Angiotensinogen Gene in Human Hypertension
Lack of an Association of the 235T Allele Among African Americans

Charles Rotimi, Linda Morrison, Richard Cooper, Catherine Oyejide, Eme Effiong, Modupe Ladipo, Babatunde Osotemihen, Ryk Ward

**Abstract** The frequency of the 235T and 174M alleles of the angiotensinogen gene, previously reported to be associated with hypertension in Caucasians and Japanese, was compared between 57 hypertensive African Americans and 130 normotensive African Americans sampled as part of a community survey of hypertension in the Chicago area. The frequency of the 235T allele was unrelated to hypertension status (cases, 83%, control subjects, 82%), as was true for the 174M allele. Compared with Caucasians, the frequency of the 235T allele was twice as high in this African American population, while the frequency of the 174M allele was similar. Even higher frequencies of the 235T allele (93%) were noted in a sample of 122 Nigerians. It appears that the 235T allele is very common in populations of West African origin, although we found no evidence that it confers risk of hypertension. (Hypertension. 1994;24:591-594.)

**Key Words** • hypertension, essential • angiotensinogen • genes • blacks

As an essential substrate for the renin-angiotensin system, angiotensinogen (AGT) plays an important role in hydromineral balance and the control of blood pressure.1-4 Walker et al5 observed a highly significant correlation between plasma AGT concentration and blood pressure in a large cross-sectional epidemiological study. Within the context of a family study, Watt and coinvestigators6 reported higher plasma AGT levels in young adults with an elevated blood pressure whose parents also had high blood pressure compared with young adults with low blood pressure whose parents also had low blood pressure. Plasma AGT is also reported to be higher in hypertensive subjects and in the offspring of hypertensive parents.7 In addition, overexpression of the AGT gene causes elevated blood pressure in transgenic mice carrying the rat AGT gene.8

A recent collaborative investigation of the AGT gene in siblings from Utah and Paris sharpened these findings by reporting both linkage and association of AGT molecular variants (235T and 174M) with hypertension, suggesting that these AGT polymorphisms may represent markers of an inherited predisposition to essential hypertension in humans.9 These findings have recently been extended to a Japanese population, where a significant association was also noted between hypertension and the 235T allele, along with a substantial increase in the population frequency of the 235T allele.10 Most recently, despite the failure to identify an association with either the 235T allele or the 174M allele, linkage between essential hypertension and the AGT gene has been demonstrated in a set of British families.11 The probable involvement of the AGT genomic region with blood pressure regulation is strengthened by two reports of an association between proteinuric preeclampsia and AGT polymorphisms: one with the 235T allele,12 the other with a microsatellite polymorphism.13

We report the findings of an investigation of the population frequency of the molecular variants 235T and 174M of the AGT gene and their association with blood pressure in samples from black populations of Chicago, Ill., and Ibadan, Nigeria.

**Methods**

**Participants**

African Americans were recruited from among the participants of an ongoing population survey of hypertension in the village of Maywood, a western suburb of Chicago. Of the 27,139 residents of Maywood, 84% are African Americans. A total of 1525 people 25 to 74 years of age (711 men, 814 women) participated in the hypertension survey, which was initiated in 1991. To study people with maximal contrasts with respect to a genetic predisposition to hypertension, participants were selected from the extremes of the bivariate age—blood pressure distribution. Cases (hypertensive subjects) were younger individuals with high blood pressure (systolic blood pressure ≥140 or diastolic blood pressure ≥90 mm Hg) or who were taking antihypertensive medication. A total of 57 cases and 130 control subjects who participated in this study were typed at both loci and had complete data for all variables.

Blood pressure, height, and weight were measured with a standardized protocol. All blood pressures were measured on the right arm with subjects in the sitting position using an appropriately sized cuff. Systolic and diastolic blood pressures were recorded to the nearest 2 mm Hg as the first and the fifth Korotkoff phases by using a standard mercury manometer. Body mass index (BMI) was calculated as the measured weight in kilograms divided by height in meters squared.
The 122 Nigerian participants included men and women recruited from a traditional Yoruba community (Idikan) in Ibadan, plus patients attending the general outpatient clinic of the University College Hospital, Ibadan. Because information regarding blood pressure and hypertension history was limited, only population allele frequencies are displayed for the Nigerian participants. Both phases of the study were reviewed and approved by the Loyola University Medical Center IRB Committee.

Identification of AGT Variants

Genomic DNA extracted from the buffy coat was adjusted to a concentration of 100 g/mL and used as a template for amplifying the second exon of the AGT gene by the polymerase chain reaction (PCR). We used the first set of second exon primers described by Jeunemaitre et al and followed their PCR protocol. Following amplification, the DNA was denatured and 100 µL of the denatured DNA was spotted onto each of two nylon membranes. The blots were neutralized, the DNA hybridized overnight with one of the following radiolabeled probes: 5'-GGCTCCCATCAGGGAGC-3' (detects the 235M allele by hybridization to the sense strand) and 5'-GCTCCCTGACGGGAGCC-3' (detects the 235T allele by hybridization to the antisense strand). Autoradiographs were obtained, and the membranes were scored to identify genotypes as above.

Statistical Analyses

Differences in the distribution of genotypes between groups (blacks versus whites; African Americans versus Nigerians; men versus women; and hypertensive versus control subjects) were determined by the χ² procedure, as was the association between allele frequencies and hypertension status. The potential confounding influences of age and BMI were assessed in a multiple logistic regression model. Statistical significance occurred if a computed two-tailed probability value was less than 5% (P<.05).

Results

The frequency of the AGT 235 TT genotype (homozygote) among African Americans and Nigerians is displayed in the Figure and compared with a sample of whites from the Salt Lake City area. The frequency of the 235T allele (Table 1) in the African American sample was 83% and increased to 93% in Nigerians, a population with little or no European admixture. Among whites, the 235T allele had a frequency of only 41% in a random sample from Utah (n=611; R. Ward et al, unpublished data, 1993). The population difference between whites and either group of blacks for this allele was highly significant (P<.001). By contrast, the frequency of the 174M allele among both African Americans and Nigerians (Table 1) was approximately only one half the reported value for whites, though the difference was significant only for the African American sample (P<.01).

Table 2 displays the characteristics of the African American participants according to hypertension status. As a result of the sampling strategy, control subjects were older and had lower systolic and diastolic blood pressures. Seventy-six percent of cases were being treated by antihypertensive medication. There was no significant difference in the frequency of either the 235T or 174M allele between the hypertensive and control participants.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Control Subjects</th>
<th>Hypertensive Subjects</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (men)</td>
<td>130 (54)</td>
<td>57 (16)</td>
</tr>
<tr>
<td>Rx, %</td>
<td>0</td>
<td>76</td>
</tr>
<tr>
<td>Age, y</td>
<td>51.4±13.1</td>
<td>42.5±9.1</td>
</tr>
<tr>
<td>Systolic blood pressure, mm Hg</td>
<td>113.8±11.4</td>
<td>137.3±21.7</td>
</tr>
<tr>
<td>Diastolic blood pressure, mm Hg</td>
<td>66.3±12.4</td>
<td>83.2±17.5</td>
</tr>
<tr>
<td>BMI, kg/m²</td>
<td>28.7±6.4</td>
<td>32.3±8.5</td>
</tr>
</tbody>
</table>

Rx indicates participants taking antihypertensive medication; BMI, body mass index.
American population, some limitations to the present study must be taken into account. First, like the other studies, our study is retrospective and thus provides only an imperfect insight into causal processes. Second, given the high frequency of the 235T allele in the African American population (80% to 90%), attempts to find an association between this putative risk factor and hypertension are inherently constrained by low statistical power. Even if the OR in African Americans were as high as in the Japanese study (OR=2.67), a sample of 200 individuals in each group would be required to give an 80% statistical power of detecting a significant effect. If the OR in African Americans were more akin to that observed in the Caucasian sample from Salt Lake City and Paris (OR=1.87), even larger sample sizes (in excess of 500 individuals per group) would be required. Clearly, our failure to identify a statistically significant association in a sample of 57 hypertensive and 130 control subjects cannot be taken as conclusive proof that no such association exists in the African American population. Against these caveats must be set the fact that in our data the frequency of the 235T allele is so similar in the two groups that, were an association with hypertension found within the African American population, the attributable risk is likely to be substantially lower than that for the Caucasian population.

Overall, the results of this study, in conjunction with previous reports, reinforce the notion that a full understanding of the genetic contribution to the pathophysiology of essential hypertension requires the evaluation of several different ethnic groups. As exemplified by the comparison of results among Caucasians, Japanese, and African Americans, the same molecular variant may exhibit very different risk associations in genetically different populations. In addition, as a recent British study demonstrated, the apparent negative findings with respect to the 235T allele cannot be taken to imply that segregation of genetic variants in the AGT genomic region has no influence on the familial distribution of hypertension. The literature to date suggests that mendelian segregation at the AGT 235T/M polymorphism may have etiologic relevance for the distribution of hypertension within the Japanese population, variable relevance for the Caucasian population, but essentially no relevance for assessment of the distribution of hypertension risk within the African American population. However, none of these studies address the issue of whether the methionine to threonine substitution at position 235 has direct relevance for the physiological role of the AGT gene. Similarly, these studies do not address the issue of whether population differences in the frequency of the 235T allele are in any way related to differences in the prevalence of hypertension. This latter issue would be best addressed by using comparable methods to measure AGT plasma levels in the different ethnic groups. If the 235T allele is consistently related to AGT levels, then the population means for plasma AGT concentration should follow the rankings of the allele frequency: African American > Japanese > Caucasian. Such comparative data appear not to exist.

On balance, this study emphasizes the importance of interethnic comparisons in developing a more complete understanding of the relation between molecular variants of the various constituents of the renin-angiotensin system and trait expression. This may be a particularly relevant area of research for hypertension, whose prevalence is much higher among African Americans than among the Japanese. Indeed, the recent demonstration in African Americans that the 235T allele is close to fixation in the population suggests that the African American population might be a good model system for studies aimed at understanding complex traits with modest genetic effect in human populations.
system and pathophysiological processes. It also indicates the importance of defining genotypes at the DNA level and suggests that haplotype analyses will be required to determine whether causation is likely to be directly related to a specific DNA substitution or to a larger genomic segment. Our data indicate that compared with Caucasians, populations of African ancestry have appreciably higher frequencies of the 235T allele but lower frequencies of the 174M allele, suggesting a more negative linkage disequilibrium. The different haplotype distribution in populations of African ancestry is confirmed by the different distribution of microsatellite alleles in both the Chicago and Nigerian populations compared with those found in Caucasians from Utah (data not shown). Hence, disease risk will have to be evaluated in terms of specific haplotypes, and haplotype associations are likely to be markedly different in different ethnic groups. Similar considerations apply to the evaluation of the pathophysiological consequences associated with other components of the renin-angiotensin system, such as the relation between polymorphisms at the angiotensin-converting enzyme gene and hypertension and its determinants, and idiopathic cardiomyopathy. In each instance, the recent conclusion of an expert National Institutes of Health panel has considerable significance for designing and interpreting cross-cultural studies: “The most important genetic determinants of disease in a minority group may not be the same as in the population at large.” In particular, understanding the potential importance of genetic variants of the renin-angiotensin system as factors influencing the high prevalence of hypertension in African American populations will require a combined attack at the molecular, physiological, and epidemiological levels.

Acknowledgments

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References


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