

Histone modifications and exercise adaptations

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Exercise is known to increase expression of numerous genes in skeletal muscle and underlying mechanisms are being elucidated. The spatial association between genomic DNA and histone proteins within chromatin plays a key role in the regulation of gene expression and is largely governed by post-translational modifications on histone proteins. Such modifications include phosphorylation, acetylation and methylation. A single bout of exercise alters the intracellular distribution of histone deacetylases, thereby increasing histone acetylation on key residues and metabolic gene expression. Emerging high throughput technologies enable analysis of multiple “epigenetic marks” and gene expression after exercise interventions. Unravelling the complexities of the so-called “histone code” before and after exercise is likely to lead to a greater understanding of the regulation of exercise-induced alterations in skeletal muscle gene expression.