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Epidemiology and Sociodemographic Determinants of HBsAg Seropositivity with Complementary Liver Biomarker Analysis among Late-Adolescent and Adult Sub-Saharan African Migrants in Al-Kufra, Libya

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ABSTRACT:

Background: Hepatitis B virus (HBV) remains a major cause of cirrhosis, hepatocellular carcinoma and liver failure, while migrants from endemic settings can face substantial barriers to diagnosis, vaccination and continuity of care. We estimated hepatitis B surface antigen (HBsAg) seroprevalence and sociodemographic determinants among newly arrived late-adolescent and adult sub-Saharan African migrants in Al-Kufra, southeastern Libya, and illustrate biochemical patterns across HBV-related liver-disease stages.

Methods: We analyzed cross-sectional participant-level data collected from June 2025 to February 2026. The primary sample comprised 539 migrants aged 18-63 years; ages 18-19 were considered late adolescence and no participant was younger than 18 years. HBsAg was measured using the mini VIDAS HBsAg Ultra assay. Prevalence was summarized using Wilson 95% confidence intervals, and associations were evaluated using chi-square tests and modified Poisson regression with robust standard errors to estimate adjusted prevalence ratios (aPRs); a secondary logistic model assessed discrimination and calibration. Several liver function tests were performed on hepatitis B patients, including transaminase (AST and ALT) and total bile acid (TBA) levels, among healthy individuals, patients with chronic hepatitis B (CHB), patients with liver cirrhosis (LC), patients with hepatocellular carcinoma (HCC), and patients with liver failure (LF). The two data sets were not combined at the participant level.

Results: In the primary migrant cohort, 148/539 participants were HBsAg positive (27.5%; 95% CI 23.9-31.4). Prevalence was 32.7% in participants aged 18-19 years and varied from 9.1% among Malian to 47.8% among Eritrean participants. In adjusted analysis, Eritrean nationality was associated with higher HBsAg prevalence than Sudanese nationality (aPR 1.81, 95% CI 1.09-3.00), whereas primary education (aPR 0.63, 95% CI

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0.44-0.90) and secondary/higher education (aPR 0.20, 95% CI 0.10-0.41) were associated with lower prevalence. Each 10-year increase in age was associated with lower adjusted prevalence (aPR 0.82, 95% CI 0.69-0.97). The secondary model had AUC 0.737 (bootstrap 95% CI 0.693-0.781) with no evidence of poor calibration (Hosmer-Lemeshow p=0.745). The biochemical results of liver function tests related to hepatitis B in the participants migrating from Al-Kufra showed that the mean concentration of thiobarbituric acid (TBA) increased from 3.99 μmol/L in healthy individuals to 24.94 μmol/L in patients with chronic hepatitis B, 39.94 μmol/L in patients with cirrhosis, 45.79 μmol/L in patients with hepatocellular carcinoma, and 203.51 μmol/L in patients with liver failure. Patients with liver failure also showed the highest mean concentrations of aspartate aminotransferase (AST) (410.24 U/L) and alanine aminotransferase (ALT) (561.83 U/L).

Conclusions: HBsAg positivity was exceptionally high in this migrant sample, with marked heterogeneity by nationality and educational attainment. The findings support entry-point HBV testing linked to confirmatory assessment, vaccination of susceptible individuals and culturally responsive follow-up rather than risk-based exclusion from testing. We conclude that analyzing vital signs and biochemical tests performed on liver function in migrant participants via Kufra is important for assessing liver function associated with hepatitis B virus infection.

1. INTRODUCTION

Hepatitis B virus (HBV) infection remains a major, vaccine-preventable cause of chronic liver disease, cirrhosis and hepatocellular carcinoma. Despite the availability of highly effective infant immunization and potent nucleos(t)ide analogue therapy, global elimination remains off track. WHO reporting continues to show a large reservoir of undiagnosed infection and major losses between diagnosis, clinical assessment and treatment, making case finding and durable linkage to care central components of the 2030 elimination agenda [1-3,17,19]. The public-health importance of screening is therefore not limited to identifying infection; it also lies in connecting people with confirmatory evaluation, assessment of liver disease, treatment when indicated, vaccination of susceptible contacts and preventive counselling.

The age at HBV acquisition strongly influences the natural history of infection. Perinatal and early-childhood acquisition carries a much greater probability of chronic infection than acquisition later in life, which is why timely birth-dose vaccination, completion of the infant series and prevention of mother-to-child transmission are foundational elimination interventions [17,19]. The 2024 WHO guidance also explicitly expanded and simplified treatment recommendations for adolescents, reflecting the need to prevent decades of cumulative liver injury in people infected early in life [17]. These life-course considerations are especially relevant when interpreting HBV epidemiology in migrants from settings where historical birth-dose coverage, maternal screening and vaccine access have varied considerably.

HBV prevalence is highly heterogeneous across countries and regions, and population movement can relocate pre-existing epidemiological burden without implying that migration itself causes infection. Migrants should therefore not be treated as a biologically homogeneous risk group. A 2026 systematic review and meta-analysis estimated a pooled HBsAg prevalence of 4.4% among migrants living in high-income countries with low or intermediate endemicity, with higher prevalence among adults than among people younger than 18 years [5]. A systematic review of EU/EEA/UK data likewise demonstrated substantial heterogeneity by origin, migrant category and study setting [6]. Contemporary liver-health policy emphasizes that migrant health responses should be rights-based, non-stigmatizing and integrated into universal health coverage rather than framed as border-control interventions [20].

The observed burden in migrant populations is shaped by both pre-migration and post-migration factors. Pre-migration determinants include country-of-origin endemicity, childhood vaccination opportunities, perinatal prevention and prior healthcare access. During migration and after arrival, unstable accommodation, frequent movement, language barriers, limited documentation, fragmented vaccination records, uncertainty regarding entitlement to care, fear of administrative consequences and competing priorities can all delay screening or interrupt follow-up [7,18,20]. These barriers explain why a positive screening

test has limited public-health value unless the testing pathway is accompanied by understandable communication, referral support and continuity of care.

Al-Kufra is a strategically important transit and settlement point in southeastern Libya for people arriving from sub-Saharan Africa. The most directly comparable study screened 3,248 migrants in Al-Kufra during 2019 and reported HBsAg positivity of 23.4%, a level far above contemporary pooled estimates from many destination-country migrant studies [4-6]. The present dataset therefore offers an opportunity to examine whether a similarly high burden is observed in a more recent cohort and to identify characteristics associated with HBsAg positivity. Such updated evidence is particularly important for local laboratory planning, vaccination services, referral pathways and surveillance.

Recent implementation studies reinforce the importance of moving from one-time testing to a complete screen-and-link pathway. Community-based screening of West African migrants in Spain achieved high linkage to specialist care when testing was combined with active referral [9]. A 2026 prospective programme among asylum seekers and undocumented migrants in Rome found HBsAg positivity in 5.3% of screened participants and successfully engaged 87% of HBsAg-positive individuals in care when administrative, linguistic and logistic support were built into the pathway [10]. A multicentre analysis in northern Italy similarly identified major attrition after screening, including low uptake of indicated HBV vaccination, demonstrating that access to a test does not guarantee completion of prevention or care [21]. At a broader level, a 2025 global systematic review and meta-analysis found substantial attrition across chronic HBV care cascades and highlighted the value of integrated, decentralized and patient-centred service models [22]. Community implementation work published in 2026 further supports active navigation from screening to care rather than passive referral [26].

Interpretation of HBsAg requires diagnostic precision. HBsAg positivity identifies current HBV infection but, in a single cross-sectional specimen, cannot by itself distinguish acute from chronic infection. Confirmation of chronic hepatitis B generally requires persistence over time and should be accompanied by clinical and laboratory assessment that may include HBV DNA, alanine aminotransferase, HBeAg status, non-invasive fibrosis assessment, evaluation for hepatitis D where indicated and hepatocellular carcinoma surveillance according to risk [17,19]. Accordingly, the outcome in this study is deliberately described as HBsAg positivity or seropositivity rather than confirmed chronic hepatitis B.

Adolescent and pediatric evidence also provides useful context. Recent migrant studies in Europe have documented HBV infection among unaccompanied asylum-seeking minors [15,16], and the 2026 migrant meta-analysis reported lower pooled HBsAg prevalence among people younger than 18 years than among adults [5]. However, the present dataset contains no participant younger than 18 years. The youngest group comprises late adolescents aged 18-19 years, and any discussion of children or pediatric migrants is therefore external contextual evidence rather than a description of the study population.

Screening identifies current HBV infection, but the clinical value of diagnosis depends on downstream assessment of liver injury, fibrosis and functional reserve. Aminotransferases such as AST and ALT mainly reflect hepatocellular injury and may fluctuate substantially across the HBV disease course, whereas circulating bile acids are influenced by hepatocyte uptake, canalicular transport, enterohepatic cycling and portal-systemic shunting. Prior studies have reported associations between serum bile-acid abnormalities and cirrhosis, acute decompensation, liver failure, fibrosis and subsequent HCC risk in chronic HBV [28-31].

Against this background, the present study aimed to provide a rigorous, publication-oriented analysis of HBsAg positivity among newly arrived late-adolescent and adult sub-Saharan African migrants in Al-Kufra. The prespecified analytical objectives were to: (1) estimate overall and subgroup-specific HBsAg prevalence with 95% confidence intervals; (2) quantify variation by nationality, age, sex and educational attainment; (3) estimate adjusted prevalence ratios for independent sociodemographic determinants; (4) examine model robustness and discrimination using sensitivity and secondary logistic analyses; and (5) interpret the findings in relation to contemporary migrant-screening, service-delivery and adolescent HBV literature; and (6) provide aggregate description of AST, ALT and TBA patterns across HBV-related disease stages to contextualize downstream clinical assessment after screening. The broader goal was to generate evidence that can inform an equitable local screen-vaccinate-link-to-care pathway rather than a screening programme in isolation.

2. MATERIALS AND METHODS

2.1 Study design, reporting framework and setting

This was a cross-sectional analytical study based on participant-level data from newly arrived migrants assessed at Al-Kufra Shelter Center in southeastern Libya between June 2025 and February 2026. Al-Kufra lies on a major trans-Saharan migration route and functions as a transit and settlement point for migrants from several sub-Saharan African countries. The manuscript was prepared in accordance with the principles of the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement for cross-sectional studies [23]. The analysis used the complete dataset supplied by the investigators and did not alter the recorded laboratory outcome.

2.2 Study population, eligibility and analytic sample

The available SPSS dataset contained 539 participants aged 18-63 years. All 539 records had non-missing values for HBsAg status, age, sex, nationality, educational attainment, viral-hepatitis awareness, reported HBV vaccination and last country of residence; consequently, all records were retained in the primary analysis and no imputation was required for these variables. The available study documentation did not include participants younger than 18 years. Participants aged 18-19 years (n=52) were classified as late adolescents and those aged 20 years or older as adults. Because the source documentation does not provide a sufficiently detailed probability-sampling frame, the dataset is treated as a facility-based study sample and population-level extrapolation beyond comparable migrant populations should be cautious.

2.3 Data source, variable verification and quality control

Analyses were performed directly from the uploaded SPSS file (HBVMigrantsData090126.sav). Variable labels and coded value labels were checked against the data dictionary embedded in the SPSS file before recoding. HBsAg diagnosis was coded as negative or positive; sex as male or female; nationality in seven categories; and education in five source categories. Internal checks confirmed that the number of observations was 539 and that the principal analytic variables contained no system-missing values. Derived variables used for analysis were created reproducibly from the original variables, while the unmodified source data were retained as the reference dataset.

2.4 Laboratory testing and primary outcome

The study documentation states that HBsAg was measured using the VIDAS HBsAg Ultra assay on the mini VIDAS platform, an automated enzyme-linked fluorescent assay (ELFA) for qualitative HBsAg detection. Published evaluation of the VIDAS HBsAg Ultra assay has demonstrated high diagnostic sensitivity and specificity in laboratory settings [27]. The primary outcome was a positive HBsAg result. The primary Al-Kufra migrant dataset did not include repeat HBsAg testing after at least six months, HBV DNA, total anti-HBc, anti-HBs, HBeAg, anti-HDV, liver biochemistry or fibrosis staging; therefore, HBsAg positivity was not classified as confirmed chronic hepatitis B and liver-disease stage was assigned to these participants. Current WHO guidance supports reflex or facilitated virological and liver-disease assessment after HBsAg detection [17-19].

2.5 Exposure variables and operational definitions

Age was analysed both continuously and categorically. For regression, age was scaled per 10-year increase to provide an interpretable effect estimate. For descriptive analyses, age was grouped as 18-19, 20-27, 28-36, 37-45, 46-54 and 55 years or older. Sex was retained as recorded. Nationality was analysed in seven categories: Sudanese, Chadian, Nigerian, Eritrean, Ethiopian, Somali and Malian. Educational attainment was collapsed from the five recorded categories into illiterate, primary, and secondary-or-higher (secondary school, university and postgraduate) to reduce sparse cells and improve multivariable model stability. Male sex, Sudanese nationality and illiteracy were used as reference categories because they provided clinically interpretable comparisons and adequate group sizes.

2.6 Sample size, data completeness and precision

The analysis was based on the fixed number of eligible records available in the source dataset rather than on a newly recruited sample; therefore, no retrospective post hoc power calculation was used as a criterion for inclusion. The 539 participants included 148 HBsAg-positive events. The principal adjusted model contained age, sex, six nationality indicator terms and two education indicator terms, providing substantially more outcome events than model coefficients. Precision was communicated

through 95% confidence intervals rather than through power alone. Nationality-specific estimates based on small strata were interpreted cautiously, and a dedicated sensitivity analysis was used to test the influence of the smallest nationality group.

2.7 Statistical analysis

Continuous age was summarized using mean, standard deviation and range; categorical variables were summarized using counts and percentages. Overall and subgroup HBsAg prevalence estimates were accompanied by Wilson 95% confidence intervals, which provide more reliable coverage than the simple Wald interval when sample sizes or proportions are modest. Pearson chi-square tests were used for unadjusted comparisons of categorical distributions. All tests were two-sided, and $p<0.05$ was considered statistically significant; effect estimates and confidence intervals were emphasized over isolated p-values.

Because HBsAg positivity was common in this dataset (27.5%), odds ratios from conventional logistic regression could materially overstate prevalence-ratio associations. The primary multivariable analysis therefore used a modified Poisson generalized linear model with a log link and robust sandwich standard errors to estimate adjusted prevalence ratios (aPRs) and 95% confidence intervals, following the robust-variance approach described by Zou [24]. Age, sex, nationality and collapsed educational attainment were included simultaneously. The model was intended for etiologic description and risk stratification at the population level, not for individual clinical diagnosis.

2.8 Reproducibility, software and reporting of results

The analysis was reproduced programmatically from the original SPSS file using Python 3.13.5, pandas 2.2.3, NumPy 2.3.5, SciPy 1.17.0, statsmodels 0.14.6 and scikit-learn 1.8.0. Tables were generated from analysis objects rather than manually transcribed, and figures were produced from the same derived dataset used for modelling. Reporting was organized around person-centred surveillance principles, emphasizing denominators, confidence intervals and linkage implications rather than nationality-based labeling [25].

3. RESULTS

3.1 Participant characteristics and overall prevalence

The study included 539 participants, of whom 501 (92.9%) were male and 38 (7.1%) were female. Mean age was 29.45 years (SD 8.93; range 18-63). Fifty-two participants (9.6%) were aged 18-19 years. Overall, 148/539 participants were HBsAg positive (27.5%; 95% CI 23.9-31.4).

Table 1. Participant characteristics and HBsAg positivity.

Variable	Category	Total n	HBsAg negative n	HBsAg positive n	Positive %	p-value
Sex	Male	501	363	138	27.5	0.870
	Female	38	28	10	26.3	
Age group, years	18-19	52	35	17	32.7	0.463
	20-27	211	146	65	30.8	
	28-36	169	127	42	24.9	
	37-45	77	59	18	23.4	
	46-54	24	20	4	16.7	
	55+	6	4	2	33.3	

Variable	Category	Total n	HBsAg negative n	HBsAg positive n	Positive %	p-value
Nationality	Sudanese	209	181	28	13.4	<0.001
	Chadian	106	66	40	37.7	
	Nigerian	47	28	19	40.4	
	Eritrean	46	24	22	47.8	
	Ethiopian	47	30	17	36.2	
	Somali	62	42	20	32.3	
	Malian	22	20	2	9.1	
Education	Illiterate	261	157	104	39.8	<0.001
	Primary	136	102	34	25.0	
	Secondary or higher	142	132	10	7.0	

3.2 Prevalence by nationality, age and education

HBsAg prevalence differed strongly by nationality ($p<0.001$). The highest estimates were observed among Eritrean (47.8%), Nigerian (40.4%) and Chadian (37.7%) participants, whereas prevalence was lower among Sudanese (13.4%) and Malian (9.1%) participants. The 95% confidence intervals were wide for smaller nationality groups, emphasizing the importance of interpreting national categories as sample-specific estimates rather than fixed country-level risks.

Table 2. Nationality-specific HBsAg prevalence with Wilson 95% confidence intervals.

Nationality	N	HBsAg positive n	Prevalence %	95% CI
Sudanese	209	28	13.4	9.4-18.7
Malian	22	2	9.1	2.5-27.8
Somali	62	20	32.3	22.0-44.6
Ethiopian	47	17	36.2	24.0-50.5
Chadian	106	40	37.7	29.1-47.2
Nigerian	47	19	40.4	27.6-54.7
Eritrean	46	22	47.8	34.1-61.9

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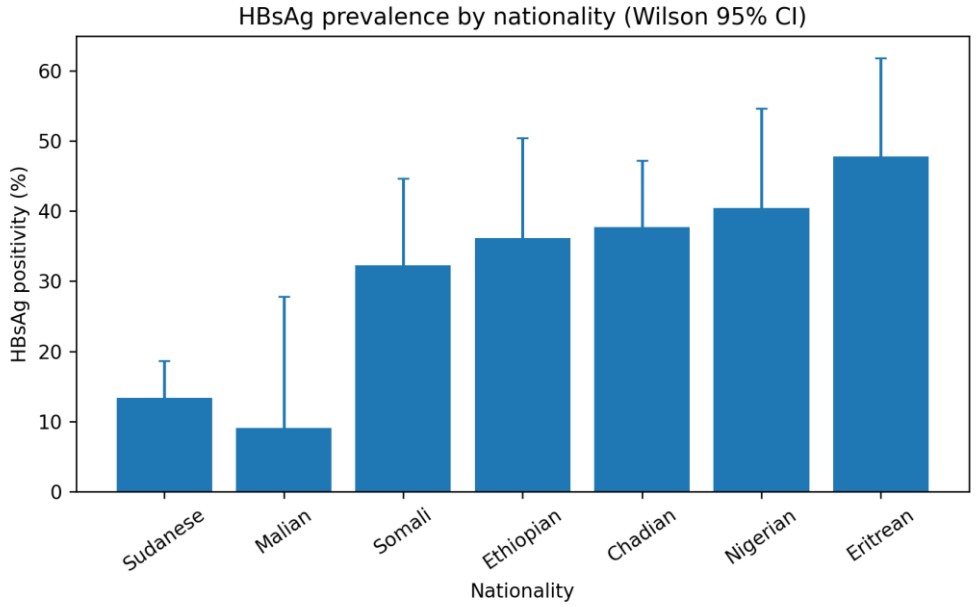

Figure 1. HBsAg prevalence by nationality with Wilson 95% confidence intervals.

Age-specific prevalence was 32.7% among late adolescents aged 18-19 years, 30.8% at 20-27 years, 24.9% at 28-36 years, 23.4% at 37-45 years and 16.7% at 46-54 years. The apparent rise in the 55+ group (33.3%) was based on only six participants and is therefore imprecise. Educational attainment showed a pronounced inverse gradient, from 39.8% in illiterate participants to 25.0% with primary education and 7.0% with secondary or higher education.

Table 3. Age-specific HBsAg prevalence with Wilson 95% confidence intervals.

Age group	N	HBsAg positive n	Prevalence %	95% CI
18-19	52	17	32.7	21.5-46.2
20-27	211	65	30.8	25.0-37.3
28-36	169	42	24.9	18.9-31.9
37-45	77	18	23.4	15.3-34.0
46-54	24	4	16.7	6.7-35.9
55+	6	2	33.3	9.7-70.0

Table 4. Education-specific HBsAg prevalence with Wilson 95% confidence intervals.

Education	N	HBsAg positive n	Prevalence %	95% CI
Illiterate	261	104	39.8	34.1-45.9
Primary	136	34	25.0	18.5-32.9
Secondary or higher	142	10	7.0	3.9-12.5

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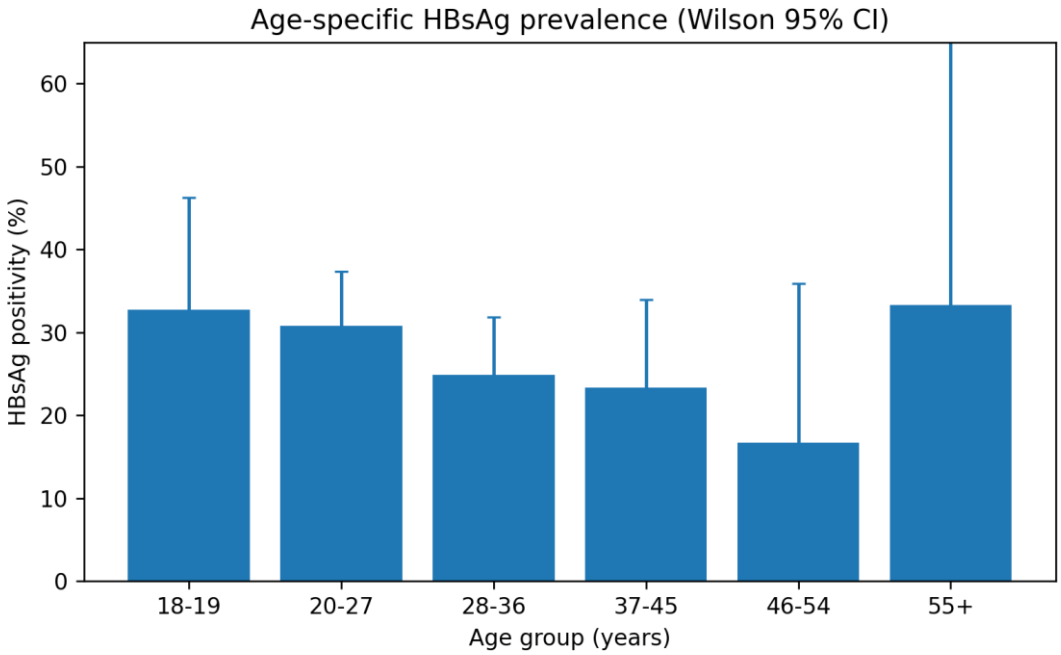

Figure 2. Age-specific HBsAg prevalence with Wilson 95% confidence intervals.

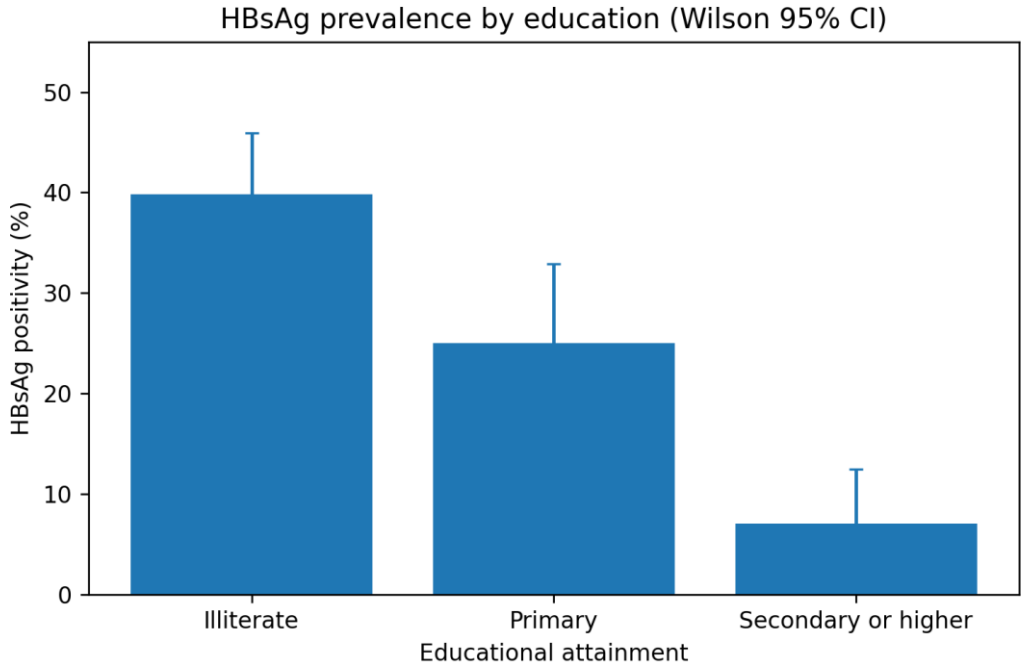

Figure 3. HBsAg prevalence by educational attainment with Wilson 95% confidence intervals.

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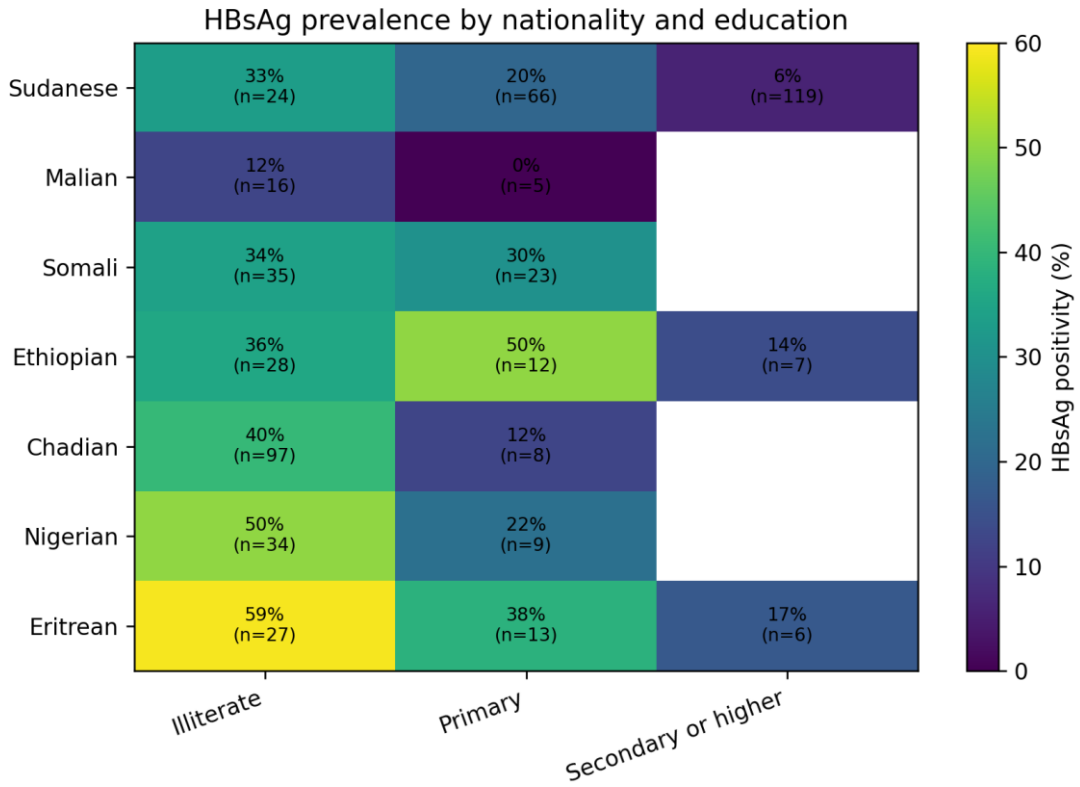

Figure 4. HBsAg prevalence by nationality and educational attainment. Cells with fewer than five participants are left blank.

3.3 Multivariable determinants

After adjustment for age, sex, nationality and education, Eritrean nationality remained associated with higher HBsAg prevalence than Sudanese nationality (aPR 1.81, 95% CI 1.09-3.00, p=0.022). Primary education was associated with lower prevalence (aPR 0.63, 95% CI 0.44-0.90), and secondary/higher education showed an even stronger inverse association (aPR 0.20, 95% CI 0.10-0.41). Each 10-year increase in age was associated with lower adjusted prevalence (aPR 0.82, 95% CI 0.69-0.97). Sex was not independently associated with HBsAg positivity.

Table 5. Modified Poisson regression with robust standard errors for HBsAg positivity.

Predictor	Adjusted prevalence ratio	95% CI	p-value
Female vs male	1.21	0.73-2.01	0.466
Chadian vs Sudanese	1.31	0.79-2.15	0.293
Eritrean vs Sudanese	1.81	1.09-3.00	0.022
Ethiopian vs Sudanese	1.38	0.78-2.43	0.270
Malian vs Sudanese	0.35	0.09-1.35	0.127
Nigerian vs Sudanese	1.51	0.89-2.58	0.129
Somali vs Sudanese	1.18	0.69-2.03	0.550

Predictor	Adjusted prevalence ratio	95% CI	p-value
Primary vs illiterate	0.63	0.44-0.90	0.012
Secondary/higher vs illiterate	0.20	0.10-0.41	<0.001
Age (per 10-year increase)	0.82	0.69-0.97	0.021

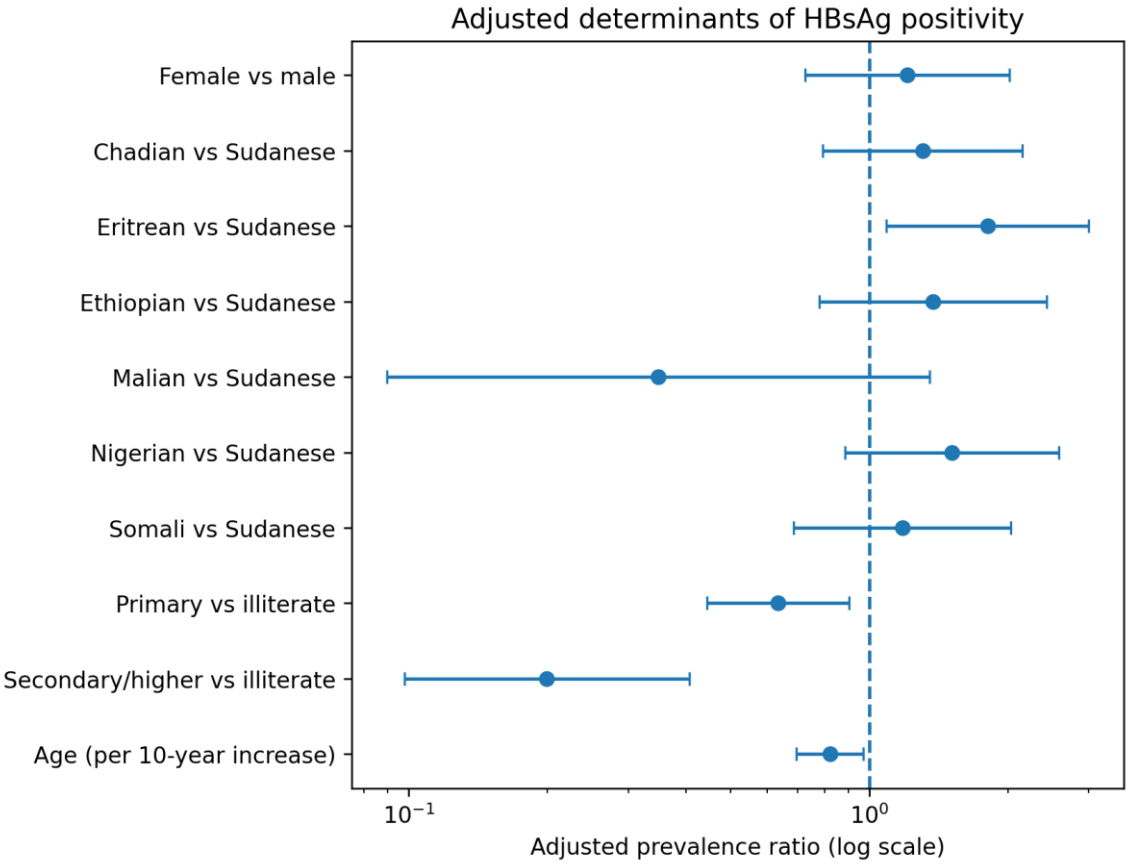

Figure 5. Forest plot of adjusted prevalence ratios for HBsAg positivity.

3.4 Model performance and sensitivity analysis

The secondary logistic model showed moderate discrimination (AUC 0.737; bootstrap 95% CI 0.693-0.781). The Hosmer-Lemeshow statistic was 5.12 (df=8, p=0.745), providing no evidence of poor calibration. Excluding Malian participants did not materially alter the direction of the principal age, education or Eritrean-nationality associations, supporting the stability of the main conclusions.

Table 6. Sensitivity analysis excluding the nationality group with n<30.

Predictor	Sensitivity aPR	95% CI	p-value
Female vs male	1.2	0.73-2.03	0.443
Chadian vs Sudanese	1.3	0.80-2.18	0.273

Predictor	Sensitivity aPR	95% CI	p-value
Eritrean vs Sudanese	1.8	1.10-3.03	0.020
Ethiopian vs Sudanese	1.4	0.79-2.46	0.252
Nigerian vs Sudanese	1.5	0.90-2.61	0.119
Somali vs Sudanese	1.2	0.69-2.05	0.524
Primary vs illiterate	0.6	0.45-0.92	0.016
Secondary/higher vs illiterate	0.2	0.10-0.41	<0.001
Age (per 10-year increase)	0.8	0.70-0.98	0.028

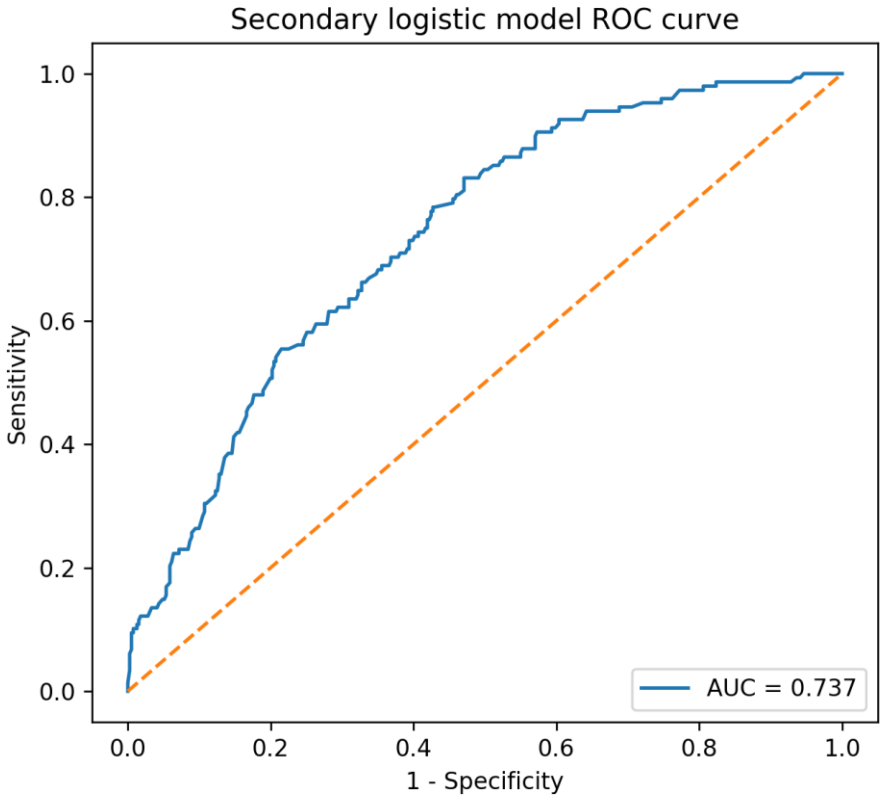

Figure 6. ROC curve for the secondary logistic regression model.

3.5 biochemical stratification in HBV disease-stage dataset from partcipate the Al-Kufra migrant cohort.

The biochemical patterns across HBV-related clinical categories. Mean AST/ALT values (U/L) were 18.22/15.86 in healthy controls, 110.45/198.33 in CHB, 44.19/39.08 in LC, 80.79/56.47 in HCC and 410.24/561.83 in LF. TBA showed a broader

stage-associated increase, rising from 3.99 µmol/L in healthy controls to 24.94 in CHB, 39.94 in LC, 45.79 in HCC and 203.51 in LF.

Table 7. biochemical profile across HBV-related clinical categories from partcipate the Al-Kufra migrant cohort.

Clinical group	Adjusted n*	AST, U/L, mean ± SD	ALT, U/L, mean ± SD	TBA, µmol/L, mean ± SD
Healthy	39	18.22 ± 4.51	15.86 ± 7.55	3.99 ± 2.63
CHB	151	110.45 ± 216.04	198.33 ± 379.87	24.94 ± 56.04
LC	150	44.19 ± 49.50	39.08 ± 61.57	39.94 ± 53.31
HCC	140	80.79 ± 140.99	56.47 ± 127.79	45.79 ± 80.58
LF	59	410.24 ± 572.09	561.83 ± 716.99	203.51 ± 124.24

**These data are inked to the migrant HBsAg cohort. CHB, chronic hepatitis B; LC, liver cirrhosis; HCC, hepatocellular carcinoma; LF, liver failure; TBA, total bile acids.*

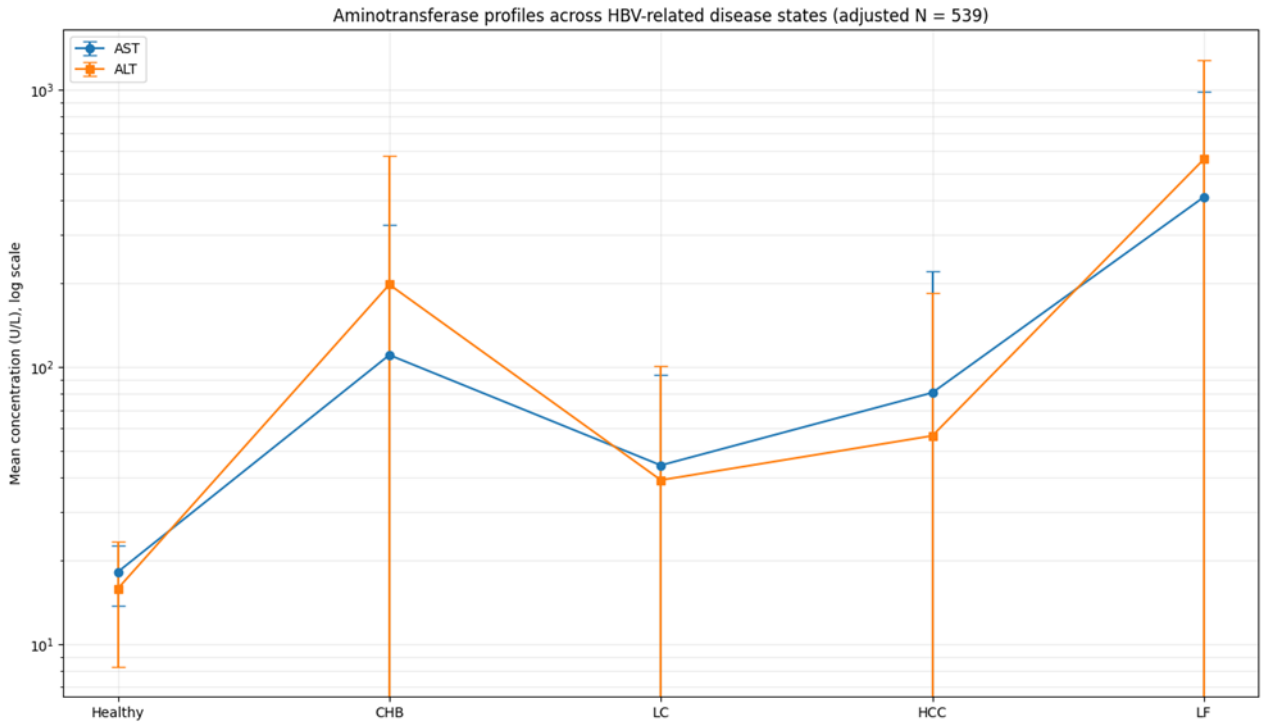

Figure 7. Mean AST and ALT across clinical categories in the ancillary aggregate HBV dataset; error bars show SD and the y-axis is logarithmic. The figure is derived from the Al-Kufra migrant participant-level dataset.

Table 8. Derived fold changes in ancillary liver biomarkers relative to the healthy reference.

Clinical group	AST fold vs healthy	ALT fold vs healthy	TBA fold vs healthy	Group-mean AST/ALT ratio†
Healthy	1.00×	1.00×	1.00×	1.15
CHB	6.06×	12.51×	6.25×	0.56
LC	2.43×	2.46×	10.01×	1.13

Clinical group	AST fold vs healthy	ALT fold vs healthy	TBA fold vs healthy	Group-mean AST/ALT ratio†
HCC	4.43×	3.56×	11.48×	1.43
LF	22.52×	35.42×	51.01×	0.73

†Ratio of group mean AST to group mean ALT; it is not the mean of individual-patient AST/ALT ratios. Fold changes are descriptive.

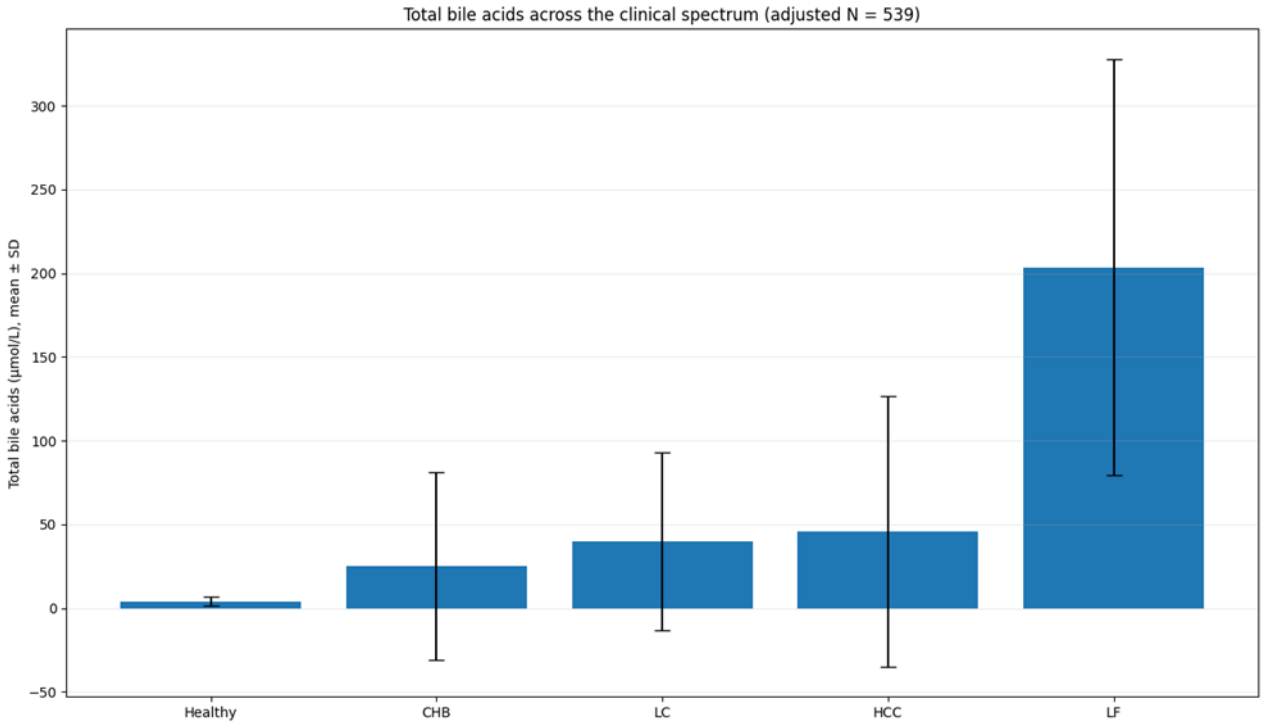

Figure 8. Mean total bile acids (TBA) across clinical categories in the HBV dataset; error bars show SD. The figure is contextual and is a liver-function analysis of the Al-Kufra migrant participants.

Relative to the healthy reference, TBA was 6.25-fold higher in CHB, 10.01-fold in LC, 11.48-fold in HCC and 51.01-fold in LF. The aminotransferase pattern was less monotonic, with marked ALT elevation in CHB and very large AST/ALT elevations in LF. This contrast supports the clinical concept that hepatocellular injury markers and bile-acid handling reflect overlapping but non-identical aspects of HBV-related liver disease [28-31].

4. DISCUSSION

This study identifies an exceptionally high burden of HBsAg positivity among newly arrived late-adolescent and adult sub-Saharan African migrants in Al-Kufra. More than one in four participants tested positive, with prevalence approaching one half in the Eritrean subgroup. Three findings were particularly consistent: substantial heterogeneity by nationality, a strong inverse gradient with educational attainment, and lower adjusted prevalence with increasing age. The multivariable model was stable in sensitivity analysis, although its moderate discrimination indicates that sociodemographic variables alone are not sufficiently accurate to determine who should or should not be tested.

The overall prevalence of 27.5% is striking when placed beside recent international evidence. The 2026 meta-analysis by Sun and Pourmarzi estimated pooled HBsAg prevalence of 4.4% among migrants in high-income countries [5], while community and reception-centre programmes in Spain, Belgium and Rome have commonly reported single-digit prevalence [9-11]. In contrast, the previous Al-Kufra study reported 23.4% HBsAg positivity among 3,248 sub-Saharan African migrants in 2019 [4]. The broad similarity between two independent Al-Kufra samples several years apart strengthens the argument that the transit population encountered in this setting may have a particularly high burden. It does not, however, establish a temporal trend:

differences in country composition, migration routes, recruitment, length of stay and laboratory pathways preclude a direct incidence comparison.

Table 9. Contextual comparison with selected migrant and migrant-minor HBV screening studies. Estimates are descriptive and not directly comparable because populations, settings and tests differ.

Study	Setting	Population	N	HBsAg %	Notes
Current study	Al-Kufra, Libya	Newly arrived sub-Saharan African migrants, age 18-63	539	27.5	Participant-level HBsAg assay
Saaed & Ongerth, 2023 [4]	Al-Kufra, Libya	Sub-Saharan African migrants, age 18-53 (2019)	3248	23.4	Rapid HBsAg with ELISA confirmation
Picchio et al., 2023 [9]	Catalonia, Spain	West African migrants	444	9.2	Community HBsAg rapid testing
D'Aquila et al., 2026 [10]	Rome, Italy	Asylum seekers/undocumented migrants	435	5.3	HBsAg/anti-HBc/anti-HBs screening
Ho et al., 2024 [11]	Belgium	Migrant ethnic minorities in outreach screening	677	3.4	Point-of-care HBsAg testing
Sun & Pourmarzi, 2026 [5]	High-income countries	Migrants; systematic review/meta-analysis	—	4.4	Pooled HBsAg prevalence (44 studies)
Eisen et al., 2023 [15]	London, UK	Unaccompanied asylum-seeking children, age 11-18	1104	3.9	Routine infection screening
Marrone et al., 2020 [16]	Rome, Italy	Unaccompanied migrant minors, age 13-18	879	2.5	HBsAg screening

Nationality-associated differences should be interpreted carefully. Nationality is not a biological determinant of HBV infection and should not be used to stigmatize communities. In migrant health datasets it can act as a proxy for heterogeneous upstream exposures, including background endemicity, childhood vaccination coverage, birth-dose implementation, maternal transmission prevention, healthcare access and migration-route experiences. The broad confidence intervals in several nationality groups and the loss of statistical precision for some adjusted estimates reinforce the need to avoid deterministic country labels. More informative future work would incorporate documented vaccination history, birth-dose status, region of childhood residence, route and duration of migration, family HBV history and behavioral exposures.

The education gradient was one of the strongest findings. HBsAg positivity fell from 39.8% among illiterate participants to only 7.0% among those with secondary or higher education, and the association persisted after adjustment. Educational attainment may capture several mechanisms: health literacy, socioeconomic conditions during childhood, ability to access

vaccination or sterile healthcare, and differences in health-seeking behavior. It may also be confounded by country of origin and unmeasured social determinants. Because the design is cross-sectional, education should be viewed as a marker associated with infection status rather than a protective intervention proven to prevent HBV in this cohort. Nevertheless, the gradient supports low-literacy, culturally tailored communication within screening programmes [7].

Age showed an inverse adjusted association despite the high late-adolescent prevalence of 32.7%. This pattern could reflect cohort differences in the composition of migrants arriving through Al-Kufra, differential vaccination histories, or selection related to migration rather than a biological reduction in infection with age. The small number of participants aged 55 years or older further limits interpretation of the oldest category. Importantly, no children were included. The 2026 migrant meta-analysis reported lower pooled HBsAg prevalence in people younger than 18 years than in adults [5], while studies of unaccompanied migrant minors in London and Rome reported HBV prevalence of 3.9% and 2.5%, respectively [15,16]. Those pediatric data are relevant for planning future work but cannot be used to relabel the present adult-dominant cohort as a child study.

Sex was not independently associated with HBsAg positivity in the present analysis. This differs from some migrant datasets and from the 2026 meta-analysis, which found higher pooled prevalence in males [5]. The null result here may reflect a genuinely similar prevalence or, more likely, limited power because only 38 women were included. The male predominance also constrains generalizability to female migrants, pregnant women and mother-to-child transmission prevention programmes.

The secondary logistic model achieved an AUC of approximately 0.74, which is adequate for describing multivariable separation but insufficient for use as a stand-alone clinical triage tool. Risk scores can assist programmes where testing resources are severely constrained, and the large STRADA study demonstrated that questionnaire-based prediction can discriminate HBV risk among migrants [12]. In Al-Kufra, however, the overall HBsAg positivity of 27.5% is so high that restricting testing to a demographic risk score could miss many infections. Universal or very broad opt-out testing within the relevant service population is therefore more defensible than selective testing based only on nationality, education or age.

A screen-and-link pathway is the logical public-health response. An HBsAg-positive result should be followed by clinical confirmation, assessment of liver disease and infectivity, and linkage to longitudinal HBV care. Conversely, HBsAg-negative people should be assessed for susceptibility and offered hepatitis B vaccination when appropriate. Recent migrant programmes show that high linkage can be achieved when testing is decentralized, culturally responsive and immediately connected to navigation support and specialist referral [9-11]. The WHO elimination agenda similarly requires expansion of diagnosis and treatment coverage, not simply identification of positive tests [2,3].

The findings also have implications for surveillance. Repeated cross-sectional sampling at Al-Kufra with a standardized protocol could distinguish real epidemiological change from shifts in migrant composition. A stronger surveillance package would include HBsAg, anti-HBc and anti-HBs to distinguish current infection, previous exposure and vaccine-induced immunity; HBV DNA and liver assessment for HBsAg-positive participants; vaccination documentation; and route, duration and prior healthcare exposures. Prospective linkage indicators would allow the programme to measure whether diagnosis translates into evaluation, treatment when indicated and vaccination of susceptible individuals.

The ancillary liver-biomarker analysis adds a clinical bridge between screening and downstream assessment. In the separate disease-stage dataset, aminotransferases were strongly elevated but did not rise in a simple stepwise pattern from CHB through cirrhosis and HCC, consistent with the fact that AST and ALT predominantly reflect current hepatocellular injury rather than fibrosis or functional reserve. In contrast, TBA increased across CHB, cirrhosis and HCC and rose sharply in liver failure. This pattern is biologically plausible because circulating bile acids are affected by hepatocyte uptake, canalicular export, cholestatic retention, enterohepatic cycling and portal-systemic shunting. Previous studies have similarly linked bile-acid abnormalities with cirrhosis, acute decompensation, fibrosis and HCC risk in HBV-related disease [28-31]. These observations reinforce the principle that HBsAg screening is the beginning of a care pathway rather than a complete assessment of disease severity.

5. CONCLUSIONS

HBsAg positivity affected 27.5% of newly arrived late-adolescent and adult sub-Saharan African migrants in this Al-Kufra sample. Nationality-specific prevalence was heterogeneous, while higher educational attainment and older age were independently associated with lower prevalence. The burden greatly exceeds pooled estimates from many destination-country

migrant studies and is similar in magnitude to a previous Al-Kufra survey. These findings justify a strong, non-stigmatizing screen-and-link strategy with vaccination and longitudinal care. Pediatric research should be conducted separately because the present dataset contains no children younger than 18 years. The biomarker analysis suggests that AST, ALT and especially TBA may provide complementary information during downstream liver-disease assessment.

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