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Leucocytic DNA methylation of interleukin-6 promoter reduction in pre-hypertensive young adults (Article) (Open Access)

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Abstract

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Background: Pre-hypertension is associated with increased risk of cardiovascular disease. Chronic inflammation plays an important role in the pathophysiology of essential hypertension, with epigenetic dysregulation involvement. Nevertheless, the role of DNA methylation in prehypertensive state is unknown. The aim of this study was to investigate the association between DNA methylation level of interleukin-6 (IL-6) promoter in pre-hypertensive (PreHT) and normotensive (NT) young adults . Methods: A total of 80 NT and 80 PreHT healthy subjects aged between 18–45 years were recruited in Kuantan, Pahang, Malaysia using an observational cross-sectional study approach. DNA methylation level of IL-6 promoter in peripheral leukocytes were measured using bisulphite conversion and MethyLight assay. Results: There was no significant difference in age between NT and PreHT (P = 0.655). The mean blood pressure was 110(8)/73(5) mmHg in NT and 125(7)/82(5) mmHg in PreHT subjects. The IL-6 promoter methylation level was significantly lower in PreHT compared to NT subjects (P < 0.001). Conclusion: The current study demonstrates that hypomethylation of IL-6 promoter was associated with pre-hypertension in young adults . Thus, IL-6 methylation could be used as an early indicator for predicting hypertension and related risk of cardiovascular diseases in prehypertensive subjects. Gene expression and longitudinal studies are warranted to examine the methylation effect on IL-6 expression over time. © Penerbit Universiti Sains Malaysia.

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MethyLight, Omron HEM-7130

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