

## 論文の内容の要旨

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論文題目	<i>NFκB2</i> gene as a novel candidate that epigenetically responds to interval walking training (インターバル速歩トレーニングに対しエピジェネティックに応じる新候補遺伝子, <i>NFκB2</i> )
(論文の内容の要旨)	<p>Physical fitness has been reported to decrease the risk of lifestyle-related diseases. The present study evaluated genome-wide methylation under the hypothesis that interval walking training (IWT) imparted beneficial effects on health, particularly by epigenetically ameliorating susceptibility to inflammation. We screened DNA from peripheral blood samples via genome-wide microarray for genes whose methylation was affected by IWT, paying special attention to promoter regions, and identified over 40 hyper- or hypo-methylated genes following IWT that were not witnessed in controls. We next selected genes in which the degree of methylation change in the promoter region was correlated with energy consumption following IWT. In this way, we found the <i>NFκB2</i> gene to have increased methylation in multiple regions of its promoter sequence following participation in an exercise regimen. Next, IWT-induced <i>NFκB2</i> hyper-methylation was confirmed by a quantitative PyroSequencing assessment of methylation in samples obtained from independent subjects who also underwent IWT. The increase in <i>NFκB2</i> gene promoter methylation by IWT indicates that this regimen may suppress pro-inflammatory cytokines. Thus, these results provide an additional line of evidence that IWT is advantageous in promoting health from an epigenetic perspective by ameliorating susceptibility to inflammation.</p>