A Quantitative Trait Loci–Specific Gene-by-Sex Interaction on Systolic Blood Pressure Among American Indians
The Strong Heart Family Study


Abstract—Age-adjusted systolic blood pressure is higher in males than females. Genetic factors may account for this sex-specific variation. To localize sex-specific quantitative trait loci (QTL) influencing blood pressure, we conducted a genome scan of systolic blood pressure, in males and females, separately and combined, and tested for aggregate and QTL-specific genotype-by-sex interaction in American Indian participants of the Strong Heart Family Study. Blood pressure was measured 3 times and the average of the last 2 measures was used for analyses. Systolic blood pressure was adjusted for age and antihypertensive treatment within study center. We performed variance component linkage analysis in the full sample and stratified by sex among 1168 females and 726 males. Marker allele frequencies were derived using maximum likelihood estimates based on all individuals, and multipoint identity-by-descent sharing was estimated using Loki. We detected suggestive evidence of a QTL influencing systolic blood pressure on chromosome 17 at 129 cM between markers D17S784 and D17S928 (logarithm of odds [LOD]=2.4). This signal substantially improved when accounting for QTL-specific genotype-by-sex interaction (P=0.04), because we observed an LOD score of 3.3 for systolic blood pressure in women on chromosome 17 at 136 cM. The magnitude of the linkage signal on chromosome 17q25.3 was slightly attenuated when participants taking antihypertensive medications were excluded, although suggestive evidence for linkage was still identified (LOD=2.8 in women). Accounting for interaction with sex improved our ability to detect QTLs and demonstrated the importance of considering genotype-by-sex interaction in our search for blood pressure genes. (Hypertension. 2006;48:266-270.)

Key Words: epidemiology ▪ blood pressure ▪ gender

Sexual dimorphism in the regulation of blood pressure has been demonstrated in several population studies and in experimental animal models. Age-adjusted blood pressure is consistently higher in men than women, but these differences are attenuated when women enter menopause. These findings suggest the presence of distinct mechanisms of blood pressure regulation in males and females and stress the importance of the sex hormonal environment in determining blood pressure.

Genetic factors account for 30% to 40% of the blood pressure variation in a population, and the effect of some genes may be apparent only in the setting of appropriate sex hormonal milieu. Several genome scans of blood pressure variation have been published, but limited success has been achieved in identifying genes influencing blood pressure in the general population. One reason that few studies have identified significant linkage to blood pressure variation may be genotype-by-sex interaction, which, when present, could reduce the power to localize quantitative trait loci (QTL). Indeed, none of the previous gene mapping studies have accounted for genotype-by-sex interaction on blood pressure variation. In this article, we examine the evidence for genotype-by-sex interaction on resting systolic blood pressure (SBP) in American Indian participants of the Strong Heart Family Study (SHFS). The identification of sex-specific QTL may allow us to identify functional genes that influence the variation in blood pressure not recognized previously because of sex differences in the expression of the phenotype.

Methods

Population
The Strong Heart Study (SHS), supported by the National Heart, Lung, and Blood Institute, is a population-based observational study...
of cardiovascular disease and its risk factors among American Indians. Subjects were recruited from 3 field centers located in Arizona, North and South Dakota, and Oklahoma and have been followed since 1989. The family component of the SHS, known as the SHFS, was initiated in 1998 and has enrolled ~1200 participants from each center. This study uses family data of participants recruited from 2001 to 2003. Participating communities are tribes from Southwestern Oklahoma, 3 tribes from Arizona, and 3 tribes from South/North Dakota. The SHS and SHFS protocols were approved by the Indian Health Service Institutional Review Board, by the institutional review boards of the participating institutions, and by the 13 American Indian tribes participating in these studies. All of the subjects gave informed consent. The study was conducted in accordance with the principles of the Declaration of Helsinki and Title 45, US Code of Federal Regulations, Part 46.

Phenotyping

During a clinic visit, family members were interviewed to obtain clinical history and environmental exposures, and a physical examination was performed. After 5 minutes of rest, forearm seated blood pressure was measured 3 times by a trained technician using a mercury sphygmomanometer (WA Baum Co) and size-adjusted cuffs. The first and fifth Korotkoff sounds were recorded. The average of the last 2 measures was used for all of the analyses. Anthropometric measurements of height, weight, and waist circumference were also obtained at the clinic visit. Waist circumference was measured using a standard protocol. Body mass index (BMI) was calculated as weight (kg)/height (m²). Body fat mass was measured using an RJL bioelectric impedance meter (RJL Systems) and estimated by the RJL formula based on total body water. Fasting blood samples were obtained for measurements of lipids, glucose, insulin, glycohemoglobin, and serum creatinine. Albumin and creatinine were measured in a random urine sample using nephelometric immunochemistry and alkaline picrate methods, respectively. Urinary albumin excretion was estimated by the albumin:creatinine ratio (mg/g). Hypertension was defined by an SBP ≥140 mm Hg or diastolic blood pressure ≥90 mm Hg or use of antihypertensive drugs. Diabetes was defined using the American Diabetes Association criteria as fasting plasma glucose levels ≥126 mg/DL or treatment with oral agents or insulin.

Genotyping

The SHFS genotyping procedures have been described previously. All of the family members were genotyped for ~400 markers spaced at intervals that averaged 10 cm. Marker allele frequencies were derived using maximum likelihood methods estimated from all of the individuals, and multipoint identity-by-descent sharing was estimated using Loki. Pedigree relationships have been verified using the pedigree relationship statistical tests (PREST) package, which uses likelihood-based inference statistics for genome-wide identity-by-descent allele sharing. Mendelian inconsistencies and spurious results of the linkage analyses, and, therefore, were not included in the final model (data not shown). Different models were explored to account for hypertension treatment (which changes blood pressure levels), including models restricted to nontreated individuals combined, n=1481; females, n=907; males, n=574) and models adjusting for BMI, hypertension medication usage, and other covariates, such as percentage of body fat, waist circumference, history of diabetes, serum creatinine, lipid measures, fasting glucose, and urine albumin excretion, did not substantially change the results of the linkage analyses. We calculated the empirical distribution of logarithm of odds (LOD) scores under the assumption of multivariate normality, using 10 000 replicates and simulation methods. We determined the robust LOD score by multiplying the observed LOD score by a correction coefficient calculated by regressing the expected LOD scores on the observed simulated LOD scores. In addition, we determined the 1-LOD unit drop support interval for all of the linkage results with LOD score ≥1.8.

Results

Women comprised 60% of 1894 genotyped individuals, and the mean age was 42 years (Table 1). The prevalences of hypertension and diabetes were 34% and 24%, respectively. Hypertension was more prevalent in men (40%) than women (30%), and men were less often treated with medications (52% of hypertensive men versus 74% of hypertensive women). Resting SBP was higher in men than in women, even when excluding treated individuals (Table 1). Average SBP increased with age in both sexes but was consistently higher in men than women until ages 55 to 60 years (data not shown). On average, participants were obese (BMI >30 kg/m²), and ~85% of men and women were overweight (BMI >25 kg/m²). Urine albumin:creatinine ratio was ≥30 mg/g in 19% of participants (n=363).

Genetic data were available for >18 000 relative pairs, with 7000 female-female relative pairs, 2700 male-male relative pairs, and 8300 male-female relative pairs (Table I, available online at http://hyper.ahajournals.org). Estimated heritability (h²) for SBP was 0.28±0.06 for the combined sample, 0.28±0.04 for women, and 0.35±0.10 for men, after accounting for the covariate effects of age, age², center, and antihypertensive medications. SBP genetic
effects were higher in models restricted to untreated individuals (n = 1481, $h^2 = 0.49 \pm 0.06$ for the combined sample, $h^2 = 0.46 \pm 0.08$ for women, and $h^2 = 0.53 \pm 0.12$ for men). These differences may be because of a more homogenous study group after removing participants with high blood pressure.

We tested for an additive genotype-by-sex interaction using the combined sample of subjects. The estimated genetic correlation between men and women for SBP was not significantly different from 1 ($\rho_{G(f \times m)} = 0.82; P = 0.19$). The genetic SD for women ($\sigma^2_g$, females) was 0.47 and for men ($\sigma^2_g$, males) was 0.55, but they were not significantly different from the fit of a model in which the sex-specific SDs were constrained to be equal ($P = 0.42$).

To further investigate genotype-by-sex interaction, we compared linkage analysis results in sex-stratified analyses to those in the combined sample (Table 2). We identified 1 chromosome region with a robust LOD score of 3.3 in women on chromosome 17 at 136 cM (Table 2 and Figure), with a 1-LOD unit support interval spanning 17 cM from 122 to 139 cM (q-terminus). This linkage signal on 17q25.3 was consistently localized, although the magnitude of effect was attenuated in models not accounting for drug treatment, all individuals; Model 2 was adjusted for age, age2, sex, and hypertension treatment, all individuals; Model 2 was adjusted for age, age2, center, and sex, all individuals; Model 3 was restricted to untreated individuals, adjusted for age, age2, sex, and center. The genetic SD for the combined sample is 0.820 in Different Models: SHFS.

### Discussion

Gender differences in blood pressure are well-documented in different populations and have been largely attributed to sex hormonal effects. Estradiol and testosterone affect several pathways of blood pressure regulation, including the autonomic nervous system and the kidneys, but also have direct effects on blood vessels. However, the underlying genetic mechanism of blood pressure variation in men and women has not been explored. Sex-dependent genetic effects on blood pressure may be because of genes located on sex chromosomes. For example, Harrap et al have described suggestive linkage of SBP to the X chromosome in the Vitoria Family Heart Study. Alternatively, the effects of autosomal genes involved in blood pressure regulation may be modulated by the hormonal environment, which may differentially affect blood pressure in men and women.

Five additional regions with LOD scores $\geq 1.8$ were identified (Table 2). The regions on chromosomes 1, 2, and 8 were limited to men; a second region on chromosome 2 was identified only in women. All of these 4 regions showed significant QTL-specific gene-by-sex interaction ($P < 0.01$). A linkage on chromosome 9 was observed in the combined sample.

### Table 1. Clinical Characteristics of 1984 Subjects Participating in the SHFS: Participants With Complete Genotype and Phenotype Data by Gender

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Combined</th>
<th>Females</th>
<th>Males</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of individuals</td>
<td>1894</td>
<td>1171</td>
<td>723</td>
</tr>
<tr>
<td>Age, y</td>
<td>42±16</td>
<td>43±17</td>
<td>41±16</td>
</tr>
<tr>
<td>SBP, mm Hg, all individuals</td>
<td>123±17</td>
<td>121±17</td>
<td>126±15</td>
</tr>
<tr>
<td>DBP, mm Hg</td>
<td>77±11</td>
<td>75±10</td>
<td>80±11</td>
</tr>
<tr>
<td>Hypertension, n (%)</td>
<td>643 (34)</td>
<td>357 (30)</td>
<td>286 (40)</td>
</tr>
<tr>
<td>% Hypertensives on treatment</td>
<td>64</td>
<td>74</td>
<td>52</td>
</tr>
<tr>
<td>SBP, mm Hg, untreated individuals*</td>
<td>120±15</td>
<td>117±15</td>
<td>124±14</td>
</tr>
<tr>
<td>Diabetes, n (%)</td>
<td>450 (24)</td>
<td>286 (24)</td>
<td>164 (23)</td>
</tr>
<tr>
<td>Body mass index, kg/m$^2$</td>
<td>32±8</td>
<td>33±8</td>
<td>32±8</td>
</tr>
<tr>
<td>% Body fat</td>
<td>38±10</td>
<td>42±8</td>
<td>30±8</td>
</tr>
<tr>
<td>Waist circumference, cm</td>
<td>105±18</td>
<td>105±18</td>
<td>106±19</td>
</tr>
<tr>
<td>Serum creatinine, mg/dL</td>
<td>0.8±0.4</td>
<td>0.8±0.3</td>
<td>1.0±0.4</td>
</tr>
<tr>
<td>Urine albumin/creatinine, mg/g</td>
<td>105±597</td>
<td>110±644</td>
<td>99±513</td>
</tr>
</tbody>
</table>

Values are means±SD unless otherwise stated. DBP indicates diastolic blood pressure.

* n = 1481 for combined; n = 907 females; n = 574 males.

### Table 2. Regions of the Genome Linked to SBP With LOD Scores $\geq 1.8^{29}$ in Different Models: SHFS

<table>
<thead>
<tr>
<th>Models</th>
<th>Chromosome</th>
<th>cM</th>
<th>Cytogenic Location</th>
<th>Robust LOD Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males</td>
<td>Model 1</td>
<td>1</td>
<td>113</td>
<td>1p31.1</td>
</tr>
<tr>
<td></td>
<td>Model 2</td>
<td>2</td>
<td>61</td>
<td>2p22.3</td>
</tr>
<tr>
<td></td>
<td>Model 3</td>
<td>59</td>
<td></td>
<td>2.19</td>
</tr>
<tr>
<td>Females</td>
<td>Model 1</td>
<td>2</td>
<td>164</td>
<td>2q22.3</td>
</tr>
<tr>
<td></td>
<td>Model 2</td>
<td>165</td>
<td></td>
<td>2.08</td>
</tr>
<tr>
<td>Males</td>
<td>Model 1</td>
<td>8</td>
<td>15</td>
<td>8p23.1</td>
</tr>
<tr>
<td></td>
<td>Model 2</td>
<td>13</td>
<td></td>
<td>2.72</td>
</tr>
<tr>
<td></td>
<td>Model 3</td>
<td>13</td>
<td></td>
<td>2.35</td>
</tr>
<tr>
<td>Combined</td>
<td>Model 1</td>
<td>9</td>
<td>61</td>
<td>9p13.3</td>
</tr>
<tr>
<td></td>
<td>Model 2</td>
<td>60</td>
<td></td>
<td>1.89</td>
</tr>
<tr>
<td></td>
<td>Model 3</td>
<td>65</td>
<td></td>
<td>1.88</td>
</tr>
<tr>
<td>Combined</td>
<td>Model 1</td>
<td>17</td>
<td>129</td>
<td>17q25.3</td>
</tr>
<tr>
<td></td>
<td>Model 3</td>
<td>129</td>
<td></td>
<td>2.41</td>
</tr>
<tr>
<td>Females</td>
<td>Model 1</td>
<td>136</td>
<td></td>
<td>3.25</td>
</tr>
<tr>
<td></td>
<td>Model 2</td>
<td>136</td>
<td></td>
<td>2.56</td>
</tr>
<tr>
<td></td>
<td>Model 3</td>
<td>126</td>
<td></td>
<td>2.76</td>
</tr>
</tbody>
</table>

Model 1 was adjusted for age, age$^2$, center, sex, and hypertension treatment, all individuals; Model 2 was adjusted for age, age$^2$, center, and sex, all individuals; Model 3 was restricted to untreated individuals, adjusted for age, age$^2$, sex, and center.
sex interactions in the identification of QTLs influencing blood pressure variation.

Several other studies have identified genetic effects on SBP in the same or nearby regions on chromosome 17 but none have accounted for sex-specific genetic effects (Table II, available online at http://hyper.ahajournals.org). Suggestive linkage to SBP was identified at region 17q25.3 for age of onset of hypertension among blacks from the Hypertension Genetic Epidemiology study (HyperGEN; LOD = 1.7).28 This is the same region identified in our study in women. Near our peak linkage signal at 17q24.2, suggestive linkage to pulse pressure was identified in Hispanics participating in the National Heart, Lung, and Blood Institute Family Blood Pressure Program (FBPP).29 In addition, genome-wide evidence for linkage was identified at region 17q23.2 for blood pressure factor in Hispanic participants of the FBPP (LOD = 3.6). Interestingly, some evidence for linkage was observed in white HyperGEN participants (which is 1 of the 4 networks of the FBPP) in this same region (LOD = 1.5).30 Levy et al described linkage of longitudinal SBP to 17q21.2 (LOD = 4.7) and 17q21.3 (LOD = 2.2) in the Framingham Heart Study. A significant gene-by-age interaction for SBP at the 17q21.2 region was later described by Diego et al in the same cohort. Suggestive linkage to the region 17q21.3 has also been described in a sibling-pair analysis of essential hypertension among United Kingdom and French families and for SBP among Icelandic hypertensive families.34

When restricting the analysis to subjects untreated for high blood pressure, the linkage signal on 17q25.3 was decreased by 0.5 LOD units. Similar findings have been reported previously.35 These reductions are partly related to the individuals who were removed from analyses when excluding treated participants (n = 413 exclusions). Nonetheless, even with decreases in LOD score, we find suggestive evidence for linkage on chromosome 17. This evidence offers strong support for the presence of a blood pressure–related QTL on chromosome 17 and speaks to the robustness of this signal. Moreover, our results show a high degree of overlap with other studies and may indeed provide probable locations for candidate gene follow-up studies.

Approximately 182 genes underlie the 1 LOD unit drop support interval (17 cM) of the 17q signal. A candidate gene, urotensin II receptor or orphan G protein–coupled receptor (GPR14), is located at 17q25.3. Urotensin II is a potent systemic vasoconstrictor but has natriuretic and vasodilatory effects in the kidneys.36 Urotensin II has been associated with hypertension and heart failure. The expression of GPR14 is confined to neuronal and cardiovascular tissues, and this distribution suggests that it contributes to blood pressure regulation.

Another plausible candidate gene, angiotensin I converting enzyme (ACE) gene, is located at 17q23.3, which is ~19.5 million base pairs from the peak LOD score. ACE is a key component of the renin–angiotensin–aldosterone system, which influences vascular tone and salt and fluid retention and is an important player in blood pressure regulation. ACE gene variants, angiotensin I to angiotensin II, a potent vasoconstrictor, and promotes aldosterone secretion. In addition, ACE inactivates bradykinin, a vasodilatory peptide. The ACE deletion/deletion (D/D) polymorphism has been associated with hypertension in men but not in women.37 ACE gene may enhance the hypertensive effects of Angiotensinogen gene variants, another component of the renin–angiotensin–aldosterone system.38 ACE variants have also been associated with increased SBP among smokers.39

Although no other genome-wide significant evidence of linkage was detected, suggestive evidence of linkage to SBP was detected on chromosomes 1p, 2p, 2q, 8p, and 9p. Some of these regions have been described previously. For example, linkage to chromosome 2p22.3 has been identified by Krushkal et al for SBP (P < 0.01) and by Angius et al (LOD = 2.0) and Rao et al (LOD = 2.08) for hypertension traits. Although these signals do not meet the genome-wide significance threshold, they suggest regions worthy of further study and may help to distinguish between true and false positives.

**Perspectives**

Our findings suggest that 1 or more genes on chromosome 17q regulate variation in SBP, particularly among female participants of the SHFS. Indeed, QTL-specific genotype-by-sex interaction on blood pressure variation was identified, which suggests that the effects of some autosomal genes for blood pressure variation may be modulated by sex-dependent factors. This region on chromosome 17q has been identified by several studies and may, therefore, have broad significance for blood pressure regulation, given the general lack of previous genome-wide evidence for linkage to SBP. Thus, future research should pursue this region with comprehensive linkage disequilibrium mapping. Identification of the risk alleles underlying this linkage peak may suggest novel mechanisms in the development and regulation of blood pressure.

**Acknowledgments**

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Disclosures

None.

References


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