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Heritability of Blood Pressure in an Iranian Population

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ABSTRACT

The fact that life styles and personal interests, aggregate within families suggests that shared environment in addition to shared bioligical factors could play a role in determining the phenotypic similarity of idividuals 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 dauther. 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 clustring 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 lipoprote in 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 babons with high and low BP –with statistically significant differences in BP level of babons- 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, consitituting 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 pportion of variance of the variables that is attributable to genetic influences, heritability analysis as performed by used of estimation of regression equations separately for each of these veriables between mothers and duathers. 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 then 0.05 were considered statistically significant.

Estimated hertability 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

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

The means ±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 dauthers.

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 estimates, 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 migth 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 unreveal physiological mechanisms causing hypertension and lead to improvements in prevention, diagnosis, and treatment of at high-risk individuals.

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REFERENCES

1. An P, Rice T, Gagnon J, Borecki IB, Perusse L, Leon AS and Skinner JS (1999): Familial aggregation resting blood Pressure and heart rate in a sedentary population: the HERITAGE family study health risk factors, exercise, training, and genetics. *Am J Hypertens*, **12**: 264-70.
2. Austin MA, King MC, Bawol RD, Hulley SB and Friedman GD (1987): Risk factors for coronary heart disease in adult female twins. Genetic heritability and shared environmental influenese. *Am J Epidemiol*, **125**: 308-18.
3. Brenn T (1994): Genetic and enviromental effects on coronary heart disease risk factors in nothern Norway. The cardiovascular disease study in Finnmark. *Ann Hum Genet*, **58**: 369-79.
4. Carey D, Kammerer CM, Sade RE, Ricek S and Mc Gill HC (1993):Selective breeing to develop lines of baboons with high and low blood pressure. *Hypertension*, **21**: 1076-9.
5. Chen CJ, Cohen BM, Diamond EL, Lin TM and Chen JS (1984): Genetic variance and heritability of cardiovascular risk factors in Chinese adolescent twins. *Acta Genet Med Gemellol Roma*, **33**: 363-73.
6. Falconer DS (1989): *Introduction to quantitative genetics.* Thrid edition Longman Scientific & Technical.
7. Friedlander Y, Kark JD and Stein K (1988): Biological and environmental sources of familial aggregation of blood pressure: the Jerusalem Lipid Research. *Clin Int J Epidemiol*, **17**:70-6.
8. Friedlander Y, Austin MA, Newman B, Edwards K, Mager-Davis EJ and King MC (1997): Heritability of longitudinal changes in coronary-heart disease risk factors in women twins. *Am J Hum Genet*, **60**: 1562-12.
9. Heller DA, de Faire U, Pedersen NL, Dahlen G and Mc Clearn GE (1993): Genetic and environmental influences on serum lipid levels in twins. *N Engl J Med*, **328**: 1150-6.
10. Iselins L, Morton NE and Rao DC (1983): Family resemblance for blood pressure. *Hum Hered*, **33**: 277-86.
11. Jensen AR (1967): Estimation of the limits of heritability of traits by comparison of monozygotic and dizygotic twins. *Proc Natl Acad Sci USA*, **58**: 156-79.
12. Krieger H, Morton NE, Rao DC and Azevedo E (1980): Familial determinants of blood pressure in northeastern Barzil. *Hum Genet*, **53**: 415-8.
13. Kuniman MW, Divitini MC, Welborn TA and Batholomew HC (1996): Familial correlation, cohabitation effects, and heritability for cardiovascular risk factors. *Ann Epidemiol*, **6**:188-94.
14. Longini IM, Higgins MW, Hinton PC, Moll PP and Keller JB (1984): Environmental and genetic sources of familial aggregation of blood pressure in Tecumseh, Michigan. *Am J Epidemiol*, **120**: 131-41.
15. Majumder PP, Bhattacharyo SK, Mukherjee BN and Rao DC (1990): Genetic epidemiological study of blood pressure in a sedentary rural agricultural population of west Bengal, India. *Am J Phys Anthropol*, **81**: 563-72.
16. Mitchell BD, Kammerer CM, Blangero J, Mahaneg MC, Rainwater DL, Dyke B, Hixson JE, Henkel RD, Sharp M, Comuzzie AG, VandeBerg JL, Stern MP and Mac Cluer JW (1996): Genetic and environmental contributions to cardiovascular risk factors in Mexican Americans. The San Antonio Family Heart study. *Circulation*, **14**: 2159-70.
17. Perusse L, Rice T, Bouchard C, Vogler GP and Rao DC (1989): Cardiovascular risk factors in a French-Canadian population:Relation of genetic and familial environmental effect on blood pressure by using extensive information on environmental correlates. *Am J Hum Genet.* **45**: 240-51.
18. Rao BP and Wagner WD (1993): Heritability estimates of blood pressure in genetically selected White Carneau pigeons. *Clin Exp Hypertens*, **15**: 367-78.
19. Rapp JP (2000):Genetic analysis of inherited hypertension in the rat. *Physiol Rev*. **80**: 135-72.
20. Rice T, Nirmala A, Reddy PC,Ramana PV, Krishna KS, and Rao DC (1992): Familial resenblance of blood pressure with residual household environmental effects in consanguineous and non-consanguineous families from Andhra Pradesh, India. *Hum Biol*, **64**: 869-89.
21. Rotimi CN, Cooperm RS, Cao G, Ogunbiyi O, Ladipo M, Owoaje E and Ward R (1999): Meximum-likelihood generalized heritability estirnate for blood pressure in Nigerian families. *Hypertension*, **33**: 874-8.
22. Schlager G, Barber BR and Bianchi G (1986): Genetic analysis of blood pressure in the Milan hypertensive strain of rat (Rattus norvegicus). *Can J Genet Cytol*, **28**: 9967-70.
23. Slattery ML, Bishop DT, French TK, Hunt SC, Meikle AW and Williams RR (1988):Lifestyle and blood pressure levels in male twins in Utah. *Genet Epidemiol*, **5**: 277-87.
24. Wang ZQ, Ouyang Z, Wang DM and Tang XZ (1990): Heritability of blood pressure in 7-to 12-year-old Chinese twins, with special reference to body size efffects. *Genet Epidemiol*, **7**: 447-52.