strongly recommended, as early detection may facilitate timely clinical intervention and reduce disease burden. Public health strategies should include awareness campaigns, widespread hepatitis B immunization, and enhanced healthcare infrastructure. While interferon-based therapy offers modest benefits, emerging treatments such as prenylation inhibitors hold promise for improving clinical outcomes. Universal HDV screening among chronic hepatitis B patients could also contribute to broader efforts to limit HDV transmission. Education of both HDV-negative and HDV-positive individuals on prevention and management remains essential to mitigating the overall impact of this co-infection.

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