Mitochondrial genetic variants identified to be associated with posttraumatic stress disorder.

Despite the fact that mitochondrial dysfunctions are increasingly recognized as key components in stress-related mental disorders, very little is known about the association between posttraumatic stress disorder (PTSD) and mitochondrial variants. To identify susceptibility mitochondrial genes for PTSD, we analyzed a total number of 978 mitochondrial single-nucleotide polymorphisms (mtSNPs) in a sample of 1238 individuals participating in the KORA (Cooperative Health Research in the Region of Augsburg) study. Participants were classified with 'no PTSD', 'partial PTSD' or 'full PTSD' by applying the Posttraumatic Diagnostic Scale and the Impact of Event Scale. To assess PTSD-mtSNP association while taking heteroplasmy into account, we used the raw signal intensity values measured on the microarray and applied linear regression. Significant associations were obtained between full versus no PTSD and two mtSNPs: mt8414C->T (\(\beta=-0.954\pm0.06\), \(P_{\text{adjusted}}=0.037\)) located in adenosine triphosphate (ATP) synthase subunit 8 (MT-ATP8) and mt12501G->A (\(\beta=-1.782\pm0.40\), \(P_{\text{adjusted}}=0.015\)) located in the NADH dehydrogenase subunits 5 (MT-ND5). Heteroplasmy for the two variants towards a larger number of the respective minor alleles increases the risk of having PTSD. NADH dehydrogenase and ATP synthase are...
both linked to the regulation of reactive oxygen species. Our results highlight the important role of the mitochondrial genome among the factors that contribute to the risk of PTSD. Mitochondrial genetic variants may be more important than has previously been assumed, leading to further insights regarding effects of existing medications, or even to the development of innovative treatments. As this is the first mitochondrial genome-wide association study for PTSDs, further analyses are needed to follow up on the present findings.