P-40 - LACK OF ASSOCIATION BETWEEN THE VAL158MET CATECHOL-O-METHYLTRANSFERASE GENE POLYMORPHISM AND METHAMPHETAMINE DEPENDENCE

L.Hosak[1], O.Sery[2], M.Beranek[3], M.Alda[4]

[1]Dept. of Psychiatry, Charles University in Prague, Faculty of Medicine and University Hospital, Hradec Kralove, [2]Laboratory of Neurobiology and Molecular Psychiatry, Dept. of Biochemistry, Faculty of Science, Masaryk University, Brno, [3]Institute of Clinical Biochemistry and Diagnostics, Charles University in Prague, Faculty of Medicine and University Hospital, Hradec Kralove, Czech Republic, [4]Dept. of Psychiatry, Dalhousie University, Halifax, NS, Canada

Introduction: About 25 000 serious methamphetamine abusers live in the Czech Republic among the total population of 10 million. Dependence on methamphetamine is markedly related to the brain neurotransmitter dopamine, metabolised by catechol-*O*-methyltransferase enzyme.
Objectives: The objective of our study was to deepen our knowledge on the genetic background of methamphetamine dependence.
Aims: The main aim of the study was to ascertain whether the Val158Met catechol-*O*-methyltransferase gene polymorphism is associated with methamphetamine dependence in the Czech Republic.
Methods: One hundred and twenty-three subjects dependent on methamphetamine (women N=44), parents of sixty-seven dependent individuals, and four hundred healthy controls (women N=250) were involved into the study. We performed a population-based as well as family-based genetic association studies.
Results: We did not find any significant association between the Val158Met catechol-*O*-methyltransferase gene polymorphism and methamphetamine dependence using the population-based or family-based design (P=0.41-0.66; Chi-Square Test or UNPHASED program, Version 3.1.4, respectively). We found a trend toward a statistically significant difference between the Val allele carriers and Met/Met homozygotes in the frequence of psychotic symptoms induced by methamphetamine (more frequent in Val carriers; P=0.062; Chi-Square Test).
Conclusions: Further research involving haplotype analysis and other dopamine-related genetic polymorphisms in large populations is needed. More attention should also be paid to possible role of the Val158Met catechol-*O*-methyltransferase gene polymorphism in individual clinical subtypes of dependence on methamphetamine involving e.g. psychotic features or violence.

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