

Altered gene expression in gp120 transgenic mouse brains with different treatments of methamphetamine

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Human immunodeficiency virus (HIV) affects over a million people in the United States, with 69% of HIV patients experiencing some form of HIV-associated neurocognitive disorder (HAND). HAND are neurological disorders, of varying severity, that over time, can lead to a decline in cognitive function. Methamphetamine (METH) abuse and HIV comorbidity can significantly contribute to the progression of HAND. To test whether gene expression was altered by METH use, transgenic mice expressing the HIV protein glycoprotein gp120 (GP120) were injected with a single dose of METH per week, increasing each successive week (1, 5, 10 & 30 mg/kg), and compared to control mice injected with saline on the same weekly schedule. The brains were harvested one week after the last dose and segmented into three parts; front third, left hemisphere, and right hemisphere. RNA was isolated from the homogenized right hemisphere and gene expression was measured using Real Time PCR. Six targets were analyzed for changes in gene expression: GFAP, GP120, TAAR1, TIMP1, EAAT2, and IL1 β . Out of the six targets, a significant increase in GFAP expression was seen in the transgenic GP120 mice when compared to the wild type in both saline and METH injected mice. GP120 gene expression was too low to measure, even among transgenic mice specifically made to express the protein. A preamplification of GP120 may be needed to see measurable results. There were no significant differences observed for the other four targets. METH injections of 1, 5 or 10mg/kg did not cause significant changes in gene expression in these six targets, experiments for the 30mg/kg METH injected mice are in progress. More experiments are needed to determine the impact of METH abuse in HIV+ subjects.

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