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***APOL1* Genotype and Glomerular and Tubular Kidney Injury in Women With HIV**

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Abstract

Background—*APOLI* genotype is associated with advanced kidney disease in African-Americans, but the pathogenic mechanisms are unclear. Here, associations of *APOLI* genotype with urine biomarkers of glomerular and tubular injury, and with kidney function decline, were evaluated.

Study Design—Observational study.

Setting & Participants—431 HIV-infected African-American women enrolled in Women's Interagency HIV Study (WIHS).

Predictor—*APOLI* genotype.

Outcomes—Albumin-creatinine ratio (ACR), four tubular injury biomarkers (interleukin 18 [IL-18], kidney injury molecule 1 [KIM-1], neutrophil gelatinase-associated lipocalin [NGAL], and α_1 -microglobulin [α_1m]), and kidney function estimated using the CKD-EPI cystatin C equation.

Measurements—Participants were genotyped for *APOLI* single-nucleotide polymorphisms rs73885319 (G1 allele) and rs71785313 (G2 allele). Urine biomarker levels were measured using stored samples from 1999-2000. Cystatin C was measured using serum collected at baseline and 4- and 8-year follow-up.

Results—At baseline, ACR levels were higher among 47 women with 2 *APOLI* risk alleles versus 384 women with 0/1 risk allele (median, 24 vs. 11 mg/g; $p < 0.001$). Compared to women with 0/1 risk allele, women with 2 risk alleles had 104% higher ACR (95% CI, 29-223 mg/g) and 2-fold greater risk of ACR > 30 mg/g (95% CI, 1.17-3.44) after multivariable adjustment. *APOLI* genotype showed little association with urine IL-18:Cr, KIM-1:Cr, and NGAL:Cr (estimates of -5% [95% CI, -24% to 18%], -20% [95% CI, -36% to 1%], and 10% [95% CI, -26% to 64%], respectively), or detectable urine α_1m (prevalence ratio, 1.13; 95% CI, 0.65-1.97) in adjusted analyses. Compared to women with 0/1 allele, women with 2 risk alleles had faster eGFR decline, by 1.2 (95% CI, -2.2 to -0.2) ml/min/1.73 m² per year, and had 1.7- and 3.4-fold greater rates of incident chronic kidney disease (95% CI, 1.1-2.5) and 10% annual eGFR decline (95% CI, 1.7-6.7), respectively, with minimal attenuation after adjustment for glomerular and tubular injury biomarkers.

Limitations—Results may not be generalizable to men.

Conclusions—Among HIV-infected African-American women, *APOLI*-associated kidney injury appears to localize to the glomerulus, rather than the tubules.

Index Words

APOLI genotype; risk variant; risk allele; G1 allele; G2 allele; single-nucleotide polymorphism (SNP); albumin-creatinine ratio (ACR); proteinuria; tubular injury biomarker; apolipoprotein L1;

kidney disease; renal function; glomerular injury; African American; Women's Interagency HIV Study (WIHS)

African-Americans have a 3- to 4-fold greater risk of end-stage renal disease (ESRD) compared to Caucasians in HIV-infected and uninfected populations.¹⁻⁴ Two prior studies revealed strong associations between chromosome 22q and ESRD without diabetes among individuals of African ancestry.^{5,6} Subsequent studies identified two risk variants on the *APOLI* (apolipoprotein L1) gene which account for these associations.^{7,8} The G1 allele comprises two SNPs (reference single nucleotide polymorphism [SNP] identification number [rs]73885319 and rs60910145) encoding 2 amino acid substitutions and the G2 allele encodes a two amino-acid deletion (rs71785313).⁷ Heterozygosity for the risk alleles appears sufficient to confer resistance to *Trypanosoma brucei rhodesiense*,⁹ while homozygosity or compound heterozygosity leads to substantially elevated kidney disease risk.⁷

The pathogenesis of APOL1-associated kidney disease, however, is poorly understood. Madhavan *et al.* demonstrated that APOL1 localizes to podocytes, proximal tubules, and endothelium in the normal kidney, and that glomerular and proximal tubular APOL1 staining is reduced among individuals with FSGS and HIVAN.¹⁰ Ma *et al.* subsequently reported that APOL1 protein and mRNA were detectable in podocytes and renal tubular cells of cryosections from individuals with normal kidney function.¹¹ However, the specific effects of *APOLI* risk alleles on glomerular and proximal tubular function were not evaluated.

Biomarkers of tubular injury and dysfunction may be useful in earlier detection and localization of pathology within the nephron. In the Women's Interagency HIV Study (WIHS), we previously found that African-American race was a strong and independent risk factor for albuminuria, and was associated with higher levels of three urinary markers of tubular injury and dysfunction: interleukin 18 (IL-18), neutrophil gelatinase-associated lipocalin (NGAL), and α_1 -microglobulin (α_1m).^{12,13} Furthermore, albuminuria, IL-18 and α_1m were each independently associated with longitudinal kidney function decline and mortality.¹³⁻¹⁵ These findings suggest that the higher risk of kidney disease progression among HIV-infected African-Americans may be mediated through their more extensive glomerular and tubular injury. However, the specific contributions of the *APOLI* risk alleles to these observations have not been ascertained.

In this study of HIV-infected African-Americans enrolled in the WIHS, we first evaluated the cross-sectional associations of *APOLI* risk alleles with glomerular injury, quantified by albumin-creatinine ratio (ACR), as well as four biomarkers of tubular injury and dysfunction: IL-18, kidney injury molecule 1 (KIM-1), NGAL, and α_1m . We then assessed the associations of *APOLI* risk alleles with longitudinal kidney function decline, adjusting for baseline levels of the injury markers.

Methods

Study Population

The WIHS is a prospective cohort study that enrolled 3,067 HIV-infected and 1,070 uninfected women from six US locations (Bronx, Brooklyn, Chicago, Los Angeles, San Francisco, and Washington, DC) in 1994-1995, 2001-2002, or 2011-2012. Details of the study design and data collection methods were published previously.^{16,17} Participants underwent semiannual visits that included a standardized questionnaire, physical examination, and collection of laboratory specimens. Among the 795 African-American HIV-infected women who were evaluated at the WIHS clinical visits in 1999-2000, we chose *a priori* to include all 431 women who had the following: 1) consent for DNA testing; 2) available DNA for *APOLI* genotyping, and 3) stored urine available from the 1999-2000 visits for biomarker measurements.

The institutional review boards of participating institutions approved the study protocol at all WIHS study sites, and informed consent was obtained from all study participants. This cross-sectional study was also approved by the Institutional Review Board at the Johns Hopkins School of Medicine.

Exposure Variable

Participants were genotyped for the *APOLI* SNPs rs73885319 (G1 allele) and rs71785313 (G2 allele) using TaqMan assays (Applied Biosystems, Foster City, CA)¹⁸ and categorized as having zero, one or two risk alleles. The G1 allele rs60910145 was not tested because rs73885319 and rs60910145 are in near perfect linkage disequilibrium.⁷ Genotyping for ancestry informative markers (AIMs) was performed using the Illumina GoldenGate platform (Illumina, San Diego, CA). Selection of AIMs in the WIHS was described previously.¹⁹ Briefly, West African, European, East Asian and Native American populations were distinguished using a subset of markers published by Smith *et al.*¹⁸ Of the larger panel of 384 AIMs, 185 were selected, and 168 passed quality control measures. Genetic ancestry components were evaluated by principal components analysis using EIGENSTRAT software.^{20,21}

Outcome Variables

All biomarkers were measured at the Cincinnati Children's Hospital Medical Center Biomarker Laboratory, using random urine samples. Urine specimen storage and coefficients of variation for the biomarker assays are described in Item S1 (provided as online supplementary material). Urine albumin and creatinine were measured by immunoturbidimetry and colorimetric enzyme assay, respectively, using a Siemens Dimension Xpand plus HM clinical analyzer (Siemens, Munich, Germany). Urine IL-18 was measured using a commercially available ELISA kit (Medical & Biological Laboratories Co., Nagoya, Japan). The urine KIM-1 ELISA was constructed using commercially available reagents (R&D Systems Inc., Minneapolis, MN).²² Urine NGAL was assayed using a human-specific commercially available ELISA (BioPorto, Grusbakken, Denmark).²³ Urine α 1m was measured by a commercially available assay (Siemens BN II Nephelometer, Munich, Germany).

Serum for cystatin C measurement was collected at baseline and two follow-up visits, occurring approximately 4 and 8 years after the initial visit. Kidney function was estimated using the CKD-EPI equation for serum cystatin C, which is less susceptible to bias by muscle mass and health status than serum creatinine.²⁴ Cystatin C was measured centrally at the University of California, Los Angeles, Clinical Immunology Research Laboratory using a particle-enhanced immunoturbidimetric assay (Gentian, Moss, Norway), which has been calibrated against the new World Standard Reference material ERM-DA471/IFCC (International Federation of Clinical Chemistry and Laboratory Medicine).²⁵ Additional details are described in Item S1.

Continuous outcomes included baseline and annual change in eGFR in ml/min/1.73m² over approximately 8 years of follow-up. Additionally, two dichotomous kidney outcomes were analyzed: 1) incident chronic kidney disease (CKD), defined as eGFR <60 ml/min/1.73m² at either of two follow-up visits among participants with baseline eGFR ≥ 60 ml/min/1.73m², and 2) rapid decline, defined as 10% or greater annual decline in eGFR.

Covariates

Demographic and clinical characteristics were ascertained at the time of urine collection (1999-2000). Hypertension was defined by self-reported use of anti-hypertensive medications, systolic blood pressure ≥ 140mmHg, diastolic blood pressure ≥ 90mmHg, or self-reported diagnosis of hypertension confirmed by any of the previous criteria within 2 years. Diabetes mellitus was defined by self-reported use of oral hypoglycemic medications or insulin, fasting blood glucose ≥ 126 mg/dl, or self-reported history of diabetes diagnosis confirmed by either of the former criteria within 2 years. Hepatitis C virus (HCV) co-infection was defined by detectable HCV RNA and positive HCV antibody result. The HIV-related characteristics included current CD4 lymphocyte count, history of clinical AIDS diagnosis,²⁶ HIV RNA level, and current highly active antiretroviral therapy (HAART) use. Historical suppression of HIV RNA was defined as the percentage of historical HIV RNA values <400 copies/mL.

Statistical Analysis

We stratified women by number of *APOLI* risk alleles and compared demographic and clinical characteristics using the chi-square and Kruskal-Wallis tests for categorical and continuous variables, respectively. We then evaluated the associations of *APOLI* risk alleles with creatinine-standardized and unstandardized ACR, IL-18, KIM-1, and NGAL, using linear regression with robust Huber-White standard errors^{27,28} (to correct for heteroscedasticity). Due to their right-skewed distributions, the continuous outcomes were log-transformed to normalize their distributions; results were back-transformed to produce estimated percentage differences.

Consistent with our previous WIHS publication,¹³ α 1m was handled as a dichotomous variable, detectable or undetectable. Because α 1m is fully reabsorbed by proximal tubular cells after filtration at the glomerulus,²⁹ its presence in the urine indicates proximal tubular dysfunction.³⁰ We used Poisson relative risk regression with a robust variance estimator³¹ to

assess the associations of *APOLI* risk alleles with detectable $\alpha 1m$, and with the clinically established threshold for $ACR >30mg/g$.

Primary analyses were performed using a recessive model of inheritance (2 vs 0/1 risk alleles). In secondary analyses, we evaluated dominant (2/1 vs 0 risk alleles) and additive (2 vs 1 vs 0 risk alleles) models of inheritance.

We then constructed multivariable regression models to determine whether *APOLI* risk genotype was independently associated with each biomarker. Model covariates were selected on the basis of known biological associations with the development and progression of kidney disease, and included age, hypertension, diabetes mellitus, body mass index, HCV infection, HIV viral load, CD4 lymphocyte count, HAART use, and baseline eGFR. Additionally, we adjusted for genetic ancestry data by including in our models the principal components that were associated with the biomarkers in univariate analyses (components 1, 3 and 5). We assessed for effect modification between *APOLI* risk genotype and historical suppression of HIV RNA for the outcome of albuminuria, by evaluating an interaction term in the overall model. To determine whether *APOLI*-associated kidney injury precedes overt CKD, we also performed subgroup analyses restricted to individuals with $eGFR >60$ ml/min/1.73m².

Finally, we evaluated the associations of *APOLI* risk genotype with kidney function at baseline and during follow-up, using a recessive model of inheritance. We used linear mixed models to evaluate the associations of *APOLI* risk alleles with annual eGFR change, with random intercepts and slopes across time to account for the correlation between repeated measures at baseline and at years 4 and 8. We then used Poisson regression with a robust variance estimator to assess the associations of *APOLI* risk alleles with incident CKD and rapid decline, expressing the results as incident rate ratios for each outcome. Women with $eGFR <60$ ml/min/1.73m² at baseline were excluded from incident CKD analyses. Multivariable models sequentially adjusted for demographics, traditional risk factors for kidney disease progression, ACR , and the tubular injury markers. To account for losses to follow-up in kidney decline analyses, we adjusted estimates using an inverse probability weighting approach by modeling the participant's probability of having a non-missing outcome, with separate weights calculated at each visit.³² The inverse of this probability was then used as a weight applied to persons with known outcomes in the multivariable regression analyses of kidney decline.

Multiple imputation with the Markov chain Monte Carlo method was used to impute missing covariates, with 10 imputations to yield ~95% relative efficiency.³³ The percentage of missing observations for each covariate ranged from less than 1% to 31% (Table S1). Right-skewed variables were log-transformed in the imputation model. Estimates obtained from imputed data were combined using the MIANALYZE procedure to reflect the uncertainty due to missing data.

Compared to the women included in this substudy, women who were excluded ($n=364$) due to missing *APOLI* genotype or urine biomarker measurements had higher prevalence of diabetes mellitus, lower CD4 lymphocyte count, and lower prevalence of HAART use

(Table S2). As an alternate approach, we used multiple imputation to include all 795 HIV-infected African-American women in the analyses (Tables S3 and S4).

Results

Study Population by *APOL1* Genotype

Among the 431 HIV-infected African-American women included in this study, 11% (n=47) and 44% (n=191) had 2 and 1 *APOL1* risk alleles, respectively, which are similar to the frequencies reported among the general African-American population in the United States.³⁴ Hypertension and HCV infection were each present in 31% and 35% of the participants, respectively, whereas diabetes was present in 10% of the cohort. There were no statistically significant differences in the prevalence of hypertension, diabetes mellitus, or HCV infection by number of *APOL1* risk alleles (Table 1). Median CD4 cell count and HIV RNA levels were similar across *APOL1* risk allele groups.

Associations of *APOL1* Genotype With Glomerular and Tubular Injury Markers

The distribution of ACR among women with two *APOL1* risk alleles was shifted to the right relative to those with 0/1 risk allele, indicating higher ACR levels (Figure 1A). By contrast, the distributions of IL-18, KIM-1, NGAL, and α 1m did not appear to differ by number of *APOL1* risk alleles (Figure 1B, Figure S1A-C).

Using a recessive model of inheritance (Table 2), the presence of 2 *APOL1* risk alleles compared with 0/1 risk allele was associated with higher levels of ACR (median, 24 vs. 11 mg/g; $p < 0.001$) and a doubling in the prevalence of ACR >30 mg/g (47% vs. 21%; $p=0.001$). After multivariable adjustment for traditional kidney risk factors and HIV-related risk factors (Table 3), the presence of 2 *APOL1* risk alleles remained associated with 104% higher ACR ($p=0.002$) and 2-fold greater prevalence of ACR >30 mg/g ($p=0.02$). There was no significant interaction between historical suppression of HIV RNA and *APOL1* genotype for the outcome of ACR ($p=0.4$).

APOL1 genotype was associated with higher ACR levels when analyzed using dominant ($p=0.02$) and additive ($p < 0.001$) models of inheritance (Table 2). After multivariable adjustment, the observed associations remained robust using the additive ($p=0.01$) but not dominant ($p=0.6$) model (Table 3).

APOL1 risk genotype was not associated with higher levels of urine IL-18, NGAL, or detectable α 1m, by recessive, dominant, or additive models of inheritance (Tables 2 and 3). In unadjusted analyses, *APOL1* risk genotype was associated with lower urine levels of creatinine-standardized but not unstandardized KIM-1, in recessive and additive models. However, after multivariable adjustment (Table 3), the association between *APOL1* risk genotype and creatinine-standardized KIM-1 levels no longer met statistical significance. Urine creatinine levels were similar across *APOL1* risk allele groups (Table 2).

Findings were similar when we restricted analyses to participants with baseline eGFR >60 ml/min/1.73m² (n=408; Tables S5 and S6), and when we used multiple imputation to

include all participants with missing *APOL1* genotype or urine biomarker measurements (n=795; Table S3).

Associations of *APOL1* Genotype With Longitudinal Kidney Function Decline

Mean baseline eGFR was 83.5 ml/min/1.73m² in women with 2 *APOL1* risk alleles and 89.1 ml/min/1.73m² in women with 0/1 risk allele (p=0.2). Over approximately 8 years of follow-up, women with 2 *APOL1* risk alleles experienced faster kidney function decline, as compared to women with 0/1 risk allele (Table 4). The unadjusted rates of annual eGFR decline were -2.6 (95% confidence interval [CI], -3.5 to -1.6) ml/min/1.73 m² among women with 2 risk alleles, and -1.3 (95% CI, -1.6 to -1.1) ml/min/1.73m² among women with 0/1 risk allele (p=0.02). Adjustment for common risk factors, ACR, and the tubular injury markers minimally affected the magnitude of difference in annual kidney function decline by *APOL1* risk genotype.

During follow-up, 100 (25%) and 34 (8%) cases of incident CKD and rapid decline occurred, respectively. Compared to women with 0/1 risk allele, women with 2 *APOL1* risk alleles experienced higher rates of incident CKD and rapid decline by 1.7- and 3.4 fold, respectively, with minimal attenuation after adjustment for the kidney injury markers (Table 4).

Findings were similar when we performed the longitudinal analyses in all 795 HIV-infected African-American participants, using multiple imputation to include individuals with missing *APOL1* genotype or urine biomarker measurements (Table S4).

Discussion

Among HIV-infected African-American women, we found that the presence of 2 *APOL1* risk alleles is associated with albuminuria, a traditional marker of glomerular injury, but not with higher levels of tubular injury markers, including IL-18, KIM-1, NGAL, and $\alpha 1m$. In longitudinal analyses, women with 2 *APOL1* risk alleles experienced faster kidney function decline, and higher rates of incident CKD and 10% annual eGFR decline, compared with women having 0/1 risk allele. Notably, adjustment for baseline levels of glomerular and tubular injury markers did not attenuate the associations of *APOL1* risk genotype with longitudinal kidney outcomes. To our knowledge, this is the first study to utilize these urine biomarkers to distinguish associations of the *APOL1* risk genotype with glomerular and tubular injury.

The strong association of the *APOL1* risk genotype with albuminuria is consistent with results of prior investigations of individuals with mild kidney disease. Among non-diabetic African-Americans in the Dallas Heart Study, individuals with 2 *APOL1* risk alleles were observed to be 2.8-fold more likely to have microalbuminuria, compared to those with 0/1 risk allele.³⁴ The *APOL1* risk genotype has also been reported to be associated with macroalbuminuria in first-degree relatives of African-Americans with nondiabetic ESRD.³⁵ Finally, among HIV-infected African-Americans without prior AIDS, we previously found that the presence of 2 *APOL1* risk alleles was independently associated with 69% higher (95% CI, 36%-108%) urine protein excretion, compared with 0/1 risk allele.³⁶ The present

study builds upon our prior work by localizing *APOLI*-associated kidney injury to the glomerulus, rather than the tubules.

Contrary to our hypothesis, albuminuria did not appreciably attenuate the associations between *APOLI* genotype and longitudinal kidney function decline. Because we measured albuminuria only at baseline, we cannot exclude the possibility that individuals with 2 *APOLI* risk alleles developed albuminuria prior to ascertainment of eGFR at the 4- or 8-year follow-up visits. Second, the relatively small sample size of individuals with 2 *APOLI* risk alleles may have reduced power to detect a smaller effect size of albuminuria on the longitudinal kidney outcomes. Finally, glomerular injury may be one of several pathways linking *APOLI* genotype with the development of overt kidney disease among HIV-infected African-Americans.

Although the pathophysiology underlying *APOLI*-associated kidney disease remains speculative, the presence of APOL1 protein in podocytes in healthy kidney samples suggests a role for APOL1 in normal glomerular health.^{10,11} APOL1 is a 43 kDa member of the Bcl-2 family of proteins, which are key regulators of programmed cell death.³⁷ When overexpressed in cancer cell lines, APOL1 induces autophagic cell death.³⁸ Recent studies suggest an important role for autophagy in the maintenance of glomerular homeostasis. Hartleben *et al.* observed that podocytes display unusually high levels of autophagic activity compared to tubular cells, and that mice lacking autophagic capability exhibit increased susceptibility to glomerular disease.³⁹ Furthermore, Lan *et al.* demonstrated that APOL1 overexpression from G1 and G2 *APOLI* genetic variants in cultured human podocytes results in podocyte necrosis, and that APOL1 variant-induced podocyte injury is augmented by the presence of HIV infection.⁴⁰ Podocyte dysregulation has been implicated in the development of HIV-associated nephropathy (HIVAN),⁴¹ although gene-environment interactions appear to be necessary for the development of overt kidney disease. Papeta *et al.* found that the introduction of HIV to mice with genetic susceptibility to HIVAN led to alterations in the expression of specific proteins important in maintaining podocyte structure and function.⁴² Collectively, these *in vitro* and animal studies suggest that host *APOLI* genotype may interact synergistically with HIV to modulate pathways involved in podocyte integrity.

In humans, the contributions of the *APOLI* genotype and HIV to the development and progression of glomerular disease have been studied in kidney biopsy series. In HIV-infected African Americans with non-HIVAN pathology, Fine *et al.* found that number of *APOLI* risk alleles correlated with the type of non-HIVAN histopathology, and with risk for end-stage renal disease (ESRD).⁴³ However, among individuals with biopsy-confirmed HIVAN, Atta *et al.* reported no differences in renal pathology or risk for ESRD by *APOLI* genotype. The discordant findings of these studies may reflect the heterogeneity of HIV-related kidney disease in African-Americans, and highlight the need for larger studies that evaluate pathophysiologic mechanisms mediating APOL1-associated kidney risk.

Of note, because APOL1 has been detected in vascular endothelium,¹⁰ albuminuria among individuals with *APOLI* risk variants could signify the presence of subclinical vascular disease. Albuminuria is an established risk factor for cardiovascular disease, even among

individuals with preserved eGFR.⁴⁴ Recent studies evaluating the associations of the *APOL1* genotype with cardiovascular outcomes have yielded conflicting results.⁴⁵ Among African-Americans in the Jackson Heart Study and the Women's Health Initiative, 2 *APOL1* risk alleles were associated with a 2-fold greater risk of atherosclerotic cardiovascular disease.⁴⁶ By contrast, Langefeld *et al.* found no association between *APOL1* risk variants and prevalent cardiovascular disease, in African-Americans enrolled in the Systolic Blood Pressure Intervention Trial,⁴⁷ while Freedman *et al.* reported lower risk for subclinical atherosclerosis and death in association with the *APOL1* risk genotype, among African-Americans in the Diabetes Heart Study.⁴⁸ Understanding the interplay between *APOL1* risk genotype, HIV suppression, kidney injury, and the development of cardiovascular disease through future studies may have substantial implications for the aging HIV-infected population.

The findings of the present study do not support a strong pathogenic role for *APOL1* risk variants in tubular injury and dysfunction among HIV-infected African-Americans with well-preserved kidney function. However, tubular injury may play a more prominent role in the absence of HIV infection, or at more advanced stages of *APOL1*-associated kidney disease. For instance, in the Focal Segmental Glomerulosclerosis Clinical Trial, in which persons with HIV were excluded, Kopp *et al.* found that individuals with the high-risk *APOL1* genotype had more extensive tubular atrophy and fibrosis on kidney biopsy.⁴⁹ Furthermore, in African-Americans with “hypertension-associated” nephropathy, Larsen *et al.* reported higher prevalence of tubular atrophy and microcystic dilatation on kidney biopsy samples of individuals with 2 vs 0/1 *APOL1* risk alleles.⁵⁰ Notably, participants of that study had advanced kidney disease, with a mean serum creatinine of 4.3 mg/dl among individuals with 2 *APOL1* risk alleles. Additional studies are needed to validate these findings, and to investigate the contributions of tubulointerstitial damage to prognosis at later stages of *APOL1*-associated kidney disease.

Our study has several limitations. First, as a study of women, the results are not generalizable to men, although there is currently no evidence to suggest a gender-based interaction between *APOL1* genotype and kidney disease risk. Second, as a cross-sectional study nested within a cohort, our study is subject to selection bias due to study dropout or competing events, and we cannot make conclusions regarding causality. Third, almost half of the HIV-infected African-American women in the WIHS were excluded from initial analyses, due to missing *APOL1* genotype or urine biomarker measurements, which could reduce power or bias the results. However, our findings remained robust when we repeated the analyses, using multiple imputation to include the participants with missing data. Fourth, urine samples were collected over a decade prior to biomarker measurement, so degradation over time may have contributed to the null associations between *APOL1* genotype and tubular biomarkers. Alternatively, the tubular injury markers may lack sensitivity for detection of tubular dysfunction at very early stages. However, these urine biomarkers had strong associations with subsequent eGFR decline and mortality risk.^{14,15} Finally, despite our adjusting for multiple potential confounders, the possibility of residual confounding remains.

In summary, among HIV-infected women of African ancestry, APOL1-associated kidney injury appears to localize to the glomerulus, rather than the tubules. Additionally, the *APOL1* risk genotype was strongly predictive of kidney function decline. Future studies should evaluate the pathophysiologic mechanisms by which variant forms of APOL1 result in glomerular injury, as well as targeted therapies to slow progression of APOL1-mediated kidney disease.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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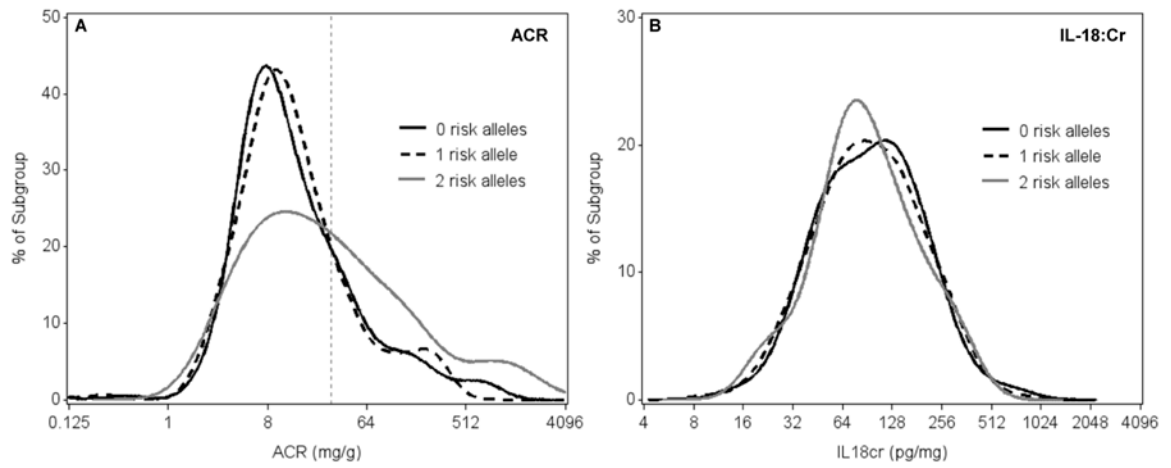


Figure 1. Distribution of albumin-creatinine ratio (A) and interleukin 18-creatinine ratio (B) in HIV-infected African-American women, stratified by number of *APOL1* risk alleles. Dashed vertical line in panel A indicates ACR threshold of 30 mg/g. Abbreviations: ACR, albumin-creatinine ratio; IL-18:Cr, interleukin 18-creatinine ratio.

Table 1
Baseline characteristics of HIV-infected African-American women, stratified by number of *APOL1* risk alleles

<i>Characteristic</i>	0 allele (n = 193)	1 allele (n = 191)	2 alleles (n = 47)	P-value
Baseline Age (y)	41 [35-46]	42 [37-47]	37 [35-47]	0.1
Hypertension	50 (26%)	67 (35%)	17 (36%)	0.1
Diabetes mellitus	13 (7%)	26 (14%)	6 (13%)	0.08
HCV infection	66 (35%)	67 (35%)	16 (34%)	0.9
Current CD4+ cell count (cells/mm ³)	380 [246-563]	388 [242-583]	474 [318-673]	0.09
History of AIDS	86 (45%)	96 (50%)	25 (53%)	0.4
HIV RNA load				0.8
80 copies/mL	52 (28%)	56 (29%)	13 (28%)	
81-1999 copies/mL	42 (22%)	47 (25%)	10 (22%)	
2000-9999 copies/mL	30 (16%)	29 (15%)	11 (24%)	
10,000 copies/mL	65 (34%)	59 (31%)	12 (26%)	
Historical HIV suppression ¹	68 (35%)	73 (38%)	15 (32%)	0.7
Current cART use	117 (61%)	116 (61%)	23 (49%)	0.3

Note: Values for categorical variables are given as number (percentage); values for continuous variables, as median [interquartile range]. P-values from chi-square and Kruskal-Wallis tests for categorical and continuous variables, respectively.

¹ Defined as percentage of historical HIV RNA values less than 400 copies/mL for each study participant.

Abbreviations: cART, combination antiretroviral therapy; HCV, hepatitis C virus

Table 2
Urine biomarker levels in HIV-infected African-American women, stratified by number of *APOL1* risk alleles

	0 allele (n = 193)	1 allele (n = 191)	2 alleles (n = 47)	P-value		
				Recessive ¹	Dominant ²	Additive ³
Glomerular Injury						
Cr-standardized						
ACR (mg/g)	10 (7-29)	11 (7-24)	24 (8-88)	<0.001	0.02	<0.001
ACR >30 mg/g	44 (23%)	38 (20%)	22 (47%)	0.001	0.1	0.005
Unstandardized						
Urine Albumin (mg/mL)	0.16 (0.08-0.37)	0.16 (0.09-0.37)	0.40 (0.11-1.10)	<0.001	0.009	<0.001
Tubular Injury						
Cr-standardized						
IL-18:Cr (pg/mg)	97 (55-149)	94 (56-150)	79 (59-148)	0.3	0.4	0.3
KIM-1:Cr (pg/mg)	323 (228-493)	325 (219-568)	265 (171-465)	0.007	0.06	0.01
NGAL:Cr (ng/mg)	29 (15-65)	34 (16-58)	27 (14-75)	0.9	0.7	0.9
Unstandardized						
IL-18 (pg/mL)	122 (66-247)	131 (70-253)	119 (83-215)	0.9	0.9	0.9
KIM-1 (pg/mL)	459 (241-874)	530 (310-866)	415 (252-845)	0.3	0.6	0.3
NGAL (ng/mL)	39 (19-86)	44 (21-91)	38 (21-159)	0.5	0.3	0.4
Tubular Dysfunction						
Detectable A1M	118 (61%)	130 (68%)	30 (64%)	0.7	0.8	0.9
Urine Cr (mg/mL)	1.50 (0.91-2.10)	1.54 (0.96-2.08)	1.51 (0.98-2.27)	0.5	0.4	0.4

Note: Values for categorical variables are given as number (percentage); values for continuous variables, as median [interquartile range].

¹ P-value for 2 risk alleles vs 0/1 risk alleles, adjusted for age and ACR.

² P-value for 2/1 risk alleles vs 0 risk alleles, adjusted for age and ACR.

³ P-value for trend (2 vs 1 vs 0 risk alleles), adjusted for age and ACR.

Abbreviations: ACR, albumin-creatinine ratio; A1M, α_1 -microglobulin; Cr, creatinine; IL-18, interleukin 18; KIM-1, kidney injury molecule 1; NGAL, neutrophil gelatinase-associated lipocalin.

Table 3
Adjusted associations of *APOLI* risk alleles with biomarkers in HIV-infected African-American women

	% Estimate ⁵ (95% CI)	Prevalence Ratio ⁶ (95% CI)	P Values by Model of inheritance		
			Recessive ²	Dominant ³	Additive ⁴
Continuous Outcomes					
ACR (mg/g)	104 (29, 223)	--	0.002	0.6	0.01
IL-18:Cr (pg/mg)	-5 (-24, 18)	--	0.6	0.5	0.5
KIM-1:Cr (pg/mg)	-20 (-36, -1)	--	0.06	0.5	0.06
NGAL:Cr (ng/mg)	10 (-26, 64)	--	0.6	0.9	0.6
Dichotomous Outcomes					
ACR > 30 mg/g	--	2.00 (1.17, 3.44)	0.02	0.8	0.08
Detectable AIM	--	1.13 (0.65, 1.97)	0.8	0.7	0.9

Note: Multivariable models adjust for age, hypertension, diabetes mellitus, body mass index, hepatitis C virus infection, HIV viral load, CD4 cell count, current combination antiretroviral therapy, creatinine-based estimated glomerular filtration rate, and principal components 1, 3, and 5.

² P-value compares 2 vs 0/1 *APOLI* risk alleles

³ P-value compares 2/1 vs 0 *APOLI* risk alleles

⁴ P-value for trend (2 vs 1 vs 0 *APOLI* risk alleles)

⁵ Estimated percentage difference attributable to having 2 vs 0/1 *APOLI* risk alleles.

⁶ Adjusted prevalence ratio among individuals with 2 vs 0/1 *APOLI* risk alleles.

Abbreviations: ACR, albumin-creatinine ratio; AIM, α 1-microglobulin; CI, confidence interval; Cr, creatinine; IL-18, interleukin 18; KIM-1, kidney injury molecule 1; NGAL, neutrophil gelatinase-associated lipocalin.

Table 4
Associations of *APOLI* risk alleles with kidney function outcomes in HIV-infected African-American women

Outcome	0 allele (n = 193)	1 allele (n = 191)	2 alleles (n = 47)
Baseline eGFR (ml/min/1.73 m ²)			
Mean (95% CI)	90.8 (88.0, 93.5)	87.3 (84.4, 90.3)	83.5 (76.1, 91.0)
Estimated difference, 2 vs 0/1 alleles (95% CI) ¹			
Unadjusted	Reference	Reference	-5.5 (-13.0, 1.9)
Adjusted + ACR	---	---	-4.7 (-10.4, 1.0)
Adjusted + ACR, IL-18, KIM-1, NGAL, A1M	---	---	-4.1 (-9.4, 1.2)
Annual change in eGFR (ml/min/1.73 m ²)			
Mean (95% CI)	-1.4 (-1.8, -1.1)	-1.2 (-1.6, -0.9)	-2.6 (-3.5, -1.6)
Estimated difference, 2 vs 0/1 alleles (95% CI) ²			
Unadjusted	Reference	Reference	-1.2 (-2.2, -0.2)
Adjusted + ACR	---	---	-1.1 (-2.1, -0.1)
Adjusted + ACR, IL-18, KIM-1, NGAL, A1M	---	---	-1.1 (-2.1, -0.1)
Incident CKD			
No. of Events	42	42	16
No. at risk	181	174	41
Incident Rate Ratio, 2 vs 0/1 alleles (95% CI) ³			
Unadjusted	Reference	Reference	1.65 (1.08, 2.52)
Adjusted + ACR	---	---	1.74 (1.15, 2.64)
Adjusted + ACR, IL-18, KIM-1, NGAL, A1M	---	---	1.68 (1.15, 2.46)
10% annual eGFR decline			
No. of Events	13	11	10
No. at risk	193	191	47
Incident Rate Ratio, 2 vs 0/1 alleles (95% CI) ³			
Unadjusted	Reference	Reference	3.40 (1.74, 6.67)
Adjusted + ACR	---	---	3.20 (1.48, 6.91)
Adjusted + ACR, IL-18, KIM-1, NGAL, A1M	---	---	2.82 (1.21, 6.54)

Note: Adjusted models control for age, hypertension, diabetes mellitus, hepatitis C virus infection, HIV viral load, CD4 lymphocyte count, combination antiretroviral therapy use, and kidney injury markers listed.

Abbreviations: CI, confidence interval; CKD, chronic kidney disease; eGFR, estimated glomerular filtration rate. A1M, α_1 -microglobulin; ACR, albumin-creatinine ratio; IL-18, interleukin 18; KIM-1, kidney injury molecule 1; NGAL, neutrophil gelatinase-associated lipocalin

¹ Estimated difference in baseline eGFR attributable to having 2 vs 0/1 *APOLI* risk alleles

² Estimated difference in annual eGFR change attributable to having 2 vs 0/1 *APOLI* risk alleles

³ Incident rate ratio for 2 vs 0/1 *APOLI* risk alleles