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INVESTIGATION OF THE RS4680 POLYMORPHISM OF THE COMT GENE IN INDIVIDUALS DEPENDENT ON SYNTHETIC CATHINONES AND CANNABINOIDS

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Abstract

This study investigates the rs4680 polymorphism of the COMT gene in individuals dependent on synthetic drugs and healthy individuals. Using molecular-genetic methods and statistical analysis, the research identifies differences in AA genotype frequency and specific haplotypes in addicts, suggesting their potential as markers for susceptibility to synthetic drug dependence.

The study's significance stems from the rising use of synthetic drugs and their severe medical and social consequences. Numerous studies indicate that synthetic cannabinoids and cathinones cause more serious negative effects and are more frequently associated with psychosis compared to their natural predecessors [1, 2]. The COMT gene, encoding an enzyme responsible for the metabolism of catecholamines, plays a key role in regulating neurotransmitters, influencing mental disorders and addictions [3].

The aim of this work is to investigate the rs4680 polymorphism of the COMT gene in individuals dependent on synthetic cathinones and cannabinoids compared to healthy individuals, and to analyze haplotypes of DBH genes: 5'-ins/del (rs141116007), IVS5 C195T (rs2519152), G444A (rs1108580) to identify genetic markers of addiction risk [4].

The study employed polymerase chain reaction, restriction analysis, and statistical methods. These methods were used to analyze DNA samples from 165 individuals dependent on synthetic drugs and 150 healthy individuals.

Statistical analysis included Hardy-Weinberg equilibrium testing and chi-square tests to assess differences in genotype and allele frequencies. The Matplotlib library in Python was used to visualize genotype distribution under the Hardy-Weinberg equilibrium. Haplotypes were analyzed to identify specific combinations associated with addiction.

Analysis of the rs4680 COMT gene revealed differences in AA homozygote frequency between dependent and healthy individuals, but no statistically significant differences were found due to limited sample size. Both groups conformed to the Hardy-Weinberg equilibrium. Among three subgroups of dependents (1. Cathinones, 2. Cannabinoids, 3. Mixed group), the rare AA genotype frequency was higher in the mixed group, while the rare A allele frequency was elevated in the cathinone-dependent group. The highest number of mental disorders was observed in the cathinone-dependent group (13 of 26 cases). Four haplotypes unique to dependent individuals were identified for COMT and DBH genes.

For the first time, frequently occurring combinations of polymorphic loci of the COMT gene (rs4680) (haplotypes) were identified, which may be considered potential markers of risk for developing dependence on synthetic psychoactive substances, contributing to understanding the genetic basis of this condition.

References

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