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THE INTERACTION OF CATECHOL-O-METHYLTRANSFERASE GENE WITH ENVIRONMENTAL FACTORS IN CONTRIBUTION TO RELAPSE OF HEROIN DEPENDENCE PATIENTS IN CHINA

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Introduction: Previous studies have shown that the polymorphisms in COMT gene and environmental factors affect the risk of drug dependence, but there's no research shown in relapse of heroin dependence, and the mechanism underlying remains uncertain.

Objective: Examine the interaction between allelic variants of the catechol-O- methlytransferase (COMT) gene and environmental factors (encountering drug-related environmental situations, social support) in contribution to relapse in heroin dependence.

Aims: Construct the gene-environment interaction model in order to understand the mechanism for relapse in heroin dependence.

Methods: The 249 heroin dependent subjects who followed up at one year after abstinent by using the natural history interview (NHI), social support rateing Scale (SSRS), and other questionnaires were genotyped for eight tagging single nucleotide polymorphisms (SNP) on the COMT gene. General Multifactor Dimensionality Reduction (GMDR) was used to construct the gene-environment interaction model which impacting relapse in heroin dependence.

Results: The relapse group had higher frequencies of encountering drug-related environment (EDE) and G allele and GG genotype frequencies on COMT gene rs4680 locus and less Social Support Scale scores than that in the abstinence group. Logistic regression analysis showed that encountering more drug-related environment and GG genotype carriers were the risk factors for relapse in heroin dependence. GMDR analysis showed that the COMT gene was interact with the frequency of EDE and social support level to impact the relapse in heroin dependence.

Conclusions: Gene-environment interaction between COMT gene and the frequency of EDE and social support were related to heroin dependence relapse.

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