Genetic aspects of internet-dependence in teenagers

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Internet addiction (IA) is a relatively new psychological phenomenon having signs of a social epidemic, specifically attributed to vulnerable groups (adolescents and young adults). The prevalence of IA among adolescents varies depending on the ethnosocial groups studied and the diagnostic criteria used, from 1% to 18%.

The genetic component of developing Internet addiction was shown by twin studies using various populations, however, to date, the specific genes involved in the mechanisms of such heritability are not exactly identified. Pilot studies verified some polymorphic sites of several candidate genes, including: rs1800497 (dopamine D2 receptor (DRD2) gene, Taq1A1 allele) and rs4680 (methionine variant of dopamine degradation enzyme catecholamine-o-methyltransferase (COMT) gene) and rs2229910 (neurotrophic tyrosine kinase receptor type 3 (NTRK3) gene).

An analysis of ethnogeographic differences of Internet addiction, while taking into account the ethnic differences in the prevalence of genotypic characteristics of populations seems to be relevant and that is not sufficiently explored in modern neurogenetics of addiction in adolescents, especially in such a multinational country as Russia.

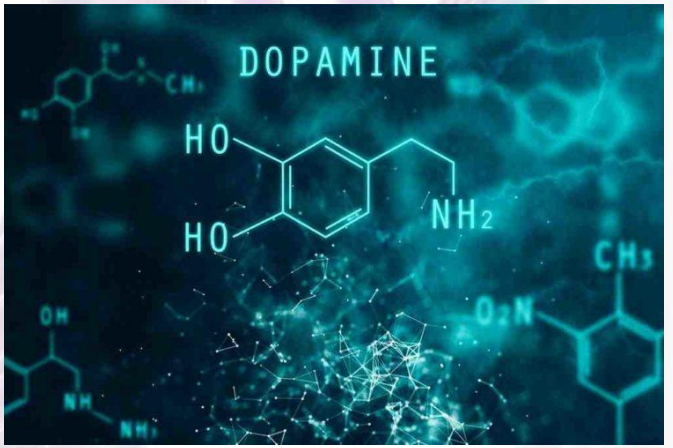
Materials and methods. The overall prevalence assessment of Internet addiction in adolescents of 13-18 years old living in the city of Krasnoyarsk was carried out using the Chen Internet addiction Scale Test (CIAS, S.-H. Chen, 2003) in randomly selected secondary schools. 233 teenagers of Caucasian origin at the age of 13-18 years old were surveyed (average age is 15.3 ± 1.6), with **111 girls** and **122 boys** being involved in the study. DNA was isolated using salting out method. Genotyping of rs1800497, rs4680 and rs2229910 was taken on 302 DNA samples of a population sampling of Caucasians in the Krasnoyarsk Territory using RT-PCR.

Results. An analysis of the content - structure of Internet addiction among adolescents in Krasnoyarsk resulted in the identification of three groups of adolescents:

(1) adolescents with no Internet addiction behavior, a control group (the expected frequency was 60-75%), the detected frequency being 80.3%;

(2) adolescents with a tendency for developing Internet addiction/pre-addictive stage (the expected frequency was 20-30%), the detected frequency being 16.7%;

(3) adolescents with Internet addiction / behavior with an internet abuse component (the expected frequency was 5-10%), the detected frequency being 3.0%.



As a result of the analysis, **7 Internet-dependent adolescents** and 39 adolescents with a tendency to Internet-dependent behavior were identified, they were also paired (corresponding to gender, age and nationality) for sampling the biological material, further DNA extraction and genetic screening of polymorphic genes on IA susceptibility.

We carried out a genotype test of the population sampling of Caucasians in Krasnoyarsk (n = 302) rs1800497 DRD2, rs4680 COMT and rs2229910 NTRK3. The frequencies of genotype distribution were obtained:

rs1800497 DRD2: *CC 59.6%, *CT 40.4%, *TT 0%;
rs4680 COMT:*AA 23.8%, *AG 52.4%, *GG 23.8%;
rs2229910 NTRK3: *CC 37.4%, *CG 46.0%, *GG 16.6%.

The frequency of allelic variants of the studied SNPs corresponds to world data on Caucasoid populations (according to www.ensembl.org).

As a result of increase in the group of teenagers, a comparative analysis of the distribution of polymorphic sites rs1800497, rs4680, rs2229910, rs25532 (serotonin transporter (SS-5HTTLPR) gene) and rs1044396 (nicotinic acetylcholine receptor subunit alpha 4 (CHRNA4) gene) is expected to carry out in adolescents of Central Siberia in order to identify candidate genes of developing Internet addiction.

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