Abstract:

Introduction: Methamphetamine is a drug frequently abused by drug-addicted pregnant women and also one of the most commonly used drugs in the Czech Republic. This drug passes easily through a placental barrier into the fetus. Thus it can negatively affect not only the mother but also the prenatal development of her offspring.

Objectives: In the framework of the grant project GA CR: 14-03708S, the long-term effects of prenatal exposure to methamphetamine were detected. It was determined whether the prenatal methamphetamine exposure affects the generation of offspring of exposed females at the level of gene expression of genes in specific regions of the brain, striatum, hippocampus and prefrontal cortex.

Methods: In the selected parts of the brain, which were removed from the rat, the microarray hybridization and the real-time PCR to express changes in expression of selected genes were performed.

Results: Statistical analysis of microarray hybridization did not show the significantly altered gene expression in tested genes significantly. Only boundary values for 13 genes were measured, which were further tested by real-time PCR. After a statistic evaluation of real-time PCR, the significantly altered expression was found in 2 genes. The significantly changed expression of DRD3 and TACR3 genes was found only in the striatum, but not in other parts of the brain. For FOXP2 gene, the threshold value of reduced gene expression in the prefrontal cortex was measured. We summarize that prenatal exposure to drug without stress load of descendant does not lead to the significant changes of gene expression in specific regions of the brain of adult offspring. This project could contribute to better understanding of the effect of methamphetamine on the developing brain of the fetus and could better understand the possible neuropsychological effects on a child, prenatally exposed to methamphetamine.

Key words: Metamphetamine, striatum, prefrontal cortex, hippocampus, prenatal exposition, microarrays, real-time PCR