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## Association between APOL 1 Risk Genotypes and Left Ventricular Hypertrophy among Sub-Saharan Africans in Trypanosoma Brucei Gambiense **Endemic Rural Area**

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#### Abstract

**Purpose.** The relationship between APOL1 variants and cardiovascular disease remains controversial, thus, this study assessed the association between APOL1 high-risk genotypes and left ventricular hypertrophy (LVH) among sub-Saharan African in T.b. gambiense endemic area.

Methodology. We enrolled 238 subjects living in the region of Masimanimba, an endemic area of T.b.gambiense HAT. We evaluated the association between LVH on echocardiography and the status of APOL1 genes in participants with or without HAT. APOL1 high-risk genotype (HRG) was defined as the presence of two risk variants (G1/G1, G2/G2, or G1/G2), and a low-risk genotype (LRG) with the presence of 0 or 1 single variant. Student's and Pearson's  $Chi^2$  tests or Fisher's exact test were used to compare means and proportions. The Wilcoxon/Mann-Whitney test was used to compare medians. A multivariate logistic regression model was used to identify independent determinants of LVH. Odds ratios were provided with their 95% confidence intervals (Cis). Statistical significance was set at p < 0.05, based on 2-tailed test.

Findings. The prevalence of LVH (31.5%) increased with age and was similar in HAT-infected and noninfected subjects (29.8% vs. 32.6%; p=0.376). The trend of a greater left ventricular mass in participants with LVH carrying APOL1 HRG compared to those with LRG was not statistically significant (141g/m<sup>2</sup> vs. 125 g/m<sup>2</sup>; p = 0.253). The frequency of HRG among participants with LVH was similar between HATinfected and non-infected (15.8% vs. 9.1%; p = 0.806). Age  $\geq 38$  years [OR 2.5 (95% CI: 1.4-4.5), p =0.001], hypertension [OR 2.4 (95% CI: 1.1-5.3), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], WHR > 0.5 [OR 2.0 (95\% CI: 1.0-3.6), p = 0.034], p =0.018] and CKD [OR 1.7 (95% CI: 1.0-3.0), p = 0.049] were associated with LVH. In multivariable logistic regression analysis age  $\geq$  38 years was the only independent determinant of LVH [ORa 2.0 (95% CI: 1.1-3.8), p = 0.020].

Unique contribution to theory, practice and policy. An assessment of cardiovascular risk is essential for individuals with LVH carrying APOL1 HRG in order to benefit from early and appropriate medical intervention. Further larger prospective follow-up survey is required to assess the incidence of LVH in individuals with APOL1 HRG variants.

Keywords: APOL1, LVH, Trypanosomiasis Endemic Area, DRC







#### Introduction

Previous reports have established the relationship between *APOL1* risk variants and CKD in African Americans (AA) and sub-Saharan Africans (1-10). However, this is not the case for subclinical and clinical cardiovascular diseases (CVD) for which the data are contradictory. Indeed, some studies demonstrated a positive correlation, while others observed no significant correlation (11-14). This disparity would be linked to the difference in methodological approaches and the genetic heritage of AA who constitute a mixed population having approximately 80% of African ancestry and 20% of European ancestry (11,14). The lack of available data on *APOL1* variants and CVD in sub-Saharan Africa requires continued research to clarify this relationship where human African trypanosomiasis (HAT) is endemic. Sub-Saharan Africans would not have the same susceptibility to CVD as AA, knowing that these variants do not confer protection against *Tb gambiense* which is prevalent in West and Central Africa (2-4). Therefore, we aimed to investigate the association between *APOL1* risk variants and left ventricular hypertrophy (LVH) in a sample of the Bantu population in a *Tb gambiense* endemic area, in Central Africa.

### Methods

### Study Design and participant sampling

We conducted this cross-sectional study from April 2019 to April 2021 in an HAT-endemic rural region of Masimanimba (Democratic Republic of Congo (DRC)), where the inhabitants belong to the Bantu ethnic group. A total of 238 individuals aged 15 years or older were enrolled using a multi-stage sampling strategy. They were accrued from two Health Zones in the region: Masimanimba and Mosango. Ten Health areas (six in Masimanimba and four in Mosango) were randomly selected. The enrolment included only subjects justifying a stay of at least one year in the region. Pregnant women were excluded from this study.

### **Clinical measurements**

Sociodemographic data (age, sex, ethnicity, and occupation) and history of cardiovascular risk factors (hypertension, diabetes, tobacco and alcohol use, and low vegetable and fruit consumption) were obtained through interviews. Anthropometric variables (height, weight, waist circumference, and body mass index), blood pressure, and heart rate were measured during the physical examination. Brachial and ankle blood pressure was measured using an automated sphygmomanometer (Omron M2 Basic (HEM-7120-E), Kyoto, Japan) with an appropriate size secured on each arm and ankle in turn after the subject had rested in the supine position for at least 5 min. The average of three measurements at 1 min intervals was used in the analysis. Pulse pressure (PP) is the difference between systolic blood pressure (SBP) and diastolic blood pressure (DBP). The ankle-brachial index (ABI) was calculated as the ratio of the highest systolic blood pressure at the two ankles to the highest systolic blood pressure at the two arms.

### Paraclinical and genetic variables assessment

Laboratory variables (serum creatinine, glucose, total cholesterol, HDL and LDL- cholesterol, uric acid, C-reactive protein (CRP), and triglycerides) were measured with a Cobas C 111 analyzer



using an enzymatic colorimetric method at the National Institute for Biomedical Research (NIBR). Estimated glomerular filtration rate (eGFR) was calculated using the MDRD (Modification of Diet in Renal Disease) formula: The albumin/creatinine ratio in freshly voided morning urine samples was evaluated. CKD was an eGFR < 60mL/min/1.73 m<sup>2</sup> and/or a urinary albumin/creatinine ratio  $\geq 30$  mg/g persistent for  $\geq 3$  months (15). HAT was diagnosed using serological [card agglutination test for trypanosomiasis (CATT)] and parasitological tests [mini anion exchange column (mAECT)].

DNA was extracted from whole blood samples according to the Maxwell method, following the manufacturer's instructions at the Genetics Laboratory of the National Institute for Biomedical Research (INRB). The extracted DNA was transferred to the Laboratory of Development and Regeneration at Katholieke University, Leuven (KU Leuven, Belgium) for storage and genotyping. APOL1 genotyping was performed for two renal risk alleles: G1 (coding variants rs73885319A>G [p.Ser342Gly] and rs60910145G>T [p.Ile384Met]) and G2 (6-bp deletion, rs71785313). Exon 7 (883 bp) of APOL1 was amplified using the gene-specific primer pairs (Fw50-Rv50-CATATCTCTCCTGGTGGCTG-30). GTCACTGAGCCAATCTCAGC-30 and Polymerase chain reaction experiments were performed on genomic DNA using GoTag Green DNA Polymerase (Promega Corporation, Fitchburg, Wisconsin) and consisted of 35 cycles at an annealing temperature of 55° C. Alkaline phosphatase and exonuclease exoSAP IT (Affymetrix, Santa Clara, CA) were used for polymerase chain reaction purification. Sanger sequencing was performed on an ABI 3100XL High-Throughput DNA Sequencer (Applied Biosystems, Foster City, CA, USA). APOL1 HRG was defined as the presence of two risk alleles (G1/G1, G2/G2, or G1/G2), and LRG was defined as the presence of zero or one risk allele.

### **Echocardiographic measurements**

Detailed two-dimensional transthoracic echocardiography was performed using an EDAN echocardiograph (D-20537, Hamburg, Germany) outfitted with a 3.5 MHz transducer. Left ventricle measurements were performed according to the 2015 American Society of Echocardiography and European Association of Cardiovascular Imaging updated guidelines for cardiac chamber quantification (16). Two-dimensional guided M-mode echocardiography was performed in the parasternal long-axis view. The interventricular septum (IVS) thickness in diastole (IVSd) in mm, left ventricular posterior wall (PW) thickness in diastole (LVPWd) in mm, and left ventricular end-diastolic diameter (LVEDd) in mm were measured at end-diastole just below the mitral valve leaflets. ECG was simultaneously recorded at the same time to correlate the measurements with the cardiac cycle. Diastolic wall thickness was measured at the onset of the QRS complex. Left ventricular mass (LVM) was calculated according to the American Society of Echocardiography simplified cubed equation linear method using the following equation: LVM  $(\text{grams}) = 0.8 \times 1.04 \times [(\text{LVEDd} + \text{IVSd} + \text{LVPWd})^3 - (\text{LVEDd})^3] + 0.6 \text{ g}$ . LVM was indexed to the BSA and height. LVM was considered high when  $\geq 115$  g/m<sup>2</sup> or  $\geq 48$  g/m<sup>2</sup> in males and  $\geq 95$  $g/m^2$  or > 44  $g/m^2$  in females. The relative wall thickness (RWT) of the left ventricle (LV) was calculated as  $(2 \times LVPWd)/LVEDd$ . LV geometric patterns were defined as follows: normal



geometry (normal LVM and RWT  $\leq$  0.43), concentric remodeling (normal LVM and RWT > 0.43), and concentric hypertrophy (high LVM and RWT > 0.43), and eccentric hypertrophy (High LVM and RWT  $\leq$  0.43). To assess LV systolic function, ejection fraction (stroke volume/diastolic volume  $\times$  100), percentage of LV systolic shortening (%) ([diastolic diameter – systolic diameter]/diastolic diameter  $\times$  100], and cardiac output (stroke volume  $\times$  heart rate) were calculated. The images were stored for subsequent validation by two cardiologists.

## **Operational definitions**

High blood pressure was SBP  $\geq$  140 mmHg or DBP  $\geq$  90 mmHg or use of antihypertensive drug treatment (17). Prehypertension was SBP of 120-139 mmHg and a DBP of 80-89 mmHg. (18). An abnormal ankle-brachial index (SBP ankle/SBP arm) < 0.9 or > 1.3 (19) determined a high cardiovascular risk.

Height (in meters) was measured using a flexible tape measure with the participants in an upright position without shoes. Body weight was measured using a digital scale (EKS, Germany), and body mass index (BMI) was calculated as weight (in kilograms) divided by the square of height (in meters). Overweight was defined as BMI of 25 to 29.9 kg/m<sup>2</sup> and obesity as BMI of 30 kg/m<sup>2</sup> (20). A tape measure was used to measure the waist circumference at the top of the hip bone. Central obesity was defined as weight circumference  $\geq$  94 cm in men and  $\geq$  80 cm in women (20). High cardiometabolic risk was defined as a waist-to-height ratio  $\geq$  0.5 (21)

HAT-infected participants were positive for both serological and parasitological tests and a CATT plasma dilution  $\geq 1/8$ , parasitology negative; non-infected participants had negative or positive CATT plasma dilution < 1/8.

Diabetes mellitus was a fasting serum glucose  $\geq 126$  mg/dl or use of antidiabetic medication (20). Dyslipidemia was defined as total cholesterol level > 1.9 g/L, triglycerides > 1.5 g/L, and HDL-cholesterol < 0.4 g/l for males and < 0.5 g/l for females) (22). Metabolic syndrome was defined according to IDF/AHA/ NHLBI (2009) by the presence of 3 out of the following 5 criteria: waist circumference  $\geq 94$  cm in males and  $\geq 80$  cm in females, - SBP  $\geq 130$  mmHg and/or DBP  $\geq 85$  mmHg or use of antihypertensive drug treatment, serum triglycerides  $\geq 1.5$  g/L, HDL-C < 0.40 g/L for males and < 50 g/L for females, fasting serum glucose  $\geq 100$  mg/dl or use of antidiabetic medication (20). C-reactive protein level > 6 mg/L was considered an inflammatory marker (23). Anemia was defined as hemoglobin (Hb) level of < 12.0 g/dl in women and < 13.0 g/dl in men (24). Elevated uric acid was considered when blood levels were > 6 mg/dl or 360 µmol/L (25)

## Statistical analysis

Data analysis was performed using SPSS for Windows software version 21. Student's and Pearson's Chi<sup>2</sup> tests or Fisher's exact test were used to compare means and proportions, where appropriate. The Wilcoxon/Mann–Whitney test was used to compare medians. A multivariate logistic regression model was used to identify independent determinants of left ventricular Hypertrophy (LVH). Odds ratios were provided with their 95% confidence intervals (Cis).



Statistical significance was set at p < 0.05, based on 2-tailed test. A chi-squared test was used to test the deviation from Hardy-Weinberg equilibrium.

#### Results

### General Characteristics of the study population

As shown in Table 1, the prevalence of LVH was 31.5% and increased with age (p = 0.002). It was similar in males (30%) and females (32%) (p = 0.404), in HAT-infected (29.8%) as well as non-infected (32.6%) individuals (p = 0.376). Participants with LVH were older than those without LVH (46.5 vs. 36.5 years; p < 0.001).

Characteristics	All	With LVH	Without LVH	p value
	N = 238	N = 75 (31,5)	N = 163 (68,5)	
Age, years	39.7 ± 17.1	$46.5\pm17.1$	$36.5\pm16.1$	< 0,001
HAT status				0.376
Infected	94 (39.4)	28 (29.8)	66 (70.2)	
Non-Infected	144 (60.6)	47 (32.6)	97 (67.3)	
Sex				0.404
Male	90 (37.9)	27 (30)	63(70)	
Female	148 (62.1)	48 (32.4)	100 (67.6)	
Age groups				0.002
< 20	29 (12.2)	4 (13.8)	25 (86.2)	
20-29	46 (19.3)	10 (21.7)	36 (78.3)	
30-39	53 (22.3)	12 (22.6)	41 (77.4)	
40-49	38 (16)	16 (42.1)	22 (57.9)	
≥ 50	72 (30.3)	33 (45.8)	39 (54.2)	

Table 1: General Characteristics of the study population

Data are expressed as mean  $\pm$  SD or absolute (n) and relative (%) frequency HAT = human African trypanosomiasis

LVH = left ventricular hypertrophy



### Distribution of Cardiovascular risk factors and APOL1 risk genotypes by LVH status

The distribution of cardiovascular risk factors in participants with and without LVH is shown in Table 2. Participants with LVH demonstrated high frequency of hypertension (20% vs. 9.2%, p = 0.019), WHR  $\ge 0.5$  (34.7% vs. 20.9%, p = 0.018) and CKD (53.3% vs. 39.3%; p = 0.029), while an abnormal ABI was noted in participants without LVH (33.7% vs. 20%, p = 0.021). The other variables did not differ between the two groups.

*APOL1* sequence analysis showed that four of 30 (13.3%) participants with LVH and six of 94 (6.4%) participants without LVH carried HRG; the difference between the two groups was not significant (p = 0.253). Participants in both groups carried G1G1, G2G2, and G1G2 genotypes. The trend of G1 (20% vs. 15.4%, p = 0.427) and G2 (11.7% vs. 8%, p = 0.434) alleles to be slightly higher in the subjects with than those without LVH was not significant.

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 Table 2: Distribution of Cardiovascular risk factors and APOL1 risk genotypes by LVH status

Cardiovascular	risk	All	With LVH	Without LVH	p value
factors		N = 238	N = 75 (31,5)	N = 163 (68,5)	-
Low consumption of fruits		231 (97)	74 (98.7)	157 (96.3)	0.295
Dyslipidemia		191 (80.2)	56 (74.7)	135 (82.8)	0.099
Alcohol intake		178 (74.7)	59 (78.7)	119 (73)	0.221
Low consumption	of	111 (46.6)	30 (40)	81 (49.7)	0.105
vegetables					
CKD		104 (43.6)	40 (53.3)	64 (39.3)	0.029
Tachycardia		102 (42.8)	31 (41.3)	71 (43.6)	0.429
Smoking		88 (36.9)	33 (44)	55 (33.7)	0.085
Albuminuria		79 (33.1)	28 (37.3)	51 (31.3)	0.219
Abnormal ABI		70 (29.4)	15 (20)	55 (33.7)	0.021
Prehypertension		66 (27.7)	20 (26.7)	46 (28.2)	0.466
WHR $\geq 0.5$		60 (25.2)	26 (34.7)	34 (20.9)	0.018
Inflammation		56 (23.5)	20 (26.7)	36 (22.1)	0.269
Hyperuricemia		39 (16.3)	12 (16)	27 (16.6)	0.538
Hypertension		30 (12.6)	15 (20)	15 (9.2)	0.019
Abdominal Obesity		28 (11.7)	12 (16)	16 (9.8)	0.124
Diabetes		9 (3.7)	2 (2.7)	7 (4.3)	0.420
Overweight - obesity		7 (2.9)	3 (4)	4 (2.5)	0.387
Metabolic Syndrome		6 (2.5)	1 (1.3)	5 (3,1)	0.386
APOL1 risk variants		N = 124	With LVH	Without LVH	P value
			n=30	N = 94	
At least one allele risk		53 (42.7)	15 (50)	38 (40.4)	0.400
High-risk genotypes		10 (8.1)	4 (13.3)	6 (6.4)	0.253
G1/G1		5 (4)	2 (6.7)	3 (3.2)	
G2/G2		2 (1.6)	1 (1.1)	1 (3.3)	
G1/G2		3 (2.4)	1 (3.3)	2 (2.1)	
Low-risk genotypes		114 (91.9)	26 (86.7)	88 (93.6)	0.253
G1/G0		28 (22.6)	7 (23.3)	21 (22.3)	
G2/G0		15 (12.1)	4 (13.3)	11 (11.7)	
G0/G0		71 (57.3)	15 (50)	56 (59.6)	
**Alleles					
G1		41(16.5%)	12 (20)	29 (15.4)	0.427
G2		22 (8.8%)	7 (11.7)	15 (8)	0.434

Data are expressed as mean  $\pm$  SD or absolute (n) and relative (%) frequency ABI = Ankle brachial index

WHR = Waist Height ratio CKD = chronic kidney disease LVH = left ventricular hypertrophy

\*\* considering all chromosomes.

### Cardiovascular risk factors in the study population by HAT infection status.

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The distribution of cardiovascular risk factors according to HAT infection status is shown in Table 3 for participants with and without LVH. HAT-uninfected subjects were older than the infected ones among participants with LVH (49.6 vs. 41.4 years, p = 0.047) as well as those without (38.1 vs. 34.1 years, p = 0.123). Men were more susceptible to HAT infection than women (p = 0.045). Albuminuria predominated in HAT-infected subjects with LVH (57.1% vs. 25.5%, p = 0.006). The frequency of HRG was similar between HAT-infected patients with and without LVH (15.8 vs. 9.1%, p = 0.806). Among participants without LVH, diabetes (9.1% vs. 1%, p = 0.018), dyslipidemia (93.9% vs. 75.3%, p = 0.001), prehypertension (39.4% vs. 20.6%, p = 0.008), hypertension (16.7% vs. 4.1%, p = 0.008), and anemia (50% vs. 26.8%, p = 0.002) predominated in HAT-infected subjects. The trend towards a higher HRG frequency in HAT-infected patients was not significant (9.6% vs. 2.4%, p = 0.220).

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Table 3: Distribution of cardiovascular risk factors by HAT infection status

Cardiovascular risk	All	With LVH			Without L	VH	
factors	N = 238	N = 75			N = 163		
		HAT <sup>+</sup> n=28	HAT <sup>-</sup> n=47	р	HAT+ n=66	HAT <sup>-</sup> n=97	р
Age (Yrs)	$39.7 \pm 17.1$	$41.4 \pm 18.6$	49.6±15.7	0.047	34.1±15.6	38.1±16.4	0.123
Sex				0.045			0.096
Male	90 (37.8)	14 (50)	13 (27.7)		30 (45.5)	33 (34)	
Female	148 (62.2)	14 (50)	34 (72.3)		36 (54.5)	64 (66)	
Smoking	88 (36.9)	12 (42.9)	21 (44.7)	0.535	12 (18.2)	43 (44.3)	< 0.001
Alcohol intake	178 (74.7)	22 (78.6)	37 (78.7)	0.603	52 (78.8)	67 (69.1)	0.116
Low fruit consumption	231 (97)	28 (100)	46 (97.9)	0.627	65 (98.5)	92 (94.8)	0.221
Low vegetable	111 (46.6)	8 (28.6)	22 (46.8)	0.093	30 (45.5)	51 (52.6)	0.232
consumption							
Diabetes	9 (3.7)	1 (3.6)	1 (2.1)	0.610	6 (9.1)	1 (1)	0.018
Dyslipidemia	191 (80.2)	24 (85.7)	32 (68.1)	0.075	62 (93.9)	73 (75.3)	0.001
Metabolic syndrome	6 (2.5)	0 (0)	1 (2.1)	0.627	4 (6.1)	1 (1)	0.087
prehypertension	66 (27.7)	9 (32.1)	11 (23.4)	0.286	26 (39.4)	20 (20.6)	0.008
Hypertension	30 (12.6)	5 (17.9)	10 (21.3)	0.483	11 (16.7)	4 (4.1)	0.008
Hyperuricemia	39 (16.3)	5 (17.9)	7 (14.9)	0.487	11 (16.7)	16 (16.5)	0.570
Abnormal ABI	70 (29.4)	5 (17.9)	10 (21.3)	0.483	18 (27.3)	37 (38.1)	0.101
Overweight-Obesity	7 (2.9)	0 (0)	3 (6.4)	0.240	1 (1.5)	3 (3.1)	0.466
Abdominal Obesity	28 (11.7)	2 (7.1)	10 (21.3)	0.096	8 (8.2)	8 (12.1)	0.289
WHR $\geq 0.5$	60 (25.2)	7 (25)	19 (40.4)	0.134	13 (19.7)	21 (21.6)	0.461
Anemia	88 (36.9)	13 (46.4)	16 (34)	0.206	33 (50)	26 (26.8)	0.002
Inflammation	56 (23.5)	8 (28.6)	12 (25.5)	0.488	16 (24.2)	20 (20.6)	0.359
Microalbuminuria	79 (33.1)	16 (57.1)	12 (25.5)	0.006	17 (25.8)	34 (35.1)	0.139
Tachycardia	102 (42.8)	11 (39.3)	20 (42.6)	0.487	27 (40.9)	44 (45.4)	0.344
Chronic Kidney	104 (43.6)	18 (64.3)	22 (46.8)	0.109	25 (37.9)	39 (40.2)	0.447
Disease							
APOL1 risk variants	N = 124	N = 19	N = 11		N = 52	N = 42	
High-risk genotypes	10 (8.1)	3 (15.8)	1 (9.1)	0.806	5 (9.6)	1 (2.4)	0.220
G1/G1	5 (4)	1 (5.3)	1 (9.1)		3 (5.8)	0 (0)	
G2/G2	2 (1.6)	1 (5.3)	0 (0)		1 (1.9)	0 (0)	
G1/G2	3 (2.4)	1 (5.3)	0 (0)		1 (1.9)	1 (2.4)	
0 risk allele	71 (57,3)	9 (47.4)	6 (54.5)	0.858	32 (61.5)	24 (57.1)	0.234
G0/G0	71 (57.3)	9 (47.4)	6 (54.5)		32 (61.5)	24 (57.1)	
1 risk allele	43 (34,7)	7 (36.8)	4 (36.4)	0.852	15 (28.8)	17 (40.5)	0.210
G1/G0	28 (22.6)	5 (26.3)	2 (18.2)		9 (17.3)	12 (28.6)	
G2/G0	15 (12.1)	2 (10.5)	2 (18.2)		6 (11.5)	5 (11.9)	

Data are expressed as mean  $\pm$  SD or absolute (n) and relative (%) frequency ABI = Ankle brachial index WHR = Waist Height ratio LVH = left ventricular hypertrophy HAT+ = infected HAT - = non-infected

### Participants' characteristics by APOL1 genotypes status.

International Journal of Health, Medicine and Nursing Practice ISSN 2710-1150 (Online)



Vol.6, Issue No.5, pp 19 - 36, 2024

Table 4 indicates that 4/30 (13.3%) subjects who carried *APOL1* HRG had higher means for all components of blood pressure (SBP, DBP, MAP, and PP), anthropometric parameters (WC, IMC, WHR), and left ventricular mass (LVM) than 26 of 30 (86.7%) subjects with LRG. However, the difference was significant only for the PP (p = 0.047). Moreover, subjects with LVH carrying HRG had an elevated median urinary ACR (p = 0.008) and LDL-C (p = 0.029). Participants without LVH who carried the HRG had a higher median u-ACR (p < 0.001) and glycaemia (p < 0.001) than those who carried the LRG. However, it should be noted that all individuals with or without LVH carrying the HRG had significant albuminuria.

Tableau 4: Clinical and paraclinical characteristics of participants by APOL1 genotype status.

	All	With LVH			Without LVH	[	
	n = 124	n = 30			n = 94		
		HRG	LRG	р	HRG	LRG	p value
		n = 4	n = 26		n = 6	n = 88	
Age (Yrs)	$38.3 \pm 17$	$48 \pm 20$	$47.6 \pm 19.8$	0.977	$49.3 \pm 13.3$	$34.4 \pm 14.7$	0.019
Gender				0.177			0.173
Male	51 (41.1)	0 (0)	10 (38.5)		1 (16.7)	40 (45.5)	
Female	73 (58.9)	4 (100)	16 (61.5)		5 (83.3)	48 (54.5)	
SBP (mm Hg)	$119.5\pm19.9$	$151.2\pm53.4$	$121.2 \pm 24.3$	0.063	$126.5 \pm 26.7$	$117.1\pm13.9$	0.139
DBP (mm Hg)	$74.1 \pm 14$	$90\pm26.6$	$76.1 \pm 17$	0.170	$74.8 \pm 18.7$	$72.7 \pm 11.6$	0.690
MAP ((mm Hg)	89.2±15.5	$110.2\pm35.6$	$91.5\pm19.4$	0.125	$90.5\pm25.2$	$87.5 \pm 11.8$	0.650
PP ((mm Hg)	$45.4 \pm 11,2$	$61.2\pm27.1$	$44.9 \pm 12.2$	0.047	$51.5 \pm 19.5$	$44.4\pm8.5$	0.080
abnormal ABI	$1.1 \pm 0.3$	$1.2 \pm 0.5$	$1 \pm 0.2$	0.359	$1 \pm 0.1$	$1.1 \pm 0.3$	0.371
WC (cm)	$72.9\pm6.7$	$80\pm10{,}7$	$75 \pm 5.8$	0.167	$73.8\pm4.6$	$71.9\pm6.7$	0.513
BMI (Kg/m <sup>2</sup> )	$19 \pm 2.7$	$21.5\pm3.1$	$19.7\pm2.1$	0.168	$19 \pm 3.2$	$18.7\pm2.7$	0.822
WHR $\geq 0.5$	$0.4 \pm 0.2$	$0.6 \pm 0.5$	$0.4 \pm 0.3$	0.465	$0.3 \pm 0.2$	$0.3 \pm 0.2$	0.239
LVM $(g/m^2 de)$	$93.5\pm25.8$	$141 \pm 31.5$	$125.1 \pm 24.4$	0.253	$78.6 \pm 11.1$	$83\pm14.3$	0.462
BS)							
HR (batt /min)	$79.1 \pm 14.6$	$86.7\pm22$	$79.3 \pm 16.4$	0.425	$82.3 \pm 13.1$	$78.5 \pm 14$	0.517
Fasting serum	78 [55-93]	76.5	77.5	0.880	111.5	78	<0.001
glucose (mg/dl)							
Total Cholestérol	$73.6 \pm 33$	$86.2\pm34.9$	$67.4 \pm 27.1$	0.222	$68 \pm 33.8$	$75.2\pm34.6$	0.619
(mg/dl)							
HDL-c (mg/dl)	$26.8 \pm 14.7$	$22 \pm 10.1$	$26.5\pm16.4$	0.595	$19.5\pm10.1$	$27.6 \pm 14.6$	0.184
LDL-c (mg/dl)	$41.8 \pm 29.3$	$61.5\pm26.8$	$35.3\pm20.3$	0.029	$44 \pm 27.3$	$42.6\pm31.6$	0.922
Triglycerides	$46.5\pm26.8$	$26.7 \pm 14.6$	$46.7\pm26.3$	0.152	$50.6\pm20.1$	$47.1\pm27.7$	0.760
(mg/dl)							
uricemia (mg/dl)	$6.1 \pm 3.1$	$5.5 \pm 0.5$	$6.3 \pm 2.8$	0.561	$6.5 \pm 2.5$	$6.1 \pm 3.4$	0.781
CRP (g/L)	$7 \pm 1.9$	$8.3 \pm 1.7$	$2\pm0.8$	0.293	$7.3 \pm 1.9$	$6.8\pm0.9$	0.912
Hematocrit (%)	$39.2 \pm 6.4$	$40.5\pm5.8$	$38.7\pm5.8$	0.586	$37.1 \pm 5.8$	39. 4 ±6.7	0.426
U-ACR (mg/g)	28 [12-72]	47	24	0.008	36.5	18.5	< 0,001
eGFR , mL/min/	$108.7\pm48.2$	$69 \pm 12.7$	$107.3\pm43.9$	0.098	$84.8\pm25.6$	$112.5\pm50.6$	0.189
$1.73 \text{ m}^2$							
CKD n (%)	54 (43.5)	4 (100)	16 (61.5)	0.272	6 (100)	28 (31.8)	0,002

International Journal of Health, Medicine and Nursing Practice ISSN 2710-1150 (Online)



Vol.6, Issue No.5, pp 19 - 36, 2024www.carijournals.orgSBP, systolic blood pressure; DBP, diastolic blood pressure; MAP, mean arterial pressure; PP,<br/>pulse pressure; ABI, ankle-brachial index; WHR, waist circumference: height ratio; WC, waist<br/>circumference: BML body mass index: HR, heart rate: CRP, C-reactive protein: U-ACR.

circumference; BMI, body mass index; HR, heart rate; CRP, C-reactive protein; U-ACR, urinary albumin-to-creatinine ratio; eGFR, estimated glomerular filtration rate. CKD, chronic kidney disease; HRG, high-risk genotype; LRG, low-risk genotype; LVH, left ventricular hypertrophy; LVM, left ventricular mass.

## Determinants of LVH in the study population

As reported in Table 5, univariate analysis showed that age  $\geq$  38 years [OR 2.5 (1.4-4.5), p = 0.001], hypertension [OR 2.4 (1.1-5.3), p = 0.034], WHR  $\geq$  0.5 [OR 2.0 (1.0-3.6), p = 0.018] and CKD [OR 1.7 (1.0-3.0), p = 0.049,] were associated with LVH. Multivariate logistic regression analysis revealed that age  $\geq$  38 years was the primary independent factor associated with LVH. Age  $\geq$  38 years was associated with a two-fold increased susceptibility to LVH [OR 2.0 (1.1-3.8), p = 0.020].

ISSN 2710-1150 (Online)

Vol.6, Issue No.5, pp 19 - 36, 2024



**Table 5.** Determinants of LVH in the study population

Variables	Univariate Analysis		Multivariate Analysis		
	OR [CI 95%]	р	OR [CI 95%]	p value	
Age (yrs)					
< 38	1		1		
$\geq$ 38	2.5 [1.4-4.5]	0.001	2.0 [1.1-3.8]	0.020	
Gender					
Female	1		1		
Male	0.8 [0.5-1.5]	0.404	0.9 [0.5-1.8]	0.951	
Hypertension					
No	1		1		
Yes	2.4 [1.1-5.3]	0.034	1.9 [0.8-4.6]	0.113	
HAT status					
Non-infected	1		1		
Infected	0.8 [0.4-1.5]	0.376	1.0 [0.5-1.9]	0.810	
Overweight-obesity					
No	1		1		
Yes	1.6 [0.3-7.5]	0.387	0.9 [0.1-5.2]	0.926	
Abdominal obesity					
No	1		1	-	
Yes	1.7 [0.7-3.9]	0.195	1.3 [0.5-3.4]	0.534	
WHR≥0.5					
Non	1		1	0	
Oui	2.0 (1.0-3.6)	0.018	1.2 (0.5-2.8)	0.654	
Dyslipidemia					
No		0.000		0.005	
Yes	0.6 [0.3-1.1]	0.099	0.6 [0.3-1.3]	0.227	
Albuminuria	1		1		
No		0.210		0.450	
Yes Character	1.3 [0.7-2.3]	0.219	0.7 [0.2-1.7]	0.459	
Chronic Kidney					
Disease	1		1		
INO Vac		0.040	l 1 0 [0 7 5 0]	0 151	
I es ADOL 1 mielt	1./[1.0-3.0]	0.049	1.9 [0.7-5.0]	0.151	
Genetypes					
$I_{OW}(0,1)$	1		1		
$\frac{1}{2} \operatorname{Low}(0,1)$	1 2 2 [0 5 8 6]	0.108	1 0.7 [0.1.2.7]	0.717	
nigli (2)	2.2 [0.3-8.0]	0.190	0.7 [0.1-3.7]	0./1/	

OR, odds ratio; CI, confidence interval; WHR, waist-to-height ratio; HAT=Human African Trypanosomiasis.

### Discussion

This study aimed to investigate the possible association between *APOL1* risk variants with LVH in a sample of the Bantu population in a *T. b. gambiense* endemic area. Salient points in the results



were a similar prevalence of LVH in HTA-infected and-uninfected participants. The presence of hypertension, albuminuria, and CKD, but not *APOL1* HRG, was associated with LVH.

## Clinical and paraclinical characteristics

LVH was observed in one of three subjects. It increased with age and was similar in HTA-infected and uninfected participants. The two groups of participants exhibited a similar frequency of *APOL1* HRG, probably because these variants do not confer protection against *T.b. gambiense* (26). Our results indicated higher blood pressure, pulse pressure and anthropometric measurements in subjects with LVH who carried an HRG than in those carrying an LRG. The observed association of age  $\geq$  38 years, hypertension, WHR > 0.5, and CKD with LVH is consistent with the literature, which reports that age and blood pressure (BP) are the main determinants of vascular remodeling (27). The stiffness of the large arterial trunks contributes to the elevation of pulse pressure, which is a factor in the development of LVH (28), as well as greater intima-media thickness of largecaliber arteries and arterioles (29,30). Remodeling of small arteries results in an increase in peripheral resistance and, thus, in mean arterial pressure. In turn, arterial stiffness increases BP and central pulse pressure, which are remodeling factors for LVH. High and uncontrolled BP leads to vascular structural and functional modifications associated with neuro-hormonal, molecular, and genetic factors that cause LVH. However, LVH also occurs in the general population of patients with coronary disease, obesity, and diabetes mellitus (31,32).

Although these factors are known to contribute to LVH development, a high prevalence of diabetes, prehypertension, hypertension, and anemia was observed in HAT-infected participants without LVH. Such an observation could be accounted for by the somewhat higher frequency of *APOL1* HRG in HAT-infected individuals than in non-infected individuals. Our findings are consistent with previous reports that *APOL1* HRG is associated with increased SBP, albuminuria, and CKD (11,33-38). One should bear in mind, however, that subclinical nephropathy can manifest as increased blood pressure (11,33,34,36), and CKD can be the cause of anemia. Finally, an association between serum level of *APOL1* and insulin resistance (HOMA-IR) has been reported to underlie the occurrence of diabetes mellitus (39).

## **Determinants of LVH**

Our results showed a similar prevalence of LVH in both HAT-infected and-uninfected subjects with a similar frequency of HRG. Individuals with LVH who carried the HRG had high u-ACR and decreased eGFR and risk of CKD, although *APOL1* HRG was not associated with LVH. Age  $\geq$  38 years emerged as the only independent correlate of LVH in the *T.b. gambiense* endemic area. Several studies have established that *APOL1* HRG is not associated with LVH in AA (33,34,40), although HRG carriage has been strongly associated with albuminuria and/or CKD (2,5,11), which are predictors of LVH (37,38,41). Subclinical CKD is a risk factor for CVD, particularly persons of African descent (42); it is known that albuminuria and reduced GFR independently increase the risk of subclinical cardiovascular events. Therefore, it is difficult to attribute increased cardiovascular risk only to the *APOL1* G1/G2 risk alleles (43). The «Jackson Heart Study (JHS) », a prospective cohort study, showed a positive association between *APOL1* HRG and incident CVD,

International Journal of Health, Medicine and Nursing Practice ISSN 2710-1150 (Online)



Vol.6, Issue No.5, pp 19 - 36, 2024

including myocardial infarction, stroke, cardiac surgery, and arterial catheterization, but not LVH, despite the presence of diabetes in some individuals (34). In contrast, the «Systolic Blood Pressure Intervention Trial «SPRINT» (33), a randomized multicenter study, did not show any association between *APOL1* HRG and the prevalence of CVD (including myocardial infarction; coronary revascularization; carotid endarterectomy or carotid stenting; peripheral arterial disease with revascularization; 50% stenosis of a coronary, carotid, or lower extremity artery; abdominal aortic aneurysm  $\geq 5$  cm with or without repair; coronary artery calcium score  $\geq 400$  Agatston units; anklebrachial index  $\leq 0.90$ ; and left ventricular hypertrophy). Some authors have identified diabetes and prior CKD as strong risk factors that may obscure any independent effects of *APOL1* risk genotypes. Thus, *APOL1* has neutral or protective effects in the presence of diabetes (44,45).

The present study is the first to investigate a possible association between *APOL1* HRG and CVD in sub-Saharan African living in a rural area endemic to *T. b. gambiense*. However, owing to its cross-sectional design we could not ascertain the cause-and-effect nature of any observed relationship. Moreover, the relatively small sample size does not allow for generalization of the findings.

### Conclusion

LVH is more prevalent in areas of DRC endemic for *T.b. gambiense*. The prevalence was similar in HAT-infected and uninfected participants, with a similar frequency of APOL1 HRG. Only age  $\geq$  38 years emerged as an independent factor for LVH in *T. b. gambiense* endemic areas. An assessment of cardiovascular risk is essential for individuals with LVH carrying APOL1 HRG in order to benefit from early and appropriate medical intervention. Therefore, a larger prospective follow-up survey is required to assess the incidence of LVH in individuals with APOL1 HRG variants<del>.</del>

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Vol.6, Issue No.5, pp 19 - 36, 2024

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Vol.6, Issue No.5, pp 19 - 36, 2024



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Vol.6, Issue No.5, pp 19 - 36, 2024



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