

Genetic Epidemiology of Blood Pressure in Two Indian Populations: Some Lessons

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Abstract A genetic epidemiological study of blood pressure was conducted in two contrasting populations: the Marwaris of Calcutta and the Hindu middle-caste agriculturists of Digha. The Marwaris are heavier and significantly more obese than the agriculturists. The prevalence of hypertension among the Marwaris (17%) is more than tenfold higher than that among the agriculturists (1.4%). Genetic analysis of blood pressure data using a path model indicates that blood pressure levels (adjusted and standardized for age, gender, education level, and disease status) are primarily determined by environmental factors, as measured by their effects on anthropometric characters. The observed familial resemblance of blood pressure levels in the two populations is primarily due to cultural rather than genetic inheritance. Genetic and familial effects on covariation between anthropometric measures of obesity and blood pressure levels are perhaps so strong that there is no residual genetic heritability of adjusted blood pressure levels.

Essential hypertension is a major risk factor for cardiovascular disease. Even mild hypertension, conventionally 90–104 mm Hg for the diastolic pressure, is viewed as a major public health burden (Labarthe 1986). An understanding of how blood pressure is influenced by genetic and environmental factors is the key to understanding the role played by hypertension in cardiovascular complications.

Blood pressure profiles and etiologic factors affecting blood pressure are different for traditional societies and for Westernized or urbanized societies (Dressler et al. 1987; Epstein and Eckhoff 1967; Marmot 1979; Siervogel 1983; Ward 1983). To gain insight into the factors that influence blood pressure and to examine whether the relative roles of the factors that influence blood pressure are similar in contrasting populations, we undertook two fam-

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ily studies in West Bengal, India. The epidemiological results of these studies have already been published (Majumder et al. 1990, 1993). Here, we primarily present results of genetic analyses performed on these data using an appropriate path model.

Materials and Methods

Study Populations. Data were collected from two populations. The first population group is the Marwari, who come from the western Indian state of Rajasthan. The families were sampled in Calcutta. They migrated to Calcutta between 100 and 300 years ago. The Marwaris are traditionally traders. The major reason for their migration was that trade thrived better in Calcutta than in Rajasthan. Because of the uncertainties associated with trading as a profession, the Marwaris, especially the adult males, are generally under high stress. (This assessment is based on close long-term interaction with the Marwari families.) Furthermore, their level of physical activity is low. They are strict vegetarians and generally consume hydrogenated and saturated fats and oils in large quantities. Although there is considerable variation in the economic status of the Marwaris of Calcutta, the families included in this study were of a similar economic level. Most families belonged to the upper middle to upper economic stratum.

Data were collected from members of Marwari families who were 12 years old or older. Two hundred ten nuclear families comprising over 1000 individuals are included in the present study. However, because of absence of complete information, many individuals had to be excluded from certain types of analyses.

The second population is a group of Hindu middle-caste agriculturists residing in villages around the town of Digha, about 160 km southwest of Calcutta. Agriculture in this region is nonmechanized and traditional, and most individuals, especially males, perform agricultural labor involving high levels of physical activity. The women are mostly engaged in household work, although they generally spend part of the day in the fields. The standard of living is low. Most of the population live in mud-walled thatched houses. They survive primarily on a carbohydrate-rich diet. Their consumption of fats, oils, and animal protein is low.

Eighty-eight nuclear families from the agricultural population—about 300 individuals, each over 15 years of age—were studied.

Variables. Systolic (SBP) and diastolic (DBP) blood pressure and pulse rate readings were taken on each individual in the sitting position using an electronic digital sphygmomanometer. Data were gathered on gender, age, education, occupation, marital status, tobacco and alcohol consumption, use of steroids, antihypertensive drugs, and oral contraceptives, and occurrence

of major tension or major disease. Anthropometric measurements taken on each individual included height, weight, and biceps, triceps, and subscapular skinfold thicknesses.

Path Model. Path analysis, developed by Sewall Wright, is a method based on algebraic manipulation of standardized regression coefficients to explain linear relationships between variables. The contemporary surge of interest in applying this method to the analysis of human family data on quantitative traits, such as blood pressure, stems primarily from the research of Morton (1974) and Rao et al. (1974). Various path models of increasing complexity have subsequently been developed [see Cloninger et al. (1983) and Rao et al. (1984) for descriptions and reviews]. In all the models the quantitative trait is assumed to be determined by the additive action of genotype and family environment.

The path model used in the present study is a special case of the one presented by Rao et al. (1979) and has already been used extensively [e.g., Rao et al. (1982)]. The model describing relationships of the variables among members of a nuclear family is presented in Figure 1. In this figure P denotes standardized phenotype (SBP or DBP), G denotes genotype, C denotes transmissible environment with index I , and B denotes common sibship environment. Details on creating standardized SBPs and DBPs are given in the next section. The subscripts F , M , C_1 and C_2 denote father, mother, and two children, respectively.

The 10 parameters of the model are defined at the bottom of Table 1. Marital resemblance, as measured by the correlation between environments of spouses (u), reflects the combined effects of social homogamy and cohabitation. (Under social homogamy mates choose each other on the basis of their group membership, which generates primary correlations between the genotypes and environments of spouses; phenotypic correlation between spouses becomes secondary.) Genetic and common environmental (cultural) heritabilities are h^2 and c^2 , respectively, in children and h^2z^2 and c^2y^2 , respectively, in adults. Thus possible intergenerational differences are taken into account in this model. Parental environmental effects are also distinguished; effects of maternal and paternal environments on the children's environments are denoted f_M and f_F , respectively. In addition to a nontransmitted common sibship environment (B), separate indexed environments and indexes are incorporated for each child.

The phenotypes and indexes of parents and children yield 16 distinct expected correlations using standard rules of path analysis (Li 1975), which are presented in Table 1. The procedures for obtaining maximum-likelihood estimates of correlations, sample sizes, and path parameters are given by Rao et al. (1979) [see also Rao et al. (1984)]. In the present study the computer program PATHMIX (Morton et al. 1983) was used to estimate the parameters.

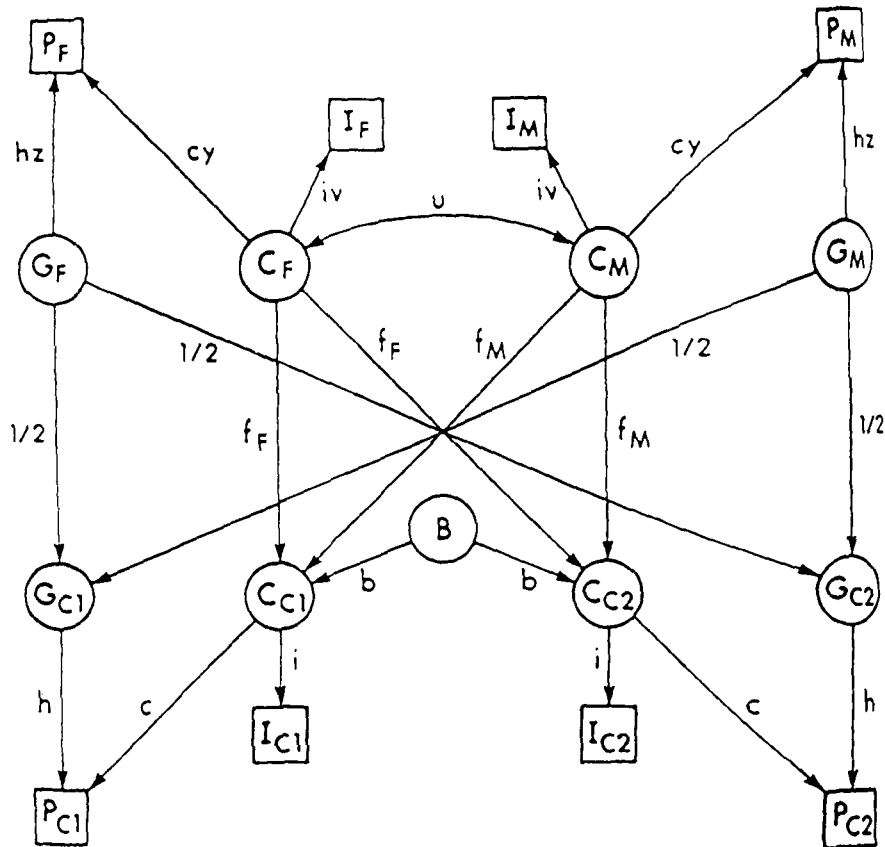


Figure 1. Path diagram depicting biological and environmental (cultural) inheritance of blood pressure in nuclear families. P denotes phenotype (standardized SBP and DBP), G denotes genotype, C denotes transmissible environment with index I , and B denotes nontransmitted common sibship environment. The subscripts F , M , C_1 , and C_2 denote father, mother, and two children, respectively.

To identify the most parsimonious model, we tested various submodels, which are nested within the general model. The submodels are obtained by specifying a null hypothesis. The various submodels tested are (1) no intergenerational differences in heritabilities ($y = z = 1$); (2) no effect of assortative mating and cohabitation ($u = 0$); (3) no extra sibling environmental effect ($b = 0$); (4) no specific maternal environmental effect ($f_F = f_M$); (5) no genetic inheritance ($h = z = 0$); and (6) no cultural inheritance ($c = y = 0, i = v = 1$). The fit of the general model is calculated by comparing the ln-likelihood obtained for estimating the correlations with that obtained under the general path model. The fit of a submodel is calculated by com-

Table 1. Expected Correlations between Variables Observed in Members of a Nuclear Family under the Path Model

Relation	Variables	Correlation
Marital	P_F, P_M	uc^2y^2
	I_F, I_M	ui^2v^2
Parental	P_F, I_M (or P_M, I_F)	$ucyiv$
	(P_F, I_F) or (P_M, I_M)	$cyiv$
Full sibs	P_{C1}, P_{C2}	$h^2/2 + c^2\psi$
	I_{C1}, I_{C2}	ψi^2
	P_C, I_C	ci
	(P_{C1}, I_{C2}) or (P_{C2}, I_{C1})	$c\psi i$
Parent-offspring	P_F, P_C	$h^2z/2 + c^2y(f_F + uf_M)$
	I_F, P_C	$civ(f_F + uf_M)$
	P_F, I_C	$cvi(f_F + uf_M)$
	I_F, I_C	$i^2v(f_F + uf_M)$
	P_M, P_C	$h^2z/2 + c^2y(f_M + uf_F)$
	I_M, P_C	$civ(f_M + uf_F)$
	P_M, I_C	$cvi(f_M + uf_F)$
	I_M, I_C	$i^2v(f_M + uf_F)$

- h : Effect of child's genotype on child's phenotype.
 - hz : Effect of adult's genotype on adult's phenotype.
 - c : Effect of child's environment on child's phenotype.
 - cy : Effect of adult's environment on adult's phenotype.
 - u : Correlation between parental environments.
 - b : Effect of nontransmitted common sibship environment on child's environment.
 - f_F : Effect of father's environment on his child's environment.
 - f_M : Effect of mother's environment on her child's environment.
 - i : Effect of child's environment on child's index.
 - iv : Effect of adult's environment on adult's index.
- $$\psi = b^2 + f_F^2 + f_M^2 + 2uf_Ff_M.$$

paring the ln-likelihood obtained under the submodel with that obtained under the general model.

Data Adjustments. Because family environment in its totality cannot be directly measured, an index I was created separately for SBP and DBP as an estimate of the environment. The index is assumed to be a measure of the family environment alone, and the genetic correlation between the index and the corresponding blood pressure variable is assumed to be zero. We note that the existence of any such genetic correlation is expected to yield an underestimate of the genetic heritability and an overestimate of the environmental heritability.

The index I was created using a stepwise multiple regression procedure. In our data set, for each individual information on age, several pertinent categorical variables (e.g., gender, education, occupation, tobacco use, tension,

Table 2. Variables Identified as Significant Predictors and Used for Creating Standardized Phenotypes and Indexes

<i>Population</i>	<i>Variables Used for Creating Standardized Phenotype</i>	<i>Variables Used for Creating Environmental Index</i>
Marwari SBP	Gender, age ³	Weight, triceps skinfold thickness
DBP	Presence of cardiovascular disease	Height, weight, biceps skinfold thickness
Hindu middle-caste agriculturists SBP	Education level, age ³	Weight, biceps skinfold thickness
DBP	Gender, age, age ³	Weight, subscapular skinfold thickness

contraceptive use, alcohol use, steroid use, major disease), and anthropometric measurements [e.g., height, weight, skinfold thicknesses (biceps, triceps, subscapular)] were used as regressors in the following model:

$$X = f(\mathbf{Z}) + g(\mathbf{M}) + \mathbf{e}, \quad (1)$$

where X is SBP or DBP; \mathbf{Z} is the vector of categorical variables including age, age², and age³; and \mathbf{M} is the vector of anthropometric variables. A stepwise multiple regression analysis was performed to identify significant regressors and to obtain estimates of regression coefficients. If \mathbf{Z}^* and \mathbf{M}^* denote the vectors of significant regressors, then the index is created as $I = g(\mathbf{M}^*)$ and the standardized phenotype is

$$P = \frac{X - f(\mathbf{Z}^*)}{\{V[X - f(\mathbf{Z}^*)]\}^{1/2}}, \quad (2)$$

where $V[X - f(\mathbf{Z}^*)]$ is the variance of the residuals $X - f(\mathbf{Z}^*)$. The standardized phenotypes have been used in the subsequent analyses. The variables identified by the stepwise regression analysis and used for creating standardized phenotypes and indexes are given in Table 2.

Anthropometric variables have significant genetic components that can be correlated with plausible genetic factors involved in the determination of blood pressure levels. Therefore the index I may contain some confounded genetic information in addition to environmental information. In view of this, it is appropriate to reinterpret the heritabilities h^2 (genetic) and c^2 (cultural) defined in the previous section. If h_i^2 and c_i^2 denote the true (unknown) genetic and cultural heritabilities, respectively, then

$$h^2 = (1 - a)h_i^2, \quad (3)$$

$$c^2 = c_i^2 + ah_i^2, \quad (4)$$

Table 3. Mean \pm SE Values of Age, Anthropometric Measurements, and Blood Pressures among Marwaris and Agriculturists

Variable	Marwari	Agriculturists
Age (yr)	37.43 \pm 0.72	35.63 \pm 0.99
Height (cm)	163.21 \pm 4.18	161.60 \pm 4.92
Weight (kg)	62.32 \pm 0.42	45.24 \pm 0.44
Skinfold thickness		
Biceps (mm)	11.48 \pm 0.28	4.87 \pm 0.13
Triceps (mm)	21.57 \pm 0.43	10.66 \pm 0.31
Subscapular (mm)	28.44 \pm 0.56	12.61 \pm 0.34
Blood pressure		
Systolic (mm Hg)	125.30 \pm 0.84	106.41 \pm 0.87
Diastolic (mm Hg)	82.28 \pm 0.74	63.90 \pm 0.70

where $0 < a \leq 1$. Thus h^2 is really the residual genetic heritability, and c^2 is the indexed (combined) heritability.

Results

Epidemiological Features. The epidemiological features of the two study populations have been published by Majumder et al. (1990, 1993). Therefore we present here only some pertinent summary information. The descriptive statistics pertaining to the anthropometric measurements and blood pressures are presented in Table 3. It can be seen from this table that the mean ages and heights of the individuals from the two populations are not significantly different. The Marwaris are significantly more obese than the agriculturists, as is reflected by higher body weight and larger skinfold thicknesses. The blood pressure distributions are significantly different; the Marwaris have about 20 mm Hg higher blood pressure values than the agriculturists. However, Majumder et al. (1993) found that the blood pressure distributions, when adjusted for age and anthropometric measurements, are not significantly different between the two populations. By using the World Health Organization's definition of hypertension (SBP $>$ 160 mm Hg and/or DBP $>$ 95 mm Hg), we found that the prevalences of hypertension were 17% and 1.42%, respectively, among the Marwaris and the agriculturists.

Familial Correlations. Sixteen correlations can be estimated between pairs of the following six variables: P_F , phenotype of father; I_F , index of father; P_M , phenotype of mother; I_M , index of mother; P_C , phenotype of a child; I_C , index of a child. However, the correlations between P_F and I_M and between P_M and I_F are equal. Also, the correlations between P_F and I_F and between P_M and I_M are equal. These correlations have been estimated by the

method of maximum likelihood developed by Rao et al. (1982). Because observations on members of a family are not all independent, the effective sample size n was estimated as

$$n = \frac{(1 - \hat{\rho}^2)^2}{V(\hat{\rho})}, \quad (5)$$

as suggested by Rao et al. (1982), where $\hat{\rho}$ denotes the estimated correlation coefficient and $V(\hat{\rho})$ denotes its variance.

Estimated familial correlations, their standard errors, and the effective sample sizes are presented in Table 4. From this table it can be seen that in both populations significant correlations for SBP are observed between the phenotype and the environmental index of the father, between phenotypes of sibs, and between phenotypes of mother and child. However, although the sib-sib correlations between environmental indexes and between the phenotype and environmental index are significant among the Marwaris, these correlations are not significant among the agriculturists. Similarly, although the correlation between phenotypes of spouses is significant for the agriculturists, it is not significant for the Marwaris.

For DBP the only correlation that is significant in both populations is between the phenotype and the environmental index of the father. Among Marwaris all sib-sib correlations—between phenotypes, between indexes, and between phenotype and index—are significant. The mother-child phenotypic correlation is significant in the agriculturists but is not significant among the Marwaris. Therefore there are notable differences in the patterns of familial correlations between the groups.

Path Analysis. The maximum-likelihood estimates of parameters of the general path model and of relevant submodels are presented in Tables 5 and 6 for SBP and DBP, respectively, along with the corresponding $-2 \ln L$ and chi-square values. It can be seen that the path model considered here provides an adequate fit to the familial correlations observed for both SBP and DBP in each of the two populations, because all chi-square values corresponding to the general model are nonsignificant at the 5% level with six degrees of freedom. From Table 5, pertaining to standardized SBP, it can be seen that the hypothesis of no cultural inheritance ($c = y = 0, i = v = 1$) is rejected in both populations. In addition, the hypothesis of no extra sibling environmental effect ($b = 0$) is rejected at the 5% level for the Marwari population. The chi-square values corresponding to all other hypotheses are nonsignificant at the 5% level. There is no evidence of any significant genetic inheritance of the standardized SBP level, although under the general model the estimated values of genetic heritability in children (h^2) are 20% among the Marwaris and 34% among the agriculturists and those in parents (h^2z^2) are 14% among both the Marwaris and the agriculturists (Table 7). There is no

Table 4. Maximum-Likelihood Estimates of Familial Correlations (r) and Their Sample Sizes (n) for Systolic and Diastolic Blood Pressure among Marwaris and Agriculturists

Variables	Systolic Blood Pressure						Diastolic Blood Pressure					
	Marwari			Agriculturists			Marwari			Agriculturists		
	r	SE	n	r	SE	n	r	SE	n	r	SE	n
P_F, P_M	-0.081	0.106	87	0.660	0.135	42	0.224	0.106	80	0.162	0.144	46
I_F, I_M	-0.088	0.110	81	-0.056	0.143	48	0.121	0.112	77	-0.065	0.141	50
P_F, I_M (or P_M, I_F)	-0.049	0.082	148	0.189	0.110	76	0.147	0.084	134	0.139	0.109	80
P_F, I_F (or P_M, I_M)	0.362	0.055	248	0.506	0.063	141	0.457	0.049	265	0.410	0.072	132
P_{C1}, P_{C2}	0.324	0.076	138	0.268	0.097	92	0.252	0.081	134	0.148	0.116	71
I_{C1}, I_{C2}	0.463	0.078	101	0.122	0.093	112	0.352	0.094	87	0.142	0.095	106
P_C, I_C	0.491	0.048	251	0.383	0.069	154	0.470	0.048	255	0.308	0.072	157
P_{C1}, I_{C2}	0.315	0.064	196	0.083	0.077	168	0.259	0.069	182	0.097	0.077	166
P_F, P_C	0.134	0.079	156	0.232	0.110	75	0.177	0.084	131	-0.001	0.089	126
I_F, P_C	0.142	0.086	130	-0.012	0.145	47	-0.027	0.096	108	0.035	0.111	80
P_F, I_C	0.078	0.091	119	0.100	0.103	93	0.078	0.093	115	0.120	0.093	112
I_F, I_C	0.075	0.102	95	0.019	0.128	61	-0.006	0.103	94	0.060	0.130	59
P_M, P_C	0.245	0.089	111	0.263	0.099	88	0.202	0.085	127	0.310	0.076	142
I_M, P_C	0.154	0.091	115	0.201	0.101	91	0.121	0.092	114	-0.040	0.058	138
P_M, I_C	0.125	0.099	98	0.096	0.099	100	0.193	0.089	116	0.114	0.101	96
I_M, I_C	0.105	0.098	102	0.159	0.097	101	0.108	0.095	109	0.110	0.098	101

Table 5. Maximum-Likelihood Estimates of Parameters and Other Statistics under Various Hypotheses Pertaining to Adjusted Systolic Blood Pressure among Marwaris and Agriculturists^a

Hypothesis	$-2 \ln L + C$	χ^2	<i>df.</i>	h^2	c^2	<i>y</i>	<i>z</i>	<i>u</i>	<i>b</i>	f_F	f_M	<i>i</i>	<i>v</i>
General													
Marwari	2868.93	4.59	6	0.201	0.346	1.222	0.841	-0.119	0.741	0.189	0.279	0.835	0.589
Agriculturists	1410.78	5.26	6	0.341	0.378	1.500	0.661	0.406	0.439	0.058	0.178	0.634	0.860
<i>y = z = 1</i>													
Marwari	2869.25	0.32	2	0.176	0.362	[1.0]	[1.0]	-0.069	0.737	0.207	0.291	0.824	0.700
Agriculturists	1411.55	0.77	2	0.178	0.796	[1.0]	[1.0]	0.430	0.400	0.0	0.221	0.435	1.299
<i>u = 0</i>													
Marwari	2869.25	0.32	1	0.199	0.348	1.110	0.851	[0]	0.735	0.182	0.283	0.834	0.648
Agriculturists	1413.78	3.00	1	0.354	0.332	1.049	0.635	[0]	0.358	0.087	0.307	0.664	1.270
<i>b = 0</i>													
Marwari	2879.31	10.38	1	0.152	0.399	0.872	0.811	-0.369	[0]	0.626	0.759	0.785	0.603
Agriculturists	1411.68	0.90	1	0.336	0.664	1.106	0.333	0.414	[0]	0.107	0.243	0.467	1.207
$f_F = f_M$													
Marwari	2869.15	0.22	1	0.203	0.344	1.204	0.835	-0.124	0.745	0.231	0.231	0.836	0.598
Agriculturists	1410.94	0.16	1	0.352	0.358	1.548	0.635	0.404	0.441	0.115	0.115	0.650	0.834
<i>h = z = 0</i>													
Marwari	2872.57	3.64	2	[0]	0.426	1.130	[0]	-0.084	0.743	0.251	0.342	0.753	0.651
Agriculturists	1411.95	1.17	2	[0]	1.0	0.970	[0]	0.388	0.404	0.146	0.197	0.379	1.382
<i>c = y = 0, i = v = 1</i>													
Marwari	2965.19	96.26	4	0.650	[0]	[0]	0.588	0.095	0.679	0.076	0.105	[1.0]	[1.0]
Agriculturists	1471.71	60.93	4	0.469	[0]	[0]	0.753	-0.082	0.313	0.078	0.153	[1.0]	[1.0]
Most parsimonious model													
<i>h = z = u = 0, y = 1, f_F = f_M</i>													
Marwari	2873.03	4.10	5	[0]	0.431	[1]	[0]	[0]	0.740	0.293	0.293	0.752	0.727
<i>h = z = u = b = 0, y = 1, f_F = f_M</i>													
Agriculturists	1419.89	9.11	6	[0]	0.823	[1]	[0]	[0]	[0]	0.314	0.314	0.452	1.364

a. Values in brackets indicate fixed values of parameters.

Table 6. Maximum-Likelihood Estimates of Parameters and Other Statistics under Various Hypotheses Pertaining to Adjusted Diastolic Blood Pressure among Marwaris and Agriculturists^a

Hypothesis	$-2 \ln L + C$	χ^2	<i>df.</i>	h^2	c^2	<i>y</i>	<i>z</i>	<i>u</i>	<i>b</i>	f_F	f_M	<i>i</i>	<i>v</i>
General													
Marwari	2763.10	2.09	6	0.153	0.328	1.425	1.539	0.332	0.683	0.0	0.274	0.815	0.686
Agriculturists	1189.34	11.00	6	0.078	0.556	1.340	0.175	0.168	0.441	0.0	0.361	0.422	0.962
<i>y = z = 1</i>													
Marwari	2770.89	7.79	2	0.205	0.224	[1.0]	[1.0]	0.175	0.610	0.0	0.137	1.0	0.917
Agriculturists	1189.96	0.62	2	0.0	1.0	[1.0]	[1.0]	0.167	0.370	0.0	0.279	0.314	1.288
<i>u = 0</i>													
Marwari	2767.44	4.34	1	0.121	0.328	1.540	1.345	[0]	0.692	0.077	0.236	0.814	0.637
Agriculturists	1190.61	1.27	1	0.058	0.583	1.310	0.0	[0]	0.427	0.0	0.369	0.411	0.984
<i>b = 0</i>													
Marwari	2772.68	9.58	1	0.147	0.379	1.216	0.928	0.325	[0]	0.0	0.498	0.752	0.799
Agriculturists	1190.18	0.84	1	0.217	0.649	1.242	0.003	0.161	[0]	0.0	0.357	0.382	1.060
$f_F = f_M$													
Marwari	2763.95	0.85	1	0.125	0.333	1.469	1.504	0.305	0.711	0.144	0.144	0.816	0.660
Agriculturists	1191.19	1.85	1	0.326	0.214	1.765	0.416	0.291	0.489	0.161	0.161	0.675	0.737
<i>h = z = 0</i>													
Marwari	2766.57	3.47	2	[0]	0.406	1.344	[0]	0.295	0.692	0.089	0.300	0.739	0.722
Agriculturists	1189.40	0.06	2	[0]	0.608	1.282	[0]	0.167	0.468	0.0	0.357	0.402	1.007
<i>c = y = 0, i = v = 1</i>													
Marwari	2881.42	118.32	4	0.478	[0]	[0]	0.727	0.132	0.612	0.0	0.111	[1.0]	[1.0]
Agriculturists	1192.26	2.92	4	0.460	[0]	[0]	0.533	-0.076	0.361	0.075	0.119	[1.0]	[1.0]
Most parsimonious model													
<i>h = z = 0, f_F = f_M</i>													
Marwari	2767.28	4.18	3	[0]	0.411	1.403	[0]	0.265	0.715	0.915	0.915	0.737	0.688
<i>h = z = u = b = 0, y = 1, f_F = f_M</i>													
Agriculturists	1198.90	9.56	6	[0]	0.412	[1]	[0]	[0]	[0]	0.335	0.335	0.502	1.145

a. Values in brackets indicate fixed values of parameters.

Table 7. Estimates of Heritabilities under General and Most Parsimonious Models for Adjusted Systolic and Diastolic Blood Pressures

Population	Heritability (and SE)					
	Genetic		Indexed Cultural		Residual	
	Children	Parents	Children	Parents	Children	Parents
Marwari						
SBP						
General	0.201 (0.154)	0.143 (0.177)	0.346 (0.084)	0.515 (0.332)	0.453 (0.134)	0.341 (0.354)
Parsimonious	0	0	0.431 (0.079)	0.431 (0.079)	0.569 (0.079)	0.569 (0.079)
DBP						
General	0.125 (0.148)	0.299 (0.351)	0.328 (0.091)	0.666 (0.261)	0.546 (0.138)	0.035 (0.447)
Parsimonious	0	0	0.411 (0.094)	0.810 (0.407)	0.589 (0.094)	0.190 (0.407)
Agriculturists						
SBP						
General	0.341 (0.246)	0.149 (0.216)	0.378 (0.427)	0.851 (0.335)	0.281 (0.302)	0.000 (0.440)
Parsimonious	0	0	0.678 (0.212)	0.678 (0.212)	0.322 (0.212)	0.322 (0.212)
DBP						
General ^a	0.074	0.022	0.565	0.998	0.361	0.000
Parsimonious	0	0	0.412 (0.162)	0.412 (0.162)	0.588 (0.162)	0.588 (0.162)

a. SEs could not be estimated.

significant evidence of any effect of assortative mating and cohabitation, and no specific maternal environmental effects could be detected.

The most parsimonious model among both the Marwaris and the agriculturists indicates that there is no genetic heritability, that there is no correlation between parental indexed environments, and that the maternal and parental indexed environmental effects on child's index are equal. For the agriculturists it was also found that there is no effect of common sibship indexed environment on child's index. The heritability estimates under the general and the parsimonious models are given in Table 7.

For standardized values of DBP it can be seen from Table 6 that the conclusions are exactly the same as those obtained for SBP, although in addition the hypotheses of no intergenerational differences in heritabilities ($y = z = 1$) and of no effect of assortative mating and cohabitation were rejected for the Marwari population. Under the general model the estimated values of genetic heritability among children were 12% among the Marwaris and 7% among the agriculturists. Among parents the estimate of genetic heritability is 0 for the agriculturists. Although this estimate for the Marwaris is 0.3, the standard error of the estimate is rather large (0.35). The most parsimonious model for DBP among the agriculturists is exactly the same as that for SBP. Among the Marwaris the most parsimonious model for DBP is basically the same as that for SBP, except that for DBP there is a significant positive correlation between parental indexed environments. The heritability estimates under the general and the parsimonious models are provided in Table 7.

Discussion

The present study was conducted among two contrasting populations. The contrasts come about from their milieu of residence (urban for the Marwaris; rural for the Hindu middle-caste agriculturists), diet (high intake of saturated fat for the Marwaris; negligible intake of saturated fat for the agriculturists), level of physical activity (low for the Marwaris; high for the agriculturists), and lifestyle stress (high for the Marwaris; low for the agriculturists). As a result of these factors, the Marwaris are much more obese than the agriculturists, and the mean blood pressure levels among the Marwaris are about 20 mm Hg higher than those of the agriculturists. The prevalence of hypertension among the Marwaris (17%) is over tenfold higher than among the agriculturists (1.42%).

Correlations between siblings are generally higher than parent-offspring correlations in both populations for the standardized levels of SBP and DBP. For DBP among the agriculturists, however, the sib-sib correlation is smaller than the mother-child correlation. The genetic analysis conducted under a specific path model reveals that the correlations of standardized blood pres-

sure levels among members of nuclear families are primarily due to the sharing of a common environment and not to the sharing of genes. This result is somewhat surprising in view of previous studies showing that there is a genetic component to the determination of blood pressure levels, although the estimated values of genetic heritability were found to differ widely across studies [see Burns and Lauer (1986) for a review].

In our own study among the agriculturists we had estimated the upper bound of genetic heritability to be 0.3 for both SBP and DBP (Majumder et al. 1990). However, the path model under which these estimates were obtained was much more restrictive than the model considered in the present study. Under that restricted model, known as the TAU model (Rice et al. 1978), in which environmental index is not used, no significant inference regarding the causes of familial aggregation of DBP could be drawn; for SBP a general pseudopolygenic model was found to be the most parsimonious.

Of relevance to the finding here that there is little or no involvement of genes in the determination of blood pressure values adjusted for covariates is a result obtained in a previous study (Majumder et al. 1993): the differences in the blood pressure profiles of the two study populations are similar when adjusted for variations of concomitant anthropometric variables, even though the unadjusted blood pressure distributions are significantly different. In the present study we have used anthropometric measurements to create an environmental index, an estimate of family environment. As mentioned, if the anthropometric measurements are genetically correlated with blood pressures, then the effect will be a reduction of the estimate of genetic heritability. In fact, some recent studies (Schork et al. 1994) have shown that there is a significant effect of shared genetic and familial factors on the covariation between some anthropometric measures of obesity and blood pressure levels.

Our present results completely support this finding. In fact, our results show that the effects of genetic factors on this covariation may be so strong that the residual genetic heritability of adjusted blood pressure levels may be negligible. We note, however, that anthropometric variables, especially obesity measures, have been used for construction of environmental indexes in many previous studies [see Rao and Wette (1990) and references therein], but their inclusion did not result in consistently high estimates of cultural heritability across studies. For example, Krieger et al. (1980), Morton et al. (1980), and Ward et al. (1979) estimated cultural heritabilities in the range of 1–10% and Perusse et al. (1989) and Rice et al. (1989) estimated cultural heritabilities in the range of 20–40%, even though all these studies used measures of obesity for construction of the environmental index. However, we also note that in a recent family study conducted in South India (Rice et al. 1992), the cultural heritability was estimated to be in the range 0.14–0.21, whereas in the present study the estimates were in the range 0.31–0.98. It should be mentioned that Rice et al. (1992) did not use a measure of adiposity for constructing the environmental index.

Thus, although consistent inferences are obtained regarding genetic influences on blood pressure levels in two contrasting populations, comparisons with previous studies reveal some consistent features and some inconsistencies. The relative genetic and environmental effects on determination of blood pressures remain an enigma and perhaps point to the fact that there may be significant genotype-environment interaction. This needs to be investigated in detail using appropriate study designs and statistical models.

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