Socioeconomic Position, But Not African Genomic Ancestry, Is Associated With Blood Pressure in the Bambui-Epigen (Brazil) Cohort Study of Aging

M. Fernanda Lima-Costa, Juliana Vaz de Mello Mambrini, Maria Lea Corrêa Leite, Sérgio Viana Peixoto, Josélia Oliveira Araújo Firmino, Antônio Ignácio de Loyola Filho, Mateus H. Gouveia, Thiago P. Leal, Alexandre Costa Pereira, James Macinko, Eduardo Tarazona-Santos

Abstract—The study objective is to examine the role of African genome origin on baseline and 11-year blood pressure trajectories in community-based ethnoracially admixed older adults in Brazil. Data come from 1272 participants (aged 260 years) of the Bambui cohort study of aging during 11 years of follow-up. Outcome measures were systolic blood pressure, diastolic blood pressure, and hypertension control. Potential confounding variables were demographic characteristics, socioeconomic position (schooling and household income), and health indicators (smoking, sedentary lifestyle, high-density lipoprotein cholesterol, waist circumference, diabetes mellitus, and cardiovascular diseases), including antihypertensive drug use. We used 370 539 single-nucleotide polymorphisms to estimate each individual’s African, European, and Native American trihybrid ancestry proportions. Median African, European, and Native American ancestry were 9.6%, 84.0%, and 5.3%, respectively. Among those with African ancestry, 59.4% came from East and 40.6% from West Africa. Baseline systolic and diastolic blood pressure, controlled hypertension, and their respective trajectories, were not significantly (P>0.05) associated with level (in quintiles) of African genomic ancestry. Similar results were found for West and East African subcontinental origins. Lower schooling level (<4 years versus higher) showed a significant and positive association with systolic blood pressure (Adjusted β=2.92; 95% confidence interval, 0.85–4.99). Lower monthly household income per capita (<USD 180.00 versus higher) showed an inverse association with hypertension control (β=−0.35; 95% confidence interval, −0.63 to −0.08, respectively). Our results support the view that favors social and environmental factors as determinants of blood pressure and hypertension control. (Hypertension. 2016;67:349-355. DOI: 10.1161/HYPERTENSIONAHA.115.06609.)

Key Words: African continental ancestry group ■ blood pressure ■ cohort studies ■ hypertension

The role of African ancestry on blood pressure or hypertension has received renewed attention with the emergence of high-throughput genotyping techniques, although most of this work has been carried out in the United States.1–4 Studying this relationship in Latin America—and in Brazil specifically—offers several opportunities because it is one of the most ethnoracially heterogeneous regions of the world.5,6 Life expectancy has increased rapidly in the region,7 generating populations with unprecedented numbers of admixed older persons at risk of hypertension. The Brazilian population—the fifth largest in the world—originates from African, European, and Native American ancestral roots.5,6 Brazilians with African ancestry generally have a high proportion of East African origin, relative to black Americans and those from the Caribbean who tend to have a higher proportion of West African ancestry.6,8,9 Previous Brazilian studies, based on ethnoracial self-classification, reported greater prevalence of high blood pressure or hypertension among self-reported black adults10 and among blacks who reported having discrimination.11

The Bambui-Epigen Cohort Study of Aging was conducted in a well-defined population of older adults in Brazil’s Southeast region.12 We used 370 539 single-nucleotide polymorphisms to examine the association between genome-wide proportions of African ancestry with baseline and 11-year blood pressure and controlled hypertension in participants of this cohort, taking into account an array of demographic...
characteristics, socioeconomic position, and health indicators that could confound this association. The large size, the community-based nature of our study, and the long period of follow-up provide a rare opportunity to address these questions in an ethnoracially admixed population.

Methods

Study Design and Population

The Bambui cohort study of aging is ongoing in Bambui, a city of ≈15,000 inhabitants in the state of Minas Gerais in Southeast Brazil. Detailed information on this cohort can be found elsewhere. Briefly, the population eligible for the cohort consisted of all residents aged ≥60 years on 1 January 1997 (1606 of 1742 inhabitants aged ≥60 years were participated). Cohort members underwent annual follow-up visits, which consisted of an interview and, on death, verification of death certificates (98.8% of which have been verified). Most participants had some degree of African, European, and Native American genome ancestry. At baseline, 2.5% of participants self-reported as black, 36.9% as brown (moreno or mulato in Portuguese), and 60.6% as white.

Blood Pressure and Use of Antihypertensive Drugs

Blood pressure was measured at baseline (1997) and in 3 subsequent waves (2000, 2002, and 2008), using the same protocols. Three measures of blood pressure were performed after 5 minutes of initial rest and after at least 30 minutes without drinking coffee or smoking. These measures were taken by using mercury sphygmomanometers with the appropriate cuff size (Tycos5097-30; Tycos, Arden) and standardized stethoscopes (Littman Cardiology II, 3M, St. Paul). Measurements were taken at the project fieldwork clinic in a quiet, isolated room with controlled temperature. Systolic and diastolic blood pressures were defined as the mean of the second and the third measures. Controlled hypertension was defined by an SBP and a DBP of <140 and 90 mm Hg, respectively, among persons undergoing antihypertensive treatment.

Use of antihypertensive medication was ascertained by examining the drug packaging or medical prescription during the interview at baseline (1997) and again in 2000, 2003, and 2008. Drugs were classified using the Anatomical Therapeutic Chemical Index (ATC/DDD Index). Drugs of the following classes were considered: CO3 (diuretics), CO7 (β-blocking agents), CO8 (calcium channel blockers), CO9 (agents acting on the renin–angiotensin system), and CO2 (antiadrenergic agents, agents acting on arteriolar smooth muscle and others).

Genetic and Ancestry Analyses

CoHort participants were genotyped with the Omni 2.5M array (Illumina, San Diego, CA). We inferred a kinship coefficient for each pair of individuals, using the approach implemented in the software Reap. Conditioning on trihybrid individual admixture proportions (see below), we used complex networks to identify families from the matrix of pair-wise kinship coefficients. In this approach (ie, families), pairs of individuals are related if they have a kinship coefficient >0.1 (first- and second-degree relatives). In this study, we performed ancestry inferences using the model-based method, implemented in the Admixture software. First, we used 370 539 single-nucleotide polymorphisms to estimate for each individual African, European, and Native American ancestry proportions, using 266 African, 262 European, and 93 Native American individuals from public data sets as parental populations. Then we used 331 790 single-nucleotide polymorphisms and the reference data set to further divide total African ancestry into its 2 components: a Western Africa/non-Bantu and an Eastern Africa/Bantu, hereafter called Western Africa and Eastern Africa, respectively. The fact that many Bambui residents are related could affect high-resolution inferences of biogeographic ancestry (such as West and East African) with the Admixture software, which assumes that individuals analyzed are unrelated. To overcome this limitation, we performed separate admixture runs to infer West and East African ancestry components, avoiding the presence of related individuals in the same run. Further details on how genetic and ancestry analyses of the Bambui cohort population were performed can be found elsewhere.

Other Study Variables

Other baseline variables in this analysis include: demographic characteristics (age and sex), socioeconomic position (schooling and household income), and health indicators (current smoking, physical activity, high-density lipoprotein cholesterol level, abdominal obesity, diabetes mellitus, and cardiovascular diseases). On the basis of its distribution, we categorized smoking into incomplete primary school (<4 years) and higher (≥4 years). We categorized monthly household income per capita into equal or superior to the median value, equivalent to 1.5x the 1997 Brazilian minimum wage (about USD 180.00). Current smokers and ex-smokers were persons who smoked at least 100 cigarettes during their lifetime and who still smoke or had stopped smoking, respectively. Physical activity levels were calculated based on the level of oxygen consumed for 25 physical activities in the previous 3 months to quantify energy expenditure in metabolic equivalent tasks. Sedentary individuals were considered to be those whose energy expenditure was <450 metabolic equivalent task minutes per week, which corresponds to at least 150 minutes per week of moderate to vigorous physical activity. Blood fasting cholesterol was determined by using standard enzymatic methods (Merck, Darmstadt, Germany). Abdominal obesity was defined by waist circumference using the cut points of >102 cm for men or >88 cm for women. Diabetes mellitus was defined by fasting blood glucose ≥126 mg/dL or treatment. Cardiovascular diseases were defined as previous medical diagnosis of myocardial infarction, symptoms of angina pectoris, stroke, and heart failure; heart failure was assessed by a plasma B-type brain natriuretic peptide level ≥100 pg/mL (MEIA/AxSYM; Abbott, Abbott Park, IL), as recommended by the manufacturer.

Statistical Analysis

Descriptive analyses were based on Pearson χ2 and 1-way ANOVA tests, for differences across frequencies and means, respectively. Because blood pressure trends could vary among participants, we used mixed effects regression to model blood pressure trajectories (using mixed effects linear regression) and hypertension control (using mixed effects logistic regression) as outcomes, based on measures taken in 1997, 2000, 2002, and 2008. All multivariable models were adjusted for baseline age (continuous), sex, monthly household income per capita, smoking, sedentary lifestyle, diabetes mellitus, any cardiovascular diseases (all categorical variables), and high-density lipoprotein cholesterol (continuous), in addition to the use of hypertensive drugs (a dichotomous time dependent variable). We retained all variables in the fully adjusted model because no pairs exhibited collinearity. All models assumed that individual trajectories could vary both with respect to the intercept and the slope of time. To take into account dropouts that could be related to outcomes, we applied a pattern mixture model. This entailed creating a factor variable representing the time of the last valid observation, which was then included in all multivariable models as both a main effect and as an interaction term with time. We also used clustered robust variance estimates to take into account intrafamilial clustering so as to avoid potential bias resulting from analysis of individuals who were related (807 participants were first- and second-degree relatives). We examined the statistical significance of multiplicative interactions between African genome ancestry and sex on baseline SBP, DBP, and controlled hypertension trajectories. Because there was no evidence of interaction with sex, all analyses were carried out with sex as a covariate. Finally, we carried out additional stratified analyses, using the above mentioned mixed effects regression models to examine the association between East and West African ancestries with each outcome. Statistical analyses were carried out using STATA 13.0 statistical software (Stata Corporation, College Station). All P values were 2 tailed (<0.05).

Ethics Assessment

The Bambui cohort study of aging was approved by the Comissão de Ética em Pesquisa (Institutional Review Board) at the Oswaldo Cruz...
Results

Of the 1606 cohort participants, 1272 persons had complete information on all study variables, and they were included in this analysis. The median proportion of African ancestry among study participants was 9.6% (interquartile range, 12.8). The corresponding values for European and Native American ancestry were 84.0% (interquartile range, 17.5) and 5.3 (interquartile range, 5.5), respectively. As shown in Table 1, at baseline, the mean age was 68.8 years, 61.2% were women and low schooling levels (<4 years) predominated (63.4%). The mean (SD) systolic and diastolic blood pressures were 137.6 (22.3) and 83.5 mm Hg (12.6), respectively. Overall, 48.9% of participants were users of antihypertensive drugs and, of these, 46.1% had their blood pressure controlled (ie, SBP and DBP <140/80 mm Hg). Statistically significant differences across African ancestry quintiles were found for age, schooling, household income, previous cardiovascular diseases, and DBP level. No significant associations (P>0.05) were found between African genomic ancestry and SBP levels, current use of antihypertensive drugs, or controlled hypertension prevalence among those being treated.

During the study period, 522 participants died, 84 (6.4%) were lost to follow-up, and a total of 3843 blood pressure measurements were taken among cohort participants. As shown in Table 2, there was no significant association (P>0.05) between quintiles of genome-wide African ancestry and baseline SBP, DBP, or controlled hypertension, or their respective trajectories, once confounders were controlled. SBP showed a positive and independent association with lower schooling levels (β=2.92; 95% confidence interval [CI], 0.85–4.99), diabetes mellitus (β=5.95; 95% CI, 2.84–9.06), and use of antihypertensive drugs (β=1.89; 95% CI, 0.29–3.49). DBP showed negative associations with age (β=–0.32; 95% CI, –0.41 to –0.23) and cardiovascular disease (β=–1.39; 95% CI, –2.51 to –0.27), and positive associations with sex (β=3.65; 95% CI, 2.25–5.04) and abdominal obesity (β=1.89; 95% CI, 0.64–3.15). Controlled hypertension showed inverse associations with household income (β=–0.35; 95% CI, –0.63 to –0.08).
and diabetes mellitus (β = −0.41; 95% CI, −0.78 to −0.04), and a positive association with being a former smoker (β = 0.44; 95% CI, 0.01−0.87).

West African ancestry predominated in the Bambui cohort population, accounting for 59.4% of the total African ancestry (the remaining 40.6% was of East African ancestry). As shown in Table 3, there was no statistically significant association between African ancestry subpopulations and baseline SBP, DBP, controlled hypertension, or their trajectories.

We carried out additional sensitivity analyses limited to those subjects who were nonrelated. The results confirmed the absence of associations between African genome ancestry levels with baseline or trajectories of SBP, DBP, and controlled hypertension and, further, the absence of any association between these outcomes and African ancestry substructures (Appendix S1 and Table S1 in the online-only Data Supplement).

**Discussion**

We used a large number of single-nucleotide polymorphisms to examine the association between African ancestry with 11-year blood pressure and hypertension control in community-dwelling admixed older adults. The key findings are: first, neither baseline nor trajectories of SBP, DBP, or controlled hypertension showed significant associations with levels of African genomic ancestry; second, socioeconomic position, as measured by schooling or household income levels, was the most important nonbiological factor associated with SBP and controlled hypertension, respectively, and these associations were independent of age, sex and an array of health indicators. Importantly, these socioeconomic disparities on SBP and controlled hypertension were observed in a population within which absolute differences in schooling and income levels were small.

To our knowledge, previous studies examining the association between hypertension or blood pressure and African ancestry have been limited to populations with larger genetic diversity differences, such as European–American and African-American populations. This is the first study to our knowledge that examined the association between African ancestry levels with blood pressure and hypertension in a population with relatively small differences in ancestry.
Table 3. Results of the Multivariable Analysis of the Association of Baseline and Trajectories of Blood Pressure and Adequate Control of Hypertension with West and East African Ancestry Proportions, The Bambui Cohort Study of Aging

<table>
<thead>
<tr>
<th>Ancestry Levels in Quintiles</th>
<th>Systolic Blood Pressure (SBP)</th>
<th>Diastolic Blood Pressure (DBP)</th>
<th>Controlled Hypertension Among Treated*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of Observations=3843</td>
<td>No. of Observations=3843</td>
<td>No. of Observations=2401</td>
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<tr>
<td></td>
<td>No. of Individuals=1272</td>
<td>No. of Individuals=1272</td>
<td>No. of Individuals=951</td>
</tr>
<tr>
<td>West African</td>
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<td></td>
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<tr>
<td>Association with baseline</td>
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<td></td>
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<tr>
<td>blood pressure outcomes</td>
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<td></td>
</tr>
<tr>
<td>Intermediate (1.7% to 13.1%; n=763) vs lowest (&lt;1.7%; n=256)</td>
<td>-1.25 (−4.11 to 1.60)</td>
<td>−0.08 (−1.70, 1.55)</td>
<td>0.15 (−0.26 to 0.57)</td>
</tr>
<tr>
<td>Highest (&gt;13.1%; n=253) vs lowest (&lt;1.7%)</td>
<td>0.28 (−3.55 to 4.11)</td>
<td>1.48 (−0.67 to 3.64)</td>
<td>−0.40 (−0.94 to 0.14)</td>
</tr>
<tr>
<td>Association with trajectory of blood pressure outcomes‡</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Intermediate vs lowest</td>
<td>0.14 (−0.23 to 0.52)</td>
<td>0.14 (−0.05 to 0.33)</td>
<td>−0.03 (−0.09 to 0.03)</td>
</tr>
<tr>
<td>Highest vs lowest</td>
<td>0.17 (−0.33 to 0.68)</td>
<td>0.18 (−0.09 to 0.44)</td>
<td>0.03 (−0.05 to 0.10)</td>
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<tr>
<td>East African</td>
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<tr>
<td>Association with baseline</td>
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<tr>
<td>blood pressure outcomes</td>
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<td></td>
</tr>
<tr>
<td>Intermediate (1.1% to 7.0%; n=763) vs lowest (&lt;1.1%; n=255)</td>
<td>1.65 (−0.96 to 4.27)</td>
<td>0.71 (−0.66 to 2.09)</td>
<td>−0.18 (−0.64 to 0.28)</td>
</tr>
<tr>
<td>Highest (&gt;7.0%; n=254) vs lowest (&lt;1.7%)</td>
<td>1.70 (−1.97 to 5.36)</td>
<td>2.13 (0.18 to 4.08)</td>
<td>−0.43 (−1.00 to 0.14)</td>
</tr>
<tr>
<td>Association with trajectory of blood pressure outcomes‡</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Intermediate vs lowest</td>
<td>0.10 (−0.28 to 0.48)</td>
<td>−0.03 (−0.21 to 0.15)</td>
<td>−0.01 (−0.08 to 0.06)</td>
</tr>
<tr>
<td>Highest vs lowest</td>
<td>0.10 (−0.42 to 0.61)</td>
<td>0.05 (−0.20 to 0.29)</td>
<td>0.03 (−0.06 to 0.11)</td>
</tr>
</tbody>
</table>

β indicates β coefficient; and CI, confidence interval.
*SBP<140 mmHg and DBP<90 mmHg among treated (n=622; 163 men and 459 women).
†Separated models (for each African origin) estimated by mixed effects regression and mutually adjusted for all variables listed in Table 2 plus intrafamilial clustering and the pattern of missing values and its interaction with time.
‡Interaction between West or East African ancestry in quintiles with time.

genoancestry were conducted in the United States and in the Caribbean and had mixed results. A large cross-sectional study in the United States showed a slight excess of African genomic ancestry in hypertensives relative to normotensives and a modest positive relationship between African ancestry and DBP. Yet another large cross-sectional study in the United States reported that European and African ancestry was not associated with diastolic or systolic blood pressure. In addition, smaller studies conducted in black Americans and those from the Caribbean showed positive or even absent relationships between African ancestry and blood pressure or hypertension.

Brazil has a more heterogeneous African ancestry than that of the United States or the Caribbean, and this ancestry varies across regions within the country. Slaves were brought to Brazil from western and central West Africa (the 2 major sources of the slave trade to all of the Americas), as well as East Africa (Mozambique). The Bambui cohort population has 40.6% of East African origin (in contrast with ≥17% in blacks). To test whether this heterogeneity might explain differences described here, we examined the influence of different African subcontinental origins on blood pressure and hypertension control trajectories, and found no evidence of an association with either East or West African ancestry. To our knowledge, this is the first study investigating this subject.

There is a scientific consensus that SBP is more highly associated with cardiovascular risk than DBP, especially after the age of 50 years. Because hypertension is a major risk factor for cardiovascular events in the elderly, improving control in this population is a public health priority. Our results indicate that 46.1% of cohort participants had their hypertension controlled in 1997, and this proportion decreased significantly in the following years. Abdominal obesity was associated with increased DBP, whereas diabetes mellitus was strongly associated with increased SBP and uncontrolled hypertension, which is in agreement with previous reports in other populations.

This study is the first investigation of the influence of African genomic ancestry on blood pressure and controlled hypertension in an admixed population to have been performed in a South American country. Major strengths include the large population-based cohort and examinations of blood pressure and antihypertensive medications during a long period of time, measured in an identical format. Another strength is the use of genome-wide measures of ancestry. Genomic ancestry does not change over time, whereas ethnoracial self-classification is prone to misclassification, particularly in admixed populations. A major limitation in this analysis is inherent to longitudinal studies in aged populations. Aged persons are at increased risk of death, which in turn might lead to differential dropouts. As an attempt to overcome this potential source of bias, we considered dropouts in our pattern-mixed models (75.3% of these were due to death). Furthermore, we included several important risk factors in our analysis. However, one cannot exclude the possibility that there may be additional unmeasured factors, including unknown genetic factors that confound our results. Finally, in this study, we focused on older
adults and can make no assertions about the generalizability of our results to persons <60 years of age.

**Perspectives**

Our results lead to the following main conclusions: first, increased blood pressure does not inevitably occur in individuals with higher levels of African genomic ancestry—at least in a multiethnic society; second, even small absolute differences in schooling and income levels may be associated with SBP levels and control of hypertension. These results support the view that favors social and environmental factors as determinants of blood pressure and hypertension control.

**Sources of Funding**

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**Disclosures**

None.

**References**


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**Novelty and Significance**

**What Is New?**

- Neither baseline systolic blood pressure, diastolic blood pressure, nor controlled hypertension trajectories showed significant associations with African genomic ancestry in an ethnoracially admixed population of older Brazilians.
- Instead, socioeconomic position (schooling and household income) were the most important nonbiological factors associated with systolic blood pressure and controlled hypertension, respectively; these associations were independent of several other demographic and health indicators.

**What Is Relevant?**

- Socioeconomic factors (and not genetic ancestry) explained differences in blood pressure and control of hypertension.

- These disparities were observed in a racially admixed population whose absolute differences in schooling and income levels were relatively small.

**Summary**

This is the first study exploring the association between genomic ancestry and blood pressure in an ethnoracially admixed population in Latin America. Our results show that increased blood pressure does not inevitably occur in individuals with higher levels of African genomic ancestry, at least in a multiethnic society and suggest an important role of social and environmental conditions.
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Running title: African genomic ancestry and blood pressure in older adults

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Table S1 – Results of the Multivariable Analysis of the Association of Baseline and Trajectories of Blood Pressure and Adequate control of hypertension with Genome Total African Ancestry, and by African sub-continental origin (West and East-Africa) among unrelated individuals, Bambui Cohort Study of Ageing.

<table>
<thead>
<tr>
<th>Ancestry</th>
<th>Systolic blood pressure (SBP)</th>
<th>Diastolic blood pressure (DBP)</th>
<th>Controlled hypertension among treated *</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>β (95%CI) †</td>
<td>β (95%CI) †</td>
<td>β (95%CI) †</td>
</tr>
<tr>
<td><strong>Total African ancestry in quintiles ‡</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Intermediate (4.1% - 19.8%) vs. lowest (&lt; 4.1%)</td>
<td>-3.05 (-6.52; 0.43)</td>
<td>-1.34 (-3.31; 0.62)</td>
<td>0.31 (-0.23; 0.85)</td>
</tr>
<tr>
<td>Highest (&gt; 19.8%) vs. lowest (&lt; 4.1%)</td>
<td>-0.77 (-5.19; 3.65)</td>
<td>0.50 (-2.03; 3.02)</td>
<td>-0.26 (-0.92; 0.40)</td>
</tr>
<tr>
<td>Interaction between African ancestry in quintiles with time §</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Intermediate vs. lowest</td>
<td>0.40 (-0.09; 0.89)</td>
<td>0.14 (-0.12; 0.40)</td>
<td>-0.02 (-0.10; 0.06)</td>
</tr>
<tr>
<td>Highest vs. lowest</td>
<td>0.32 (-0.30; 0.93)</td>
<td>0.21 (-0.11; 0.54)</td>
<td>0.03 (-0.06; 0.13)</td>
</tr>
<tr>
<td><strong>West African ancestry in quintiles ‡</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Intermediate (1.7% - 13.1%) vs. lowest (&lt; 1.7%)</td>
<td>-1.92 (-5.55; 1.70)</td>
<td>-1.20 (-3.22; 0.81)</td>
<td>0.18 (-0.35; 0.72)</td>
</tr>
<tr>
<td>Highest (&gt; 13.1%) vs. lowest (&lt; 1.7%)</td>
<td>0.09 (-4.47; 4.66)</td>
<td>0.13 (-2.45; 2.70)</td>
<td>-0.49 (-1.15; 0.17)</td>
</tr>
<tr>
<td>Interaction between West African ancestry in quintiles with time</td>
<td></td>
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</tr>
<tr>
<td>Intermediate vs. lowest</td>
<td>0.17 (-0.35; 0.69)</td>
<td>0.13 (-0.13; 0.38)</td>
<td>-0.05 (-0.13; 0.02)</td>
</tr>
<tr>
<td>Highest vs. lowest</td>
<td>0.08 (-0.57; 0.73)</td>
<td>0.19 (-0.14; 0.52)</td>
<td>0.02 (-0.08; 0.11)</td>
</tr>
<tr>
<td><strong>East African ancestry in quintiles ‡</strong></td>
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</tr>
<tr>
<td>Intermediate (1.1% - 7.0%) vs. lowest (&lt; 1.1%)</td>
<td>1.00 (-2.33; 4.33)</td>
<td>1.40 (-0.34; 3.13)</td>
<td>-0.24 (-0.75; 0.28)</td>
</tr>
<tr>
<td>Highest (&gt; 7.0%) vs. lowest (&lt; 1.7%)</td>
<td>1.59 (-2.74; 5.91)</td>
<td>2.27 (-0.05; 4.59)</td>
<td>-0.59 (-1.24; 0.05)</td>
</tr>
<tr>
<td>Interaction between East African ancestry in quintiles with time</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Intermediate vs. lowest</td>
<td>Highest vs. lowest</td>
<td></td>
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<td>----------------------</td>
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<tr>
<td></td>
<td>-0.00 (-0.47; 0.46)</td>
<td>-0.09 (-0.31; 0.13)</td>
<td>0.01 (-0.07; 0.09)</td>
</tr>
<tr>
<td></td>
<td>0.05 (-0.55; 0.64)</td>
<td>0.05 (-0.26; 0.37)</td>
<td>0.04 (-0.06; 0.14)</td>
</tr>
</tbody>
</table>

Table abbreviations: CI (confidence interval); β (beta coefficient)

- SBP < 140 mmHg and DBP < 90 mmHg; † separate models (for each African ancestry group) estimated by mixed effects regression and mutually adjusted for all variables listed in Table 2 plus intra-familial clustering, the pattern of missing values and its interaction with time; ‡ association with baseline outcomes; § association with outcome trajectories.