ORIGINAL ARTICLE

Heritability of fear: Ukrainian experience

CrossMark

O.V. Filiptsova [a,*], **L.A. Atramentova** [b], **Yu.N. Kobets** [c]

[a] Biology Department, National University of Pharmacy, Kharkov, Ukraine
[b] Genetics and Cytology Department, V.N. Karazin Kharkiv National University, Kharkov, Ukraine
[c] Management and Marketing in Pharmacy Department, National University of Pharmacy, Kharkov, Ukraine

Abstract *Background:* A wide range of normal and clinically significant behavior traits, including fears, were intensively studied and heritability coefficients were obtained for many of them. A heritability value is a population-based trait, so it may significantly vary in different human populations. In the former Soviet Union, research on human behavior traits was mostly tabooed. Ukraine is a population with a unique history and cultural background and with a specific multi-ethnic composition. Until 1991, Ukraine was part of the former Soviet Union. The current research is devoted to heritability of fear assessment in Ukrainian megapolice sample.

Subjects and methods: 2305 individuals (741 males and 1564 females), aged 14–72 years, participated in the current study. Data were collected during 2004–2007. All participants lived in Ukraine and were Slavs (predominantly Ukrainians and Russians). Most of them were Kharkov city residents (Kharkov is the second city in Ukraine by its population size after the capital Kiev city, and Kharkov region includes about 1,730,000 inhabitants). Most participants were engaged without relatives and were used only for population distribution evaluation. Some volunteers were enrolled with a relative of the first degree of relatedness (with a parent or a sibling). These formed 352 parent–offspring pairs and 104 sibling pairs. Spouses were enrolled in the experiment for a potential assortative mating effect searching. The total number of marital couples was 74.

24 emotional states of fear have been studied by Ivleva–Shcherbatyh questionnaire, which was developed and validated by Russian psychologists in Slavs samples.

Evaluation and decomposition of total phenotypic variance were performed according to the classical Falconer approach, based on correlation coefficients between relatives. Assortative mating effect was taken into account and correlation coefficients between relatives were adjusted for traits with statistically significant correlation coefficients between wives and husbands.

Results: As a result of the research, correlation coefficients of fears ρ between relatives and mates were obtained in the range 0.18–0.77. In majority of cases, correlation coefficients were higher in sibling pairs compared to «parent–offspring» pairs. For three fears (psychiatric disorders development, disease of relatives, and suicide commitment) there was a positive assortative mating in the population (correlation coefficients ρ were in the range 0.35–0.43), so for these traits, correlation

---

* Corresponding author. Address: Biology Department, National University of Pharmacy, Pushkinska Street, 53, Kharkov 61002, Ukraine. Tel.: +380 984099100.
E-mail address: philiptsova@yahoo.com (O.V. Filiptsova).

coefficients' modification between relatives was needed to be done. Heritability coefficients of nine types of fear were in the range 26–48%, among them the lowest heritability coefficient was recorded for fear of suicide commitment and the highest one was recorded for fear of aggressive behavior possibility to the relatives.

Conclusions: The conducted research demonstrated genetic component presence for nine types of fear – psychic disorder development, complications in personal life, making responsible decisions, senility, closed spaces, sexual dysfunction, suicide commission, speaking in public, and aggressive behavior possibility to relatives. It helps to consider these fear perspectives for further molecular-genetic analysis in Ukraine.

© 2014 Production and hosting by Elsevier B.V. on behalf of Ain Shams University.

1. Introduction

The final aim of genetic analysis for any trait is searching for genes, which are responsible for its formation, their localization in a genome, and possible variant. Further analysis targets how products of these genes influence metabolic pathways, leading to trait formation. Many human and other biological species can be traced this way. Generally, it is clear for relatively simple traits, such as blood groups, single-gene diseases, etc. More complicated situation is with the so named, 'quantitative traits', which are associated with many traits of behavior. Nevertheless, such analysis is possible, and its algorithm on the first stage suggests a phenotype inventory, forming heritability estimation. The phenotype inventory means an assessment of trait variability in a population.

Both environmental factors and genes influence human behavior traits. Another thing which should be taken into consideration and can attribute to phenotypes is complex interactions between genes and environment. People in a population vary in the genotypes for behavior traits. The genotypic part is due to a combined effect of all loci, including possible allelic interactions within loci (dominance) and between loci (epistasis). Heritability is the proportion of phenotypic variation (V_P) that is due to variation in genetic values (V_G). Broad-sense heritability can be calculated as $h^2 = V_G/V_P$ and demonstrates the proportion of phenotypic variation due to genetic values that may include effects due to dominance and epistasis. Narrow-sense heritability can be calculated as $h^2 = V_A/V_P$ and shows only that proportion of genetic variation that is due to additive genetic values (V_A). The value of heritability always lies between 0 and 1 (or between 0% and 100%) [1].

After heritability assessment, further analysis is conducted due to the heritability value. If a heritability coefficient is close to zero, we can make a conclusion that inter-individual differences are caused by different environmental conditions. On the contrary, if h^2 is close to one, a quite opposite conclusion can be made (inter-individual differences are mostly due to genetic differences). Proof of a genetic influence makes a sense for a further gene search. Without prior population analysis and heritability estimation, the search of these genes is ineffective [2].

A wide range of normal and clinically significant behavior traits were intensively studied and heritability coefficients were obtained for many of them, such as mental ability [3,4], altruism and aggression [5,6], suicidal behavior [7,8], borderline personality disorder [9], fears [10–12] etc.

The trait which is often under study in genetic investigations is fear. In some cases, the intensity of fear can go beyond a normal range (often in the strengthening side). Strong intensity of fear to a stimulus of inadequate strength is a component of mental disorders, particularly, panic attacks, phobias, and obsessive–compulsive syndrome. The prevalence of such disorders in the world population is relatively high [13], weakening people's health and quality of life [14].

Nonetheless, in spite of many studies done on fear, many questions are not yet clarified. Moreover, a heritability value is a population-based trait, so it may significantly vary in different human populations. In the former Soviet Union, research on human behavior traits was mostly tabooed. Ukraine is a population with a unique history and cultural background and with a specific multiethnic composition [15–18]. Until 1991, Ukraine was part of the former Soviet Union. The current research will fill some gaps on the "behavioral map" of Ukraine in relationship with fear heritability estimation.

2. Subjects and methods

2.1. Subjects

2305 individuals (741 males and 1564 females), aged 14–72 years, participated in the current study. Data were collected during 2004–2007. All participants lived in Ukraine and were Slavs (predominantly Ukrainians and Russians). Most of them were Kharkov city residents (Kharkov is the second city in Ukraine by its population size after the capital Kiev city, and Kharkov region includes about 1,730,000 inhabitants).

The volunteers were enrolled randomly in different schools, colleges, and universities of Kharkov city and Kharkov region. They were school children of 10th and 11th classes (schools of Kharkov city Nos. 22, 23, 24, 27, 56, 91, 95, 148 and 156, and the Pesochin Collegium of Kharkov region) or college (Kharkov Building Secondary Technical School) and university (V.N. Karazin Kharkiv National University, National University of Pharmacy, National Technical University "Kharkov Polytechnic Institute" and Kharkov National Medical University) students of different courses (1st–5th), so the age of this subgroup of participants varied from 14 to 23.

Most participants were engaged without relatives and were used only for population distribution evaluation. Some volunteers were enrolled with a relative of the first degree of relatedness (with a parent or a sibling). These formed 352 parent–offspring pairs and 104 sibling pairs.