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# **Original Research Article**

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# Evaluation of Serum HBV Viral Load and Transaminases in Treatment-Naïve Patients Who Tested Positive for Hepatitis B Virus in the City of N'Djamena, Chad

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# ABSTRACT

## Keywords

ALT; AST; HBV DNA; Hepatitis B; Viral load; Naïve.

### **Article Info**

Received: 05 September2025 Accepted: 30 October 2025 Available Online: 10 November 2025 Hepatitis B virus (HBV) remains a major global public health concern, particularly in developing countries. Accurate diagnosis in infected individuals requires virological and biochemical assessments, which are essential for effective management and follow-up. The objective of this study was to evaluate the serum HBV viral load and transaminase levels among patients who tested positive for the HBs antigen in the city of N'Djamena. This was a prospective, cross-sectional analytical study conducted from February 2024 to March 2025 at the Notre Dame of the Apostles Hospital (HNDA) in N'Djamena, Chad. All patients with chronic HBsAg carriage who tested positive and were reconfirmed after six months were included. An information sheet explaining the study objectives was provided to each participant, followed by an informed consent form signed by all who agreed to take part. Of the 171 patients interviewed, 157 were included in the study after signing the consent form, and their information was recorded on the data collection sheet. Transaminase levels were measured using the ABX 400 / Pentra C400 automated chemistry analyzer, and viral loads were quantified using the GeneXpert Cepheid system, an automated molecular biology platform (PCR and real-time RT-PCR). In the study population, 52.2% of participants were male and 47.8% female, with a mean age of 33.14 years (±10.37). A detectable HBV DNA rate of 83% was observed, while ASAT and ALAT levels were normal in 67.5% and 61.8% of patients, respectively. The majority of patients (74.4%) had a viral load below 2000 IU/mL, compared with 24.6% who had a viral load above 2000 IU/mL. Among those with viral loads above 2000 IU/mL, 76% were male and 24% female. This study highlights the evaluation of initial viremia and transaminase profiles among newly diagnosed HBsAg-positive patients.

#### Introduction

Hepatitis B virus (HBV) infection is a major global public health threat, particularly in developing countries (Ahmed *et al.*, 2023; Elizabeth *et al.*, 2023).

Despite the availability of an effective preventive vaccine for several decades and widely used, well-tolerated antiviral suppressive therapies since 1998, approximately 250 million people worldwide remain chronically infected with HBV. The hepatitis B virus is a leading cause of liver cancer and overall mortality globally, surpassing malaria and tuberculosis (Revill P.A. *et al.*, 2019; Mendie H. *et al.*, 2020).

Hepatitis B is often a benign disease; however, 5–10% of immunocompetent adults progress to chronic hepatitis, which may evolve into cirrhosis or hepatocellular carcinoma (HCC). Furthermore, 15–45% of children infected with HBV develop cirrhosis and/or HCC later in life (Fattovich *et al.*, 2008; Kao *et al.*, 2010).

According to the 2024 WHO report, HBV-related mortality is increasing, with 1.3 million deaths recorded in 2022 compared to 1.1 million in 2019. The highest HBV prevalence is observed in sub-Saharan Africa and East Asia. The African region alone accounts for 63% of new HBV infections; however, only 18% of newborns receive vaccination at birth.

Despite improvements in diagnostic tools, treatment options, and reduced costs of medical products, screening and treatment rates remain low (WHO, 2024). For adequate clinical management and assessment of treatment efficacy, several virological and biochemical biomarkers are used. Virological success is defined by reduced viral load or complete non-detectability depending on the sensitivity of the detection method. Highly sensitive real-time PCR assays now provide reliable quantification of serum HBV DNA. Measurement of HBV DNA is essential in the management of chronic HBV infection (Lila P. et al., 2020; Fabbio M. et al., 2021).

Serum transaminases—AST (aspartate aminotransferase) and ALT (alanine aminotransferase)—are enzymes released by the liver in response to tissue damage and disease. Their measurement is used to assess the severity of hepatic fibrosis. These biochemical markers are highly relevant for the monitoring and clinical management of

individuals with HBV infection (Meryem G. et al., 2020). ALT is the most commonly used enzyme for evaluating liver disease.

Previous studies reported that even slight increases in ALT within the upper-normal range are significantly associated with higher risk of liver-related mortality in the general population (Kim H.C. *et al.*, 2004; Wu W.C. *et al.*, 2012).

The objective of this study was to evaluate baseline serum HBV DNA levels and initial transaminases among treatment-naïve patients newly diagnosed positive for HBV infection in the city of N'Djamena, Chad.

#### **Materials and Methods**

# **Study Design**

This study was a prospective, cross-sectional analytical investigation conducted from February 2024 to March 2025 at the Notre Dame des Apôtres (NDA) Hospital in N'Djamena, Chad.

#### **Inclusion Criteria**

All chronically infected HBsAg-positive patients who had known their serological status for more than six months and who presented to the laboratory for both transaminase testing and viral load analysis were included.

#### **Sampling Method**

A non-probabilistic, voluntary sampling method was used. A total of 210 individuals presenting for transaminase and viral load testing were approached. Among the 171 individuals interviewed, 157 consented to participate and were included, while 14 declined and were excluded.

#### **Data Collection Procedures**

An information sheet explaining the purpose of the study was provided to each participant, followed by additional clarification when necessary.

A written informed consent form was then issued and signed by all participants who agreed to take part in the study.

## **Sample Collection Method**

Sample collection took place in the phlebotomy unit of the NDA Hospital laboratory. Two tubes were used for each participant: an EDTA tube and a heparinized tube.

Samples were immediately transported to the biochemistry-virology unit for analysis.

# **Biological Analyses**

EDTA tubes were used for HBV viral load quantification.

Heparinized tubes were used for transaminase measurement.

A volume of 2–3 mL of blood was drawn into each tube.

Transaminases were measured using the Pentra C400 Horiba analyzer.

HBV DNA viral load was quantified using the GeneXpert Cepheid automated molecular testing system.

# **Pentra C400 Method Principle**

The ABX 400 / Pentra C400 is a fully automated chemistry analyzer using colorimetry, turbidimetry, and potentiometry. It performs in vitro diagnostics on homogeneous samples including serum, plasma, urine, and whole blood (Technical Manual PC400, 2025).

# **GeneXpert Cepheid Method Principle**

The GeneXpert is an automated system performing molecular biology assays (PCR, nested PCR, and real-time RT-PCR) to determine the presence and quantify the amount of target genetic material (Cepheid System, 2025).

### **Analytical Workflow**

For Pentra C400: Patient registration  $\rightarrow$  sample identification  $\rightarrow$  test selection  $\rightarrow$  validation.

For GeneXpert: Patient identification  $\rightarrow$  pipetting of 1 mL of plasma into the cartridge  $\rightarrow$  barcode scanning  $\rightarrow$  cartridge loading  $\rightarrow$  automated extraction, amplification, and detection within 60 minutes.

A total of 157 samples collected from the included patients were processed for transaminase assays and HBV DNA quantification.

# **Statistical Analysis**

Data collected on paper forms were entered into Excel and exported to SPSS version 25 for statistical analysis. Chi-square and Pearson correlation tests were used where appropriate.

#### **Results and Discussion**

Regarding sociodemographic characteristics, a total of 157 patients were included in the study, of whom 52.2% were male and 47.8% were female. The mean age was 33.14 years ( $\pm$  10.37), with ages ranging from 16 to 60 years. The most represented age group was 26–35 years, accounting for 36.3% of the cases.

# **Biological Characteristics of the Patients**

All association tests were performed using a significance threshold of 5% (p < 0.05). The Chi-square test of independence was applied to evaluate the association between viral load and transaminase levels (ALT, AST), as well as other relevant variables.

# Distribution of Patients According to Detectable and Non-Detectable HBV DNA

Regarding the biological characteristics of the patients, a total of 157 samples from individuals who tested positive for HBsAg were analyzed. Among them, 130 patients had detectable HBV DNA, representing 83%, while 27 patients (17%) had non-detectable HBV DNA (p = 0.001).

# Distribution of patients according to HBV DNA viral load

Among the 130 patients with detectable HBV DNA, 106 had a viral load greater than 10 IU/mL (81.5%), while 24 had a viral load below 10 IU/mL (18.4%) (P = 0.001).

# **Distribution According to ASAT Levels**

Based on ASAT values, 106 patients (67.5%) had abnormal levels, outside the reference range, whereas 51 patients (32.5%) had normal levels within the reference

range (P = 0.24). Reference range for normal ASAT:  $\leq$  35 UI/mL.

# **Distribution According to ALAT Levels**

Regarding ALAT values, 106 patients (67.5%) had normal levels within the reference range, while 51 patients (32.5%) had abnormal levels. Reference range for normal ALAT: ≤ 45 UI/mL.

# Sociodemographic Characteristics of the Study Population

Male participants represented the majority of the study population, accounting for 52.2%. This result is similar to findings reported by Kumar *et al.*, and Mbouyap *et al.*, who observed respectively 56.1% male participants in studies conducted in India in 2024 and in Cameroon in 2025 (Kumar M. *et al.*, 2024; Mbouyap J.R. *et al.*, 2025). Diawara *et al.*, reported a higher proportion of male patients (76.1%) in a study conducted at the Principal Hospital of Dakar, Senegal in 2022 (Diawara *et al.*, 2022).

The mean age of the study population was  $33.14 \pm 10.37$  years, with extremes ranging from 16 to 60 years. The most represented age group was 26–35 years, accounting for 36.3% of participants. This predominance may be explained by the fact that this age group is sexually active and more frequently exposed to risk factors such as sharing injection drug equipment and tattooing materials.

Our findings are comparable to those of Kumar *et al.*, who reported a mean participant age of  $36.35 \pm 14.76$  years with an age range of 2.5 to 82 years, with the most represented group being young sexually active adults aged 21–40 years (Kumar M. *et al.*, 2024). Similarly, Salamata *et al.*, reported a comparable mean age of 33 years with an age range of 14 to 83 years (Salamata D. *et al.*, 2018).

Regarding professional categories, 28.66% of patients were civil servants and 20.38% were students. This distribution may be due, on one hand, to the relatively high cost of follow-up tests, and on the other, to the lack of adequate information and orientation after an initial positive HBsAg diagnosis. Other professions included housewives (15.28%), traders and pupils (14.01%), and

craftsmen (7.64%).

Most patients had a higher education level (43.94%), followed by secondary education (35.66%), while primary and non-educated participants represented less than 12%. These findings may be explained by better awareness of HBV infection among administrative workers, university students, and high-school students, as well as their greater tendency to seek medical follow-up. Ntagirabiri *et al.*, also reported that most patients were employees (41.2%) and had higher education, followed by traders, although in their study, students were less represented compared with our findings (Ntagirabiri R. *et al.*, 2016).

Among study participants, married individuals accounted for 59%, whereas single individuals represented 41%. This could be attributed to sexual transmission being one of the primary routes of HBV transmission.

# **Biological Characteristics of the Patients**

Regarding HBV DNA detectability, among the 157 samples analyzed, 130 (83%) were positive for detectable HBV DNA, while 27 samples (17%) showed no detectable DNA. This difference was statistically significant (P = 0.001).

These findings may be explained by the fact that all patients had previously tested positive for HBsAg before undergoing viral load quantification. Our results are consistent with those of Diawara *et al.*, who reported 92.48% detectable HBV DNA and 7.52% undetectable DNA among the quantified patient samples (Diawara P.S. *et al.*, 2022).

Khairy *et al.*, reported a lower proportion of detectable HBV DNA, with 65.9% DNA-positive samples and 34.1% undetectable DNA (Khairy H. *et al.*, 2025).

With respect to liver transaminases, 61.8% of patients had normal aspartate aminotransferase values (≤ 35 UI/mL), while 38.2% had elevated values (> 35 UI/mL).

Similarly, 67.5% of patients had normal alanine aminotransferase values ( $\leq$  45 UI/mL) compared with 32.5% with elevated levels (> 45 UI/mL). This could be attributed to the fact that the majority of patients had relatively low viral loads.

Presence ADN
Absence ADN

Total = 157 échantillons

Figure.1 Distribution of patients according to DNA detectability

Table.1 Summary of Sociodemographic Characteristics of the Patients

Variable	Category	Number (n)	Percentage (%)
Sex	Male	82	52.2
	Female	75	47.8
	Total	157	100
<b>Marital Status</b>	Married	92	58.5
	Single	64	40.7
	Widowed	1	0.6
	Total	157	100
Occupation	Civil servant	45	28.6
	Student	32	20.3
	Trader	22	14.0
	Pupil	22	14.0
	Housewife	24	15.2
	Skilled worker / Artisan	12	7.6
	Total	157	100
<b>Educational Level</b>	Higher education	69	43.9
	Secondary education	56	35.6
	Primary education	20	12.7
	No schooling	12	7.6
	Total	157	100
Age Group (years)	15–25	40	25.5
	26–35	57	36.3
	36–45	41	26.1
	46–55	15	9.6
	>55	4	2.5
	Total	157	100

**Table.2** Distribution of patients according to DNA detectability

DNA Status	Count	Percentage (%)	P value
<b>Detectable DNA</b>	106	81.5	0.001
<b>Undetectable DNA</b>	24	18.4	_
Total	130	100.0	_

**Table.3** Distribution According to ASAT Levels

<b>ASAT Status</b>	Count	Percentage (%)	P value
Normal	97	61.8	0.24
Abnormal	60	38.2	_
Total	157	100.0	_

**Table.4** Distribution According to ALAT Levels

ALAT Status	Count	Percentage (%)	P value
Normal	106	67.5	0.37
Abnormal	51	32.5	_
Total	157	100.0	_

Distribution According to HBV DNA > 2000 UI/mL by Sex

**Table.5** Distribution of DNA Levels > 2000 UI/mL by Sex

Sex	Count	Percentage (%)	P value
Male	19	76	0.02
Female	6	24	_
Total	25	100.0	_

Distribution According to HBV DNA Viral Load

Table.6 Distribution According to HBV DNA Viral Load

HBV DNA Viral Load	Count	Percentage (%)	P value
< 2000 UI/mL	81	74.4	0.47
≥ 2000 UI/mL	25	23.6	_
Total	104	100	

Our findings are comparable to those of Khairy *et al.*, who reported normal alanine aminotransferase levels in 79.8% of cases and normal aspartate aminotransferase levels in 85.7% of cases (Khairy H. *et al.*, 2025). However, they differ from the results of Kumar *et al.*, who found 77.17% abnormal alanine aminotransferase values and 22.83% normal values, while aspartate aminotransferase values were normal in 52.66% and abnormal in 47.34% of cases (Kumar M. *et al.*, 2024). There was a low viral load in the study population, with 74.41% showing HBV DNA levels below 2000 UI/mL, compared to 23.59% above this threshold. This pattern could be explained by the fact that most patients were newly diagnosed with HBsAg and were undergoing

initial viral load assessment. Our findings are similar to those of Mbouyap *et al.*, who observed viral loads below 2000 UI/mL in 68.5% of patients (Mbouyap J.R. *et al.*, 2025).

According to the analytical results, there was a significant association between viral load and alanine aminotransferase levels (P = 0.006). In contrast, aspartate aminotransferase levels did not show a significant association with viral load (P = 0.085). Esmaeelzadeh *et al.*, in their study conducted in Mashhad, Iran in 2017, reported a significant association between HBV DNA and transaminase levels (Esmaeelzadeh A. *et al.*, 2017). Our findings also align

with those of Mbouyap *et al.*, who found a correlation between viral load and alanine aminotransferase levels in their 2025 study in Cameroon (Mbouyap J.R. *et al.*, 2025).

Regarding viral load and age, the analysis showed no significant correlation between age and HBV DNA detection (P = 0.386). The number of male patients with viral loads exceeding 2000 UI/mL was higher than that of female patients, with a statistically significant difference (P = 0.0001). Our results are comparable to those of Diawara *et al.*, who reported in 2022 that viral loads were higher among men than women (Diawara P.S. *et al.*, 2022).

In conclusion, this study assessed baseline viral load levels and liver transaminases among treatment-naïve patients in the city of N'Djamena. Overall, the viral load was low in the study population, and transaminase levels were within the normal range for most patients.

The evaluation of viral load and transaminases is essential when initiating clinical follow-up in patients who test positive for HBsAg. These parameters confirm or rule out the presence of HBV DNA and help assess liver enzyme levels, which are key indicators of disease progression.

#### **Author Contributions**

Nan-arabé Lodoum conceptualized the study. coordinated field activities, performed laboratory analyses, and drafted the manuscript. Mbaihodji Jules contributed to the validation of the database, as well as the analysis and interpretation of the data. Mbainadji Lodoum contributed by reviewing the contextual relevance of the manuscript and performing corrections. Hassan Mahamat Ali contributed to the validation and revision of the manuscript. Ndjelassem Ferdinand contributed to the study design and manuscript revision. Diamaladine Mahamat Doungous contributed to manuscript reading and corrections. Naibi Keitoyo Amedé contributed to manuscript reading and corrections. Asbagui Faysala Oscar contributed to manuscript reading and corrections. Koulbou Mahamat contributed to manuscript reading and corrections. Dahabaye Adoum Mahamat contributed to manuscript reading and corrections. Adawaye Chatté contributed to the study design, critically revised the manuscript, and provided overall supervision.

## **Data Availability**

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

#### **Declarations**

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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