Familial and Genomic Analyses of Postural Changes in Systolic and Diastolic Blood Pressure

Stephen B. Harrap, Jisheng S. Cui, Zilla Y.H. Wong, John L. Hopper

Abstract—The physiological adaptation to the erect posture involves integrated neural and cardiovascular responses that might be determined by genetic factors. We examined the familial- and individual-specific components of variance for postural changes in systolic and diastolic blood pressure in 767 volunteer nuclear adult families from the Victorian Family Heart Study. In 274 adult sibling pairs, we made a genome-wide scan using 400 markers for quantitative trait loci linked with the postural changes in systolic and diastolic pressures. Overall, systolic pressure did not change on standing, but there was considerable variation in this phenotype (SD = 8.1 mm Hg). Familial analyses revealed that 25% of the variance of change in systolic pressure was attributable to genetic factors. In contrast, diastolic pressure increased by 6.3 mm Hg (SD = 7.0 mm Hg) on standing and there was no evidence of contributory genetic factors. Multipoint quantitative genome linkage mapping suggested evidence (Z = 3.2) of linkage of the postural change in systolic pressure to chromosome 12 but found no genome-wide evidence of linkage for the change in diastolic pressure. These findings suggest that genetic factors determine whether systolic pressure decreases or increases when one stands, possibly as the result of unidentified alleles on chromosome 12. The genetics of postural changes in systolic blood pressure might reflect the general buffering function of the baroreflex; thereby, the predisposition to sudden decreases or increases in systolic pressure might cause postural hypotension or vessel wall disruption, respectively. (Hypertension. 2004;43:586-591.)

Key Words: blood pressure ■ population ■ baroreflex

A n effective cardiovascular physiological response to erect posture maintains cerebral blood flow, despite gravitational redistribution of blood to the lower extremities. The baroreflex of the autonomic nervous system reacts to increasing heart rate, myocardial contractility, and total peripheral resistance to counter the decrease in cardiac output and blood pressure that occurs immediately after standing.1 The baroreflex of the autonomic nervous system reacts to gravitational redistribution of blood to the lower extremities. The Atherosclerosis Risk in Communities (ARIC) Study suggested that subjects at the extremes of the distribution for the postural change in SBP (ΔSBP) are more likely to be hypertensive4 and experience coronary heart disease and stroke.5,6

In contrast to SBP, diastolic pressure (DBP) tends to increase on average on standing (ΔDBP) by approximately 4 mm Hg, although decreases and larger increases in DBP are observed.2 Increases of 10 mm Hg or more in DBP on standing have been associated with increased risk of subsequent coronary heart disease.7

Explanations for these features of ΔSBP and ΔDBP are not fully understood. A certain amount of the variation in postural pressure changes in individuals appears to be associated with age, gender, and race, as well as exposures to cigarettes and antihypertensive drug treatments.2 Twin and family studies can provide information regarding the contribution of genes and environment to the overall variation, but to our knowledge no such analyses have been reported for ΔSBP and ΔDBP. One genome-wide analysis of quantitative trait loci (QTL) and postural changes in SBP has been reported,8 but this study was restricted to hypertensive siblings, most of whom were receiving antihypertensive treatment that might have interfered with their inherent physiological responses to posture.

In this study, we have used data and material from the Victorian Family Heart Study (VFHS) to address the familial correlations of lying and standing pressures and their changes with posture. VFHS families are enriched with those containing twins, thereby increasing the usefulness of biometric analyses in providing estimates of the genetic and environmental components of variance.9 We also conducted a genome-wide linkage analysis in relation to ΔSBP and ΔDBP.
Methods

Subject Recruitment and Phenotype Measurement

The details of the recruitment of subjects for the VFHS have been published previously. In brief, a volunteer sample of 767 white adult families enriched with twins (66 monozygotic pairs, 84 dizygotic pairs) was recruited from a variety of community-based sources. A family history of heart disease was not a prerequisite for recruitment. Families comprised parents aged 40 to 70 years and at least one natural offspring aged 18 to 30 years.

The Ethics Review Committee of the Alfred Hospital in Melbourne approved the study, and informed consent was obtained from all participants. Participants attended research clinics where trained research nurses obtained relevant information regarding drug treatment and smoking, measured cardiovascular phenotypes, and took blood samples as detailed previously.

After resting for 10 minutes, 3 measurements of SBP and DBP were taken in the supine position, the last 2 of which were recorded. Subjects then stood for 2 minutes and 3 further measurements of SBP and DBP were measured, the last 2 of which were used in these analyses. For subjects receiving antihypertensive treatments, we adjusted the recorded pressures by adding 10 mm Hg and 5 mm Hg to SBP and DBP, respectively, as detailed previously. The ΔSBP and ΔDBP pressures were calculated as the average of the standing pressures minus the average of the supine pressures. Mean arterial pressure (MAP) was calculated as DBP+ (SBP–DBP)/3 and presented as the average of lying and standing values.

Genome-Wide Scan

A genome-wide scan was undertaken in 274 sibling pairs as described previously. DNA from the sibling pairs was extracted and purified. We used the ABI PRISM Human Linkage Mapping Set version 2 that comprises 400 microsatellite markers with approximately 10-cM resolution as detailed previously.

Statistical Methods

Variance component analyses were performed following the modeling procedures used for previous analyses of data from this study under a multivariate normal model for pedigree analysis using the FISHER software. The means of all phenotypes were adjusted for age by sex and by generation, and the variances, correlations, and/or variance components, standard errors, and confidence intervals were estimated under large-sample maximum likelihood theory. The genetic and environmental modeling decomposes the total variance into additive genetic, σ2a, shared environment, σ2e, and individual-specific, σ2i, components. The individual-specific component includes a component for measurement error, σ2me. The “split-plot” model was used to estimate the variance for the individual measurement error σ2me from the repeated measures. The variance of the average of 2 repeated measurements was assumed to be half the variance of the individual measures. Ordinary, polytomous, and ordered logistic regression analyses were used to test for associations between smoking and postural changes in SBP or DBP (data not shown).

Multipoint nonparametric linkage analysis was conducted by GENEHUNTER II, using the information from all genetic markers jointly to infer the full probability distribution of identity-by-descent status in offspring and taking into account blood pressure phenotypes of all offspring and their parents. Adjustments to phenotypes were made for age and sex. The probability of linkage was expressed as nonparametric Z scores. The data were checked for pedigree and genotyping errors as described previously.

Results

Table 1 shows that within each sex by generation group, there was no evidence of change in mean SBP from lying to standing (all P > 0.05). Nevertheless, ΔSBP varied substantially, with SD ranging from 6.65 to 8.89 mm Hg across the four groups. In contrast, in all groups there was a significant increase in mean DBP on standing, with group means ranging from 4.68 to 9.79 mm Hg. Again, there was substantial variation, with SD ranging from 5.79 mm Hg to 8.53 mm Hg across the groups.

Table 2 shows the characteristics of subjects by tertiles of ΔSBP and ΔDBP. There was a weak correlation between ΔSBP and MAP in parents (r = 0.08, P = 0.02) and in male (r = 0.15, P < 0.001) and female offspring (r = 0.19, P < 0.001). Reported antihypertensive treatment was more frequent in the low and high tertiles than in the middle tertile of ΔSBP (P = 0.03). In contrast, ΔDBP did not correlate with MAP and there was no evidence of differences in the frequency of antihypertensive treatment between the tertiles of ΔDBP (P > 0.05). However, higher ΔDBP was weakly associated with greater postural changes in heart rate (ΔHR) in fathers (r = 0.10, P = 0.008), mothers (r = 0.09, P = 0.02), sons (r = 0.19, P < 0.001), and daughters (r = 0.15, P < 0.001). We could find no evidence of an association between smoking and postural changes in SBP or DBP (data not shown).

Table 3 shows the correlations between relatives for the measured and derived pressures. For lying and standing SBPs and DBPs, the magnitudes of the correlations were greatest for monozygotic (MZ) twin pairs and least for spouse pairs. Higher correlations between MZ twins than dizygotic (DZ) twins were observed for all phenotypes except ΔDBP (for which neither correlation was significant statistically) (Table 3) and reflect the greater genetic similarity between MZ (100%) than DZ twins (on average 50%). The differences in correlations between first-degree relatives who on average are 50% genetically similar (DZ twins, non-twin sibling pairs, parent–offspring pairs) reflect the influence of shared environments. For SBP phenotypes, the differences in correlations between different categories of first-degree relatives were most obvious between the generations (Table 3); but for DBP phenotypes, the differences in correlations were more apparent between DZ twins and non-twin siblings (Table 3). The strongest correlation for ΔDBP was observed for spouse pairs, indicative of the effects of shared environment.

Table 4 shows the estimates from the univariate variance component analyses. For lying SBP, the genetic and shared

<p>| Table 1. Descriptive Statistics of Blood Pressure Phenotypes by Generation and Gender |
|---------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|</p>
<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Parents</th>
<th>Offspring</th>
<th>Parents</th>
<th>Offspring</th>
<th>Parents</th>
<th>Offspring</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>767</td>
<td>663</td>
<td>714</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SBP (mm Hg)</td>
<td>129.8 (15.4)</td>
<td>122.3 (11.2)</td>
<td>113.6 (9.8)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Standing</td>
<td>130.1 (16.1)</td>
<td>122.4 (11.4)</td>
<td>112.7 (10.9)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DBP (mm Hg)</td>
<td>79.7 (9.2)</td>
<td>67.1 (10.7)</td>
<td>65.0 (9.1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lying</td>
<td>84.7 (9.4)</td>
<td>76.9 (9.9)</td>
<td>71.3 (9.4)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔSBP (mm Hg)</td>
<td>0.31 (8.69)</td>
<td>0.10 (7.92)</td>
<td>−0.87 (6.65)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔDBP (mm Hg)</td>
<td>5.02 (6.05)</td>
<td>4.68 (5.79)</td>
<td>9.79 (8.53)</td>
<td>6.33 (7.39)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
environment components of variance accounted for 43% and 29% of the total variance, respectively. The remaining 28% were accounted for by individual-specific factors, of which 2% were estimated to be attributable to measurement error. Genetic and shared environmental factors, respectively, accounted for 45% and 30% for standing SBP, 21% and 24% for lying DBP, and 42% and 12% for standing DBP.

For the derived variable ΔSBP, 11% of variance (7.3 mm Hg²) could be attributed to measurement error. Genetic and shared environmental factors accounted for 25%...
We also tested separately the effects of genetic (19.6 to 1.8 mm Hg$^2$) and shared environment (22.6 to 39.1 mm Hg$^2$) components.

Variance was attributable to shared environment. In terms of the shared environmental factors, the coefficients were greater within the generations ($\gamma_{se}$) than between the generations ($\gamma_{se}$) for lying and standing SBP and DBP and for $\Delta$SBP (Table 4). In contrast, the coefficients within the generations ($\gamma_{se}$) were less for $\Delta$DBP than between the generations ($\gamma_{se}$).

When lying SBP was adjusted for standing SBP, the estimates of total variance decreased considerably (196.8 to 216.1 mm Hg$^2$), reflecting the strong cross-sectional correlation between the two traits. The genetic component of variance showed the greatest decrease after adjustment (85.2 to 14.5 mm Hg$^2$). There was also substantial reduction in the shared environment component of variance (56.5 to 6.1 mm Hg$^2$). A similar pattern was observed when lying DBP was adjusted for standing DBP, with a decrease in genetic (19.6 to 1.8 mm Hg$^2$) and shared environment (22.6 to 7.7 mm Hg$^2$) components.

In contrast, when $\Delta$SBP was adjusted for $\Delta$DBP, there was only a relatively small decrease in the total variance (66.1 to 62.9, 57.2, and 65.5 mm Hg$^2$, respectively) or the genetic component (from 16.5 to 17.6, 14.5, and 16.0 mm Hg$^2$, respectively). There was also little change in variance components for $\Delta$DBP after separate adjustments for lying DBP, standing DBP, and the average of lying and standing DBPs (data not shown).

Within individuals, there were strong correlations between lying and standing SBP and between lying and standing DBP, but relatively weak correlations between $\Delta$SBP and $\Delta$DBP (Table 5). The cross-trait correlations between lying and standing SBP and between lying and standing DBP for relative pairs showed evidence suggestive of genetic influences (higher correlations between MZ than DZ pairs) and of shared environmental influences (greater correlations between DZ twins than between non-twin siblings and greater correlations between non-twin siblings than between parent–offspring pairs) (Table 5). The cross-trait correlations between $\Delta$SBP and $\Delta$DBP were low and showed little difference between relative pairs (Table 5).

The results of bivariate variance component analyses indicated that genetic factors were highly correlated for lying and standing SBP ($R=0.92$) and for lying and standing DBP ($R=0.89$). There was also a substantial correlation for shared environmental factors between lying and standing SBP ($R=0.92$). No significant shared environment correlation was observed between lying and standing DBP. The weak cross-

### Table 4. Genetic and Environmental Components of Variance

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Lying</th>
<th>Standing</th>
<th>Lying</th>
<th>Standing</th>
<th>$\Delta$SBP</th>
<th>$\Delta$DBP</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma^2$</td>
<td>85.2 (10.4)</td>
<td>96.8 (11.5)</td>
<td>19.6 (21.6)</td>
<td>39.1 (20.7)</td>
<td>16.5 (3.2)</td>
<td>0.03 (8.2)</td>
</tr>
<tr>
<td>$\sigma^2$</td>
<td>56.5 (12.0)</td>
<td>64.6 (12.3)</td>
<td>22.6 (17.1)</td>
<td>11.3 (16.4)</td>
<td>9.8 (3.0)</td>
<td>9.3 (4.5)</td>
</tr>
<tr>
<td>$\sigma^2$</td>
<td>55.1 (9.8)</td>
<td>54.7 (9.5)</td>
<td>50.7 (7.6)</td>
<td>41.9 (7.3)</td>
<td>39.8 (3.3)</td>
<td>39.4 (4.1)</td>
</tr>
<tr>
<td>$\sigma^2$</td>
<td>196.8</td>
<td>216.1</td>
<td>92.9</td>
<td>92.3</td>
<td>66.1</td>
<td>48.7</td>
</tr>
<tr>
<td>$\gamma_{SP}$</td>
<td>0.71 (0.21)</td>
<td>0.73 (0.18)</td>
<td>0.47 (0.24)</td>
<td>0.36 (0.56)</td>
<td>1 (bound)</td>
<td>0.75 (0.19)</td>
</tr>
<tr>
<td>$\gamma_{se}$</td>
<td>0 (bound)</td>
<td>0 (bound)</td>
<td>0.38 (0.24)</td>
<td>0.24 (0.62)</td>
<td>0 (bound)</td>
<td>1 (bound)</td>
</tr>
<tr>
<td>$\rho_{SP}$</td>
<td>0.10 (0.03)</td>
<td>0.14 (0.03)</td>
<td>0.14 (0.04)</td>
<td>0.17 (0.03)</td>
<td>0.12 (0.03)</td>
<td>0.36 (0.04)</td>
</tr>
</tbody>
</table>

Means were adjusted for age, sex, age–sex interaction, and generation.

Variance units are mm Hg$^2$.

The model estimates the following components of the total phenotype variance ($\sigma^2$): additive genetic ($\sigma^2_{a}$), shared environment ($\sigma^2_{e}$), and individual-specific ($\sigma^2_{i}$) effects; shared environment coefficients for non-twin sibling pairs ($\gamma_{se}$) and parent–offspring pairs ($\gamma_{se}$); and the correlation coefficient between spouse pairs ($\rho_{SP}$). Standard errors of estimates are given in parentheses.

SBP indicates systolic blood pressure; DBP, diastolic blood pressure; $\Delta$SBP, standing SBP–lying SBP; $\Delta$DBP, standing DBP–lying DBP.

### Table 5. Cross-Trait Correlation Coefficients of Measured and Derived Phenotypes

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Spouse–Spouse</th>
<th>Parent–Offspring</th>
<th>Non-twin Siblings</th>
<th>DZ Twins</th>
<th>MZ Twins</th>
<th>Within Individuals</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>767</td>
<td>2754</td>
<td>473</td>
<td>84</td>
<td>65</td>
<td>2911</td>
</tr>
<tr>
<td>Lying SBP and Standing SBP</td>
<td>0.10 (0.03, 0.17)</td>
<td>0.20 (0.16, 0.23)</td>
<td>0.39 (0.31, 0.46)</td>
<td>0.43 (0.24, 0.59)</td>
<td>0.67 (0.51, 0.79)</td>
<td>0.87</td>
</tr>
<tr>
<td>Lying DBP and Standing DBP</td>
<td>0.08 (0.01, 0.15)</td>
<td>0.17 (0.13, 0.21)</td>
<td>0.21 (0.12, 0.30)</td>
<td>0.32 (0.11, 0.50)</td>
<td>0.49 (0.27, 0.65)</td>
<td>0.80</td>
</tr>
<tr>
<td>$\Delta$SBP and $\Delta$DBP</td>
<td>0.09 (0.02, 0.16)</td>
<td>0.10 (0.06, 0.14)</td>
<td>0.09 (0.01, 0.18)</td>
<td>0.13 (–0.08, 0.33)</td>
<td>0.18 (–0.06, 0.41)</td>
<td>0.28</td>
</tr>
</tbody>
</table>

Cross-trait correlations measure the association between the first trait in one relative with the second trait in the relative pair (eg, the correlation between lying SBP in fathers and standing SBP in mothers).

Means were adjusted for age, sex, age–sex interaction. and generation. 95% CIs given in parentheses.

N indicates number of pairs; SBP, systolic blood pressure; DBP, diastolic blood pressure; $\Delta$SBP, standing SBP–lying SBP; $\Delta$DBP, standing DBP–lying DBP.
trait correlations between ΔSBP and ΔDBP afforded little power to resolve the degree to which common genetic and shared environmental factors might explain these two phenotypes.

None of the variance component analyses was altered materially when analyses were repeated excluding the 244 subjects who reported using antihypertensive medication (data not shown).

Genome Linkage

The Figure shows the probability plots of nonparametric Z-score values for linkage of ΔSBP and ΔDBP, respectively, across all 22 autosomes and the X chromosome. We identified suggestive QTL as those with Z scores of 3.1 or greater according to the guidelines of Lander and Kruglyak. Such values were observed for one region on chromosome 12 (Figure, peak at 69 cM from p telomere [pter]) for ΔSBP (Z = 3.2). A Z peak of 2.9 was also observed for ΔSBP on chromosome 17 (Figure, 78 cM from pter) and a peak of 2.7 was found on the X chromosome (Figure, 100 cM from pter). Other than a Z score of 2.8 at the p telomere of chromosome 4, no Z values exceeded 2.5 for ΔDBP across the genome.

Discussion

Postural blood pressure responses are of interest because they are simple measures of cardiovascular reactivity and they appear to be associated with cardiovascular risk. On standing, SBP shows little average change, a stability that suggests that SBP is the set point targeted by homeostatic systems in short-term physiological control. In the face of reduced venous return to the heart, the autonomic nervous system attempts to achieve a stable SBP by increasing total peripheral resistance of the circulation and minimizing the reduction in cardiac output by increasing cardiac contractility and heart rate.

However, the lack of average change in SBP belies the considerable variation in the response such that on standing, SBP decreases in some individuals yet increases in others. This study reveals for the first time to our knowledge that such variation is not entirely random and is determined to a significant extent by familial factors. Indeed, 40% of the variation in ΔSBP was familial, mostly attributable to genes (25%) but also to shared environmental factors (15%). This implies that some families are hyporeactive to the postural challenge, with a tendency for pressure to decrease on standing, whereas other families are hyperreactive, resulting in higher SBP on standing.

It appears that the dynamic change in SBP is controlled by factors other than those that determine the static pressures, because adjustment of ΔSBP for lying and standing SBP had little impact on the genetic and environmental variance components of ΔSBP. Nevertheless, we noted (as others previously) weak correlations indicating that individuals whose SBP increased on standing also tended to be those with the highest MAP. The potential importance of this association is that postural increases in SBP in those with high MAP might augment hemodynamic stresses and contribute to the observed increased long-term cardiovascular risk.

In our genome-wide scan, we observed suggestive evidence for ΔSBP of linkage to chromosome 12 and possible evidence of linkage (Z = 2.7) on chromosomes 17 and X. This contrasts with the analyses of Pankow in which no linkage between the change in SBP after 2 minutes of standing and chromosome 12 was found. Instead, Pankow reported suggestive evidence of linkage between the immediate (but not 2-minute) change in SBP and chromosome 18. The reasons for these discrepancies are uncertain. It is possible that both studies are identifying false-positive evidence of linkage expected once per genome scan at the suggestive level of genome-wide significance. The Pankow study was larger than our linkage analysis and would have been expected to have greater power to detect our chromosome 12 QTL for the postural changes after 2 minutes. However, potentially more relevant to the differences is the nature of the 2 samples. Pankow examined older hypertensive subjects, most of whom were receiving antihypertensive treatment, whereas we stud-
ied volunteer families with a prevalence of antihypertensive treatment of only 8.4%.

We have previously reported suggestive evidence of linkage between 4 loci (chromosomes 1, 4, 16, and X) and lying SBP. None of the 3 autosomal loci for lying SBP appears relevant to ΔSBP, but the suggested locus on chromosome X for lying SBP might be related to the possible QTL for ΔSBP.

The characteristics of ΔSBP and ΔDBP are distinct in a number of aspects. Only 8% of the individual variance in ΔSBP is associated with variance in ΔDBP. In contrast to ΔSBP, there was little evidence in family analyses of genetic contribution to variance of ΔDBP. We estimated that 19% of variance in ΔDBP were attributable to shared environment as reflected in the relatively high correlation between spouse pairs. We could find no evidence of linkage for ΔDBP at the sites of suggestive and possible QTL for ΔSBP on chromosomes 6, 12, 17, 18, or X reported in this and other analyses.

Interestingly, the significant association between the change in pulse rate and ΔDBP is consistent with determination of the 2 phenotypes by sympathetic activation and/or parasympathetic withdrawal. The fact that ΔSBP does not correlate with the postural change in pulse rate suggests that factors other than cardiac autonomic responses influence ΔSBP. The physiological explanations for variation in ΔSBP are not obvious, but the arterial component of the sympathetic responses or other non-autonomic factors such as arteriolar remodeling or large arterial compliance might be important. These considerations might help identify candidate genes if subsequent fine mapping replicates and refines the possible QTL for ΔSBP on chromosomes 12, 17, and X.

In these analyses, we were able to make estimates of the measurement error associated with each measured or calculated phenotype. In general, the measurement error was small, typically being 4% of total variance for individual measurements of lying and standing SBPs and DBPs. Measurement error is compounded for calculated variables; for single estimates of ΔSBP and ΔDBP, measurement errors were 22% and 20%, respectively. All other things being equal, statistical power to detect genetic linkage or association is vulnerable to measurement error, and this could be more important in the case of phenotypes derived by calculations from individual measures. Repeated measures are a simple way of reducing this source of error.

Perspectives

These analyses have revealed that although stability of SBP appears to be the aim of the postural baroreflex, some families are prone to a decrease and others to an increase in SBP on standing. Such tendencies might have long-term implications for clinical events such as postural hypotension and acute vascular disruption including coronary plaque rupture and cerebral hemorrhage. Our biometric and genomic evidence of genetic influences provide impetus for further investigation to define the detailed molecular and physiological explanations of the variation in the postural response of SBP.

Acknowledgments

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References

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