P-125 - EPIGENETICS OF PANIC DISORDER - EVIDENCE FOR MAO-A GENE HYPOMETHYLATION

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Introduction: The monoamine oxidase A (*MAO-A*) gene has been suggested as a vulnerability gene in the pathogenesis of panic disorder.
Objectives: Epigenetic processes such as methylation critically influencing gene regulation and mediating adaptation to environmental factors have so far not been investigated in panic disorder.
Aims: Thus, in the present study DNA methylation patterns in the *MAO-A* regulatory and exon1/intron1 region were investigated for association with panic disorder.
Methods: Sixty-five patients with panic disorder (m=21, f=44) and 65 healthy controls were analyzed for DNA methylation status at 42 *MAO-A* CpG sites via direct sequencing of sodium bisulfate treated DNA extracted from blood cells. The occurrence of positive and negative life events was ascertained. All subjects were genotyped for the *MAO-A* VNTR.
Results: Male subjects showed no or only very minor methylation. In female patients, significantly lower methylation was observed at ten *MAO-A* CpG sites in the promoter and exon/intron 1 in comparison to healthy controls. Additionally, in female subjects the occurrence of negative life events was associated with a decreased methylation status, while positive life events were associated with relatively increased methylation. Age, smoking status or medication did not influence methylation status, the more active MAO-A VNTR alleles were associated with increased methylation in controls.
Conclusions: The present study suggests a potentially female-specific role of epigenetic alterations, i.e. *MAO-A* gene hypomethylation, in interaction with environmental factors in the pathogenesis of panic disorder. Future studies are warranted to replicate the present finding in independent samples, preferably in a longitudinal design.

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