A pilot study for circadian gene disturbance in dementia patients

胡朝榮

Liu HC;Hu CJ;Tang YC;Chang JG

摘要

Abstract

Disturbance of circadian gene regulation might contribute to behavioral and psychological symptoms in dementia patients. This study was to evaluate the CpG island methylation status on the circadian gene promoters in dementia patients. We conducted a set of methylation specific polymerase chain reaction (mPCR) followed by nucleotide sequencing to analyze the methylation status within the promoters of nine circadian-related genes, including PER1, PER2, PER3, CRY1, CRY2, CLOCK, BMAL1, TIM and CK1epsilon, in the genomic DNA from the peripheral blood leukocytes of 80 dementia patients and 80 age- and gender-matched controls. A total of seven dementia patients (7/80) had CpG island methylation in the circadian genes and none of the controls had methylation. There were three and four patients had CpG island methylation on the promoters of PER1 and CRY1, respectively. Dementia with Lewy body (DLB) patients had the significantly highest frequency of circadian gene CpG island methylation (35.7%). It suggested that epigenetic methylation of circadian gene was more prevalent in dementia patients, especially for the DLB patients. The significance of circadian gene methylation in clinical behavior/sleep disturbance in dementia patients needs further study.