

Exercise Proteomics: Review

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Abstract

Aim: The aim of this review was to discuss the proteomics of exercise. **Results:** The sophisticated protein biochemical and mass spectrometric technologies can now be used to study subtle changes in protein concentration, isoform expression patterns, protein–protein interactions and/or post-translational modifications following physical exercise. **Conclusion:** Rapid advancements in molecular techniques and the streamlining of mass spectrometry-based proteomic workflows have enabled the establishment of global alterations in the concentration, isoform expression patterns, molecular interactions and post-translational modifications of muscle proteins following physical exercise. Recent genetic advances in the field of molecular exercise science will heavily influence the design of future proteomic studies in sports science and sports medicine.

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Introduction

Over the last decade, a large number of scientific breakthroughs have transformed the field of exercise science (Baldwin and Haddad 2010). Our understanding of gene regulation and protein alterations in response to physical exercise has dramatically improved through the application of molecular and cellular analyses of skeletal muscle adaptations. This has involved the clarification of novel structural, functional and metabolic aspects during force generation and physiological adaptability in response to different training regimes (Harridge 2007). Physical exercise triggers various physiological stimuli that involve neuronal, hormonal, metabolic and mechanical signals that are sensed, transduced and integrated in a highly coordinated manner (Flück 2006). The frequent recruitment of specific muscle groups causes long-term alterations in gene expression patterns and special changes in the concentration, isoform repertoire and/or post-translational modifications of skeletal muscle proteins (Booth and Laye 2010). During muscle adaptations, a vital relationship exists between contraction-induced signalling cascades and downstream effects in contractile fibres on the level of gene activation, mRNA processing, protein synthesis and protein assembly, as well as metabolic regulation. Novel integrative approaches attempt to study these effects of physical exercise-induced physiological disturbances on the level of the genome, transcriptome, proteome and metabolome (Petritz et al.2012; Burniston and Hoffman 2011; Hittel et al. 2007).

What is a Proteome?

A proteome indicates the quantitative protein expression profile of a cell, a tissue or an organism under exactly defined conditions. The human genome comprises about 100 000 genes and this gene inventory is applied for a cell type-specific expression of a set of 10 000 genes. One gene will result