



EXPERIENCE OF STAKES IN A RAT GAMBLING TASK INDUCES SELECTIVE GENE DOWN-REGULATION IN SEROTONIN AND DOPAMINE SYSTEMS: A POSSIBLE ROLE FOR EPIGENETIC MECHANISM IN GAMBLING PRONENESS

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Gambling Disorder (GD) is characterized by excessive gambling despite adverse effects on individual functioning. To date, in spite of some positive findings, it is difficult to draw any conclusion on the genetics of GD. Indeed, beyond DNA sequence variation, other regulatory mechanisms (like epigenetic ones) may explain the role of genes in this addiction. Rats underwent an operant-based protocol (Probabilistic-Delivery Task) for the evaluation of individual propensity to gamble. Specifically, rats initially learnt to discriminate and consequently to prefer nose-poking for a large over a small food reward. At this point, few rats were sacrificed to obtain a baseline profile of gene expression at both central and peripheral levels. Subsequently, the probability of occurrence of large-reward delivery decreased progressively to very low levels. Thus, rats were faced with temptation to nose-poke for a binge reward, whose delivery was omitted the majority of times. After 3 weeks of testing, rats showing a clear-cut and extreme profile of either gambling proneness (i.e. sustained preference for large-uncertain reward; "gamblers") or aversion (i.e. marked shift in preference towards small-certain reward; "non-gamblers") were selected and sacrificed 3 hours after last session. To assess gene abundances and to quantify gene promoters' DNA methylation, we used Real-Time RT-PCR and Pyrosequencing respectively. We found, in "gambler" vs. "non-gambler" rats, a selective down-regulation (compared to baseline) of (i) serotonin transporter in prefrontal cortex, (ii) tyrosine hydroxylase in ventral striatum, (iii) dopamine transporter in lymphocytes. Regarding DNA methylation, we observed a consistent increase in one specific CpG site at SERT gene promoter in prefrontal cortex of "gamblers" rats, whereas no changes were detected in the promoter regions of the other two genes under investigation. Elucidation of epigenetic changes occurring during GD progression may pave the way to the development of new therapeutic strategies through specific modulation of epigenetic factors.

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