

Heritability of Blood Pressure in an Iranian Population

*M Saadat¹, M Sadeqi¹, DD Farhud², A Bahaoddini¹

¹Dept. of Biology, College of Sciences, Shiraz University, Shiraz 71454, Iran.

²Dept. of Human Genetics and Anthropology, School of Public Health and Institute of Public Health Research, Tehran University of Medical Sciences, P.O.Box 14155-6446, Tehran, Iran

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ABSTRACT

The fact that life styles and personal interests, aggregate within families suggests that shared environment in addition to shared biological factors could play a role in determining the phenotypic similarity of individuals living in the same household. It is a major concern of cardiovascular epidemiologists to know how much of the familial aggregation of blood pressure is attributable to shared genes and/or shared family environment. Genetic and environmental influences on blood pressure was examined in a sample representative of the adult population of Shiraz, Fars province, south of Iran. The studied population was the 107 pairs of mother and daughter. Analysis of the data suggest that the genetic heritabilities were estimated to be 0.58, 0.30, 0.60 for systolic, diastolic, and mean blood pressure, respectively.

INTRODUCTION

Familial aggregation of the observable expression of a trait suggests either influences of heredity or influences of a common environment. In 1921, Wright introduced the method of path coefficients to estimate the relative importance of these two factors in determining the phenotype. At first, Wright's method was used primarily by animal and plant breeders (6). By the late 1960's, investigators used familial covariance to separate the proportion of a trait variability due to genetic influence from the proportion due to common environment in human populations (1).

The familial aggregation of coronary heart disease (CHD) can be accounted for in large part by a clustering of cardiovascular disease risk factors. Prospective epidemiological studies have revealed that a substantial portion of the variation in CHD risk within populations can be attributed to variation in age, gender, obesity, glucose tolerance status, blood pressure, and lipid and lipoprotein levels (8,9,16).

One strategy for identifying the genetic factors that influence CHD risk is to identify the genetic influence of intermediate traits associated with atherosclerosis, ie, traits such as dyslipidemia, obesity, glucose intolerance, and hypertension. Such investigations must account for the fact that these intermediate traits themselves are multifactorial in nature, being influenced both by genes and environmental factors.

The importance of BP as a risk factor in CHD is well established (2,17,22).

It is reported that by selective breeding and rigorous measurements of BP, two lines of baboons with high and low BP—with statistically significant differences in BP level of baboons—can be developed (4). Also it is showed that the genetic factors play a significant role in

influencing BP in White Carneau pigeon (18). BP has a strong genetic component in rats (19). The genetic analysis of BP in the Milan hypertensive strain and Milan normotensive rats, the heritability was estimated 0.64. (21). There are several reports that indicate the systolic BP (SBP) and diastolic BP (DBP) indices have heritability in human populations (1-3, 5, 7, 10, 11-15, 20,22-24).

Although the heritability of BP in western population has been well described, there is no information in Iranian population. Therefore, the purpose of the present study is to investigate

genetic influences on intra-individual variation in BP, by performing heritability analysis on an Iranian population (Shiraz, Fars province).

MATERIALS AND METHODS

A total of 214 individuals, constituting 107 families were ascertained. The maternal generation (n=107) ranged in age from 32 to 52 years. Ages of the offspring generation ranged from 16 to 19 years.

The BP was measured by a trained individual after the subjects have been seated for 10 min, by use of a standard mercury sphygmomanometer. The subjects were in a supine position. A first reading was taken followed by a second reading after a 2 min delay. The mean of two consecutive measurements which were less than 10 mmHg apart was used. The measured phenotypes were SBP and DBP. Mean BP(MBP) was estimated as $DBP + [(SBP - DBP) / 3]$.

To determine the proportion of variance of the variables that is attributable to genetic influences, heritability analysis as performed by use of estimation of regression equations separately for each of these variables between mothers and daughters. Heritability (h^2) is then calculated using equation: $h^2 = 2b$ (b means the slope of the regression line) (6). The analysis of variance for each model was employed. A P-value less than 0.05 were considered statistically significant.

Estimated heritability near 0 imply that there are no genetic effects whereas values close to 1 imply strong genetic influences under the assumption of an underlying multifactorial model.

RESULTS AND DISCUSSION

Assortative mating and length of cohabitation between members of a family may be confounded with the estimates of the contribution of shared genetic and shared environmental effects to familial aggregation. In cross-sectional population studies, the shared environmental effects on spouse correlation is not distinguishable from assortative mating when there is no information on the length of marriage or cohabitation of the parents. In such case, the heritability estimates using the formula: $h^2 = 2b / (1+r)$, when b is the slope of regression line

* Corresponding author, Tel: +98-711-2282747; Fax: + 98-711-2280926; E-mail: Saadat@susc.ac.ir

between mother and daughter and r is the correlation coefficient between the parents (6).

The means \pm SD (mmHg) for SBP, DBP, and MBP are 120 ± 12.6 , 80.6 ± 9.1 , and 94.2 ± 10.1 , respectively in mothers, and are 108.4 ± 13.5 , 72.9 ± 10.5 , and 85.1 ± 10.7 , respectively, in daughters.

Both MBP ($h^2 = 0.60$; $F = 19.82$; $df = 1, 105$; $P < 0.05$) and SBP ($h^2 = 0.58$; $F = 13.44$; $df = 1, 105$; $P < 0.05$) have high heritability^{6,7}, whereas the estimation of h^2 for DBP was more moderate ($h^2 = 0.30$; $F = 3.74$; $df = 1, 105$; $P = 0.06$).

The estimation of heritability of SBP in the studied population is remarkably higher than estimates obtained from several western populations and other populations (2, 7, 12, 15, 17). On the other hand, the genetic fractions of DBP and MBP variability are similar to estimates obtained from other studied populations (1, 3, 10, 11, 22-24). The consistency of these estimates across suggests that the fraction of variance explained by genetic variability within population might have same adaptive significance.

Direct comparisons of our result with those obtained from other studies are difficult. Because, heritability represents that portion of the total phenotypic variance that is attributable to variation at the genetic level, the heritability of the same trait would differ between population that differ in the distribution of environmental risk factors for that trait. For example, with all other factors being equal the heritability of BP will be higher in population with a low frequency of cigarette smoking than in population in cigarette which smoking varies widely.

These results confirm that substantial familial aggregation of cardiovascular risk factors occurs and that much of this aggregation has a genetic basis (8, 9, 16), although assortative mating (in spouses) and environmental influences (in offspring and sibling) are also present. The data indicate that hereditary factors must be considered the interpretation of same aspects of functional characterization of the heart in Iranian population and the showed genes in nuclear family should be considered as a point of intervention in cardiovascular diseases prevention programs.

By considering both genes and environmental risk factors together, we hope not only to identify specific genes that contribute to the high proportion of the variance in these traits, but also to determine how the environmental factors influence the expression of these genes. Finding genes for the augmentation index could help to unveil physiological mechanisms causing hypertension and lead to improvements in prevention, diagnosis, and treatment of at high-risk individuals.

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