Format: Abstract

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Differential immune system DNA methylation and cytokine regulation in post-traumatic stress disorder.

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Abstract

DNA methylation may mediate persistent changes in gene function following chronic stress. To examine this hypothesis, we evaluated African American subjects matched by age and sex, and stratified into four groups by post-traumatic stress disorder (PTSD) diagnosis and history of child abuse. Total Life Stress (TLS) was also assessed in all subjects. We evaluated DNA extracted from peripheral blood using the HumanMethylation27 BeadChip and analyzed both global and site-specific methylation. Methylation levels were examined for association with PTSD, child abuse history, and TLS using a linear mixed model adjusted for age, sex, and chip effects. Global methylation was increased in subjects with PTSD. CpG sites in five genes (TPR, CLEC9A, APC5, ANXA2, and TLR8) were differentially methylated in subjects with PTSD. Additionally, a CpG site in NPFFR2 was associated with TLS after adjustment for multiple testing. Notably, many of these genes have been previously associated with inflammation. Given these results and reports of immune dysregulation associated with trauma history, we compared plasma cytokine levels in these subjects and found IL4, IL2, and TNFα levels associated with PTSD, child abuse, and TLS. Together, these results suggest that psychosocial stress may alter global and gene-specific DNA methylation patterns potentially associated with peripheral immune dysregulation. Our results suggest the need for further research on the role of DNA methylation in stress-related illnesses.

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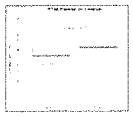


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