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DNA methylation changes associated with insufficient sleep in men

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Sufficient sleep is crucial for our health. Poor sleep affects basic physiological processes, including systemic inflammatory reaction, and leads to an increased risk for various psychiatric and somatic disorders. The assessment and early prevention of long-term risks could be enhanced by identification of key players in molecular processes associated with insufficient sleep. Though sleep is precisely regulated, the detailed mechanisms of brain processes during sleep remain unclear. Since DNA methylation plays critical role in the regulation of gene expression, study of differentially methylated positions (DMPs) might be valuable for comprehensive understanding of the mechanism underlying insomnia. The author performed epigenome-wide association studies for two independent cohorts to identify DMPs in whole blood samples of individuals suffering from insufficient sleep or diagnosed with shift-work disorder. Corresponding genes were analyzed by various tools to investigate affected biological pathways in individuals lacking sleep. The data analysis showed that processes related to neuronal plasticity and neurodegeneration were compromised in people lacking sleep, as well as there is an enrichment of genes involved in visual processing and regulation of circadian rhythm. The results give evidence for importance of the epigenetic regulation in mediating both brain-specific and systemic stress caused by compromised sleep and diurnal rhythm.