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Patterns of Inheritance of Essential Hypertension in Hundred Iranian Families

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Abstract

Background: Essential hypertension tends to a familial mode. Its pattern of inheritance is heterogeneous, but the frequencies of different mode of inheritance vary in different populations. Determining of the mode of inheritance in each family is the basic information that is needed for the risk estimation in those family members. Determination of pattern of inheritance in families with at least two members affected with essential hypertension in Hamadan city, west of Iran, was the goal of the present paper.

Methods: The present study was a cross sectional descriptive one. The cases were patients in Dr Emami Clinic in Hamadan that were diagnosed as essential hypertension and also a familial recurrence pattern among their families. Then we prepared a suitable questionnaire containing some questions about their medical and family histories as well as pedigree containing 3 to 4 generations. After drawing their pedigree we determined their patterns of inheritance based on the standard method. The data were expressed in tables according to our variables to show the results. Totally we could include 100 families in this study.

Results: The number of live patients in 100 studied families was 285 (84 males and 201 females, average=62.7 y). Our primary results showed that the ages of diagnoses were from 30 to 81 y (average 54.24) for men and 28, 90 and 54.127 y in that order for women. The consanguineous marriages were done in 10.52% of the parents of affected persons (8.07% degree 3 and 2.45% degree 4). Frequencies of patients in different age groups, according to the age of diagnosis, were statistically significant ($P<0.05$), but not significant between the males and females. Our family study and pedigree patterns of essential hypertension showed that the mode of inheritance in 40% of families was autosomal dominant. Autosomal recessive was the pedigree pattern of 8% of our cases. Although in 52% of remainders the mode of inheritance was familial, but there were not enough evidences for single gene trait. It seemed that in recent families the etiology of the defect was multifactorial.

Conclusion: Essential hypertension in our subject families was heterogenic. Their frequency orders were multifactorial, autosomal dominant and autosomal recessive trait, respectively. Such order is adopted with the literature but it seems that in our population, the essential hypertension with autosomal recessive mode is more frequent than the western populations.

Keywords: *Consanguinity, essential hypertension, pedigree pattern, genetics, population*

Introduction

An elevated arterial pressure is probably the most important public health problem in developed countries. It is common, asymptomatic, readily detectable, usually easily treatable, and often leads to lethal complication if left untreated. Patients with arterial hypertension and no definable cause are said to have primary, essential, or idiopathic hypertension (1).

Prevalence of essential hypertension (EHT) varies with age groups, sex, race etc. Hypertension affects approximately 1 in 5 of the population overall, but is relatively more common in older age groups. EHT accounts for 90 to 95%

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of all cases, with a variety of secondary causes making up the remainders (2).

EHT is considered a complex trait to which genetic, environmental and demographic factors contribute interactively (3). Genetic factors have long been assumed to be important in the genesis of hypertension. Data supporting this view can be found in animal and population studies in humans. The first genetic study to show the potential role of the angiotensinogen gene (AGT) in human essential hypertension was a sib-pair linkage of 2 large populations of hypertensive sibships (4).

In some cases, high blood pressure does appear to run in families, and many people can often find a first-degree relative with hypertension. Because the essential hypertension is a heterogenous condition (2), so it is important to know the most frequent pattern of inheritance in each given population. This will help us to estimate the rate of recurrent risk in close relatives of individuals who are affected by essential hypertension in any considered community with its own demographical, racial and environmental characteristics.

Materials and Methods

In this cross-sectional descriptive study, the patterns of inheritance of EHT in one hundred families were studied. At first, the files of affected individuals with EHT in Dr. Emami Heart Clinic, Hamadan, Iran were selected. Then the secretary called them, after a short explanation of the research work and its aims and procedures, invited them to involve in our project. If there was familial recurrence pattern, she made appointments to interview. During different days, more than 100 face to face interviews were carried out. In any interview, first we asked some questions about their background information, such as sex, age and marital status. Then we designed a series of questions about their family history. If there were patients with the same problem, as well as the first considered person (proband) in their family, were asked to come to the clinic for further tests. If the results showed that the new cases were affected with EHT as well, then we would enter that family in our study, and drew their pedigree for each family, based on the standard method (5), containing 3 to 4 generations; if not, they were rolled out from the study. At the end we had 100 families having our criteria.

In this study, the hypertension was concluded as blood pressure over 140/90 mmHg that was proven by 3 separated examinations during two weeks. When laboratory findings such as urine analysis for protein and glucose, CBC, potassium, urea, creatinin, triglyceride, cholesterol, blood sugar, uric acid and calcium, physical examinations, CXR and ECG did not show any secondary cause of hypertension, then it was considered as primary or EHT. Consanguinity was applied to marriages of couples with common ancestors. The marriages of cousins are third degree and marriage of a member from second generation with one from third, is fourth degree. Defining the inheritance pattern was carried out based on the standard criteria of Mendelian inheritance (5).

Results

Total individuals affected by essential hypertension in 100 studied families were 315 (103 men, 212 women). Thirty two individuals (19 men, 13 women) at the time of our study died, and because of lack of their complete medical information, we rolled them out, so the alive affected persons that we visited were 283 (83 men, 200 women).

Table 1 shows the frequencies of our cases in order of their age groups of their diagnosis age. Statistic comparison of the ratios between men and women did not show any significant differences (P= 0.745), but the differences between their ratios in age groups were statistically significant (P= 0.00). Table 2 shows them in order of their age groups at the time of our study. Statistic comparison of the ratios between men and women did not show any significant differ-

ences. The differences between the age groups of the age at the study time, were not statistically significant (P= 0.999).

Table 3 shows the mean, minimum and maximum age in order of the sex, also it shows diagnosis age, sickness duration and age at the time of study according to the sex. The youngest and the oldest affected males, were 36 and 92 y old, while the same parameters for females, were 30 and 100, in that order.

According to relationship with probands, the numbers and percents of first, second and third degrees were 188 (87.4%), 25 (11.6%) and 2 (0.93%), respectively. Pedigree study showed that the autosomal dominant was the mode of inheritance in 40% of families, autosomal recessive in 8% and the remainder families (52%) have not shown a single-gene or Mendelian mode.

Table1: Frequencies of the individuals with essential hypertension according to the age groups at the time of diagnosis and the sex.

	≤ 50		51-60 y		61-70 y		≥ 71		Total	
	No.	(%)	No.	(%)	No.	(%)	No	(%)	No.	(%)
Females	80	42.33	62	32.80	39	20.64	8	4.23	189*	100
Males	32	40.0	23	28.8	21	26.3	4	5.0	80*	100
Total	112	41.6	85	31.6	60	22.3	12	4.5	269*	100

* Differences between these numbers with the total number of our cases are because of missing values.

Table2: Frequencies of the individuals with essential hypertension according to the age groups at the time of study and the sex.

	≤ 50		51-60 y		61-70 y		≥ 71		Total	
	No.	(%)	No.	(%)	No.	(%)	No.	(%)	No.	(%)
Females	40	20.0	51	25.5	61	30.5	48	24.0	200	100
Males	16	19.3	21	25.3	26	31.3	20	24.1	83	100
Total	56	19.8	72	25.4	87	30.7	68	24.0	283	100

P= 0.999

Table 3: Statistical descriptive of the diagnosis ages, ages at the time of study and duration of the sickness according to the sex of individuals affected with essential hypertension.

Sex	Statistical parameters	Age of diagnosis (A1)	Age at study time (A2)	Sickness duration (A1-A2)
Females	Mean	54.127	62.14	7.92
	Minimum	28.00	30.00	0.00
	Maximum	90.00	100.00	30.00
	S.D.	11.083	12.87	7.51
Males	Mean	54.24	61.78	7.33
	Minimum	30.00	36.00	0.00
	Maximum	81.00	92.00	52.00
	S.D.	11.21	12.05	8.01
Total	Mean	54.16	62.04	7.74
	Minimum	28.00	30.00	0.00
	Maximum	90.00	100.00	52.00
	S.D.	11.10	12.61	7.65

Discussion

According to diagnosis age, the present results showed that the diagnosis in younger age groups was more frequent. This result is adopted with the other reports about the most frequent age for early-onset hypertension (2). In our results, there were no statistical differences between men and women in their distribution in different age groups of diagnosis age. In other words, the mean age of diagnosis in men and women was almost the same.

Our results showed that 10.52% of cases had parental consanguinity which was about half of the same ratio in general population of Hamadan (6). In other words, consanguinity, which is a risk factor for more frequent expression of autosomal recessive traits, was less than general population in this study. This result can show the probable high frequency of the gene or genes involving the EHT in gene pool of Hamadan. Based on the results, the most frequent group of relatives of probands was the first degree relatives (87.44%). This can lead, once more, that our cases were affected with familial essential hypertension. In our work, the multifactorial mode was 52%. Frequencies of autosomal dominant and autosomal recessive were 40% and 8%, respectively. Autosomal dominant pattern of essential hypertension have been reported by other researchers too (1), but reports of autosomal recessive form are very rare (7).

We can conclude that in our ethnic population, as other populations (8), the family history was the most important risk factor for EHT and the most frequent mode of EHT was multifactorial, so they do not obey the single-gene or Mendelian roles for transmission of responsible genes from parents to progenies.

But in notable number of our subject families with EHT the pattern of inheritance, like in some other populations (9, 10) were Mendelian forms. So it is necessary to consider the genetic counseling as a part of our attendance of such families.

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