**Proteomic response of the rat skeletal muscle after long-term high-intensity training**

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**Abstract:** High-intensity exercise is a common training method, so exploring the mechanism of skeletal muscle response is important for improving the training effect. In this study, we used poteomic analyses to investigate how gstrocnemius muscle proteins responsed to the long-term high-intensity training. 20 Sprague-Dawley rats were randomly divided into control group and exercise group. Whole protein samples of the gstrocnemius muscle were extracted from both groups and analyzed by two-dimensional gel electrophoresis. Compared to the control group, there were 36 protein spots exhibited a >1.5-fold difference in expression, 9 of which was successfully identified by mass spectrometry. The five down-regulated proteins were identified as 5-hydroxytryptamine receptor 2B (5-HTR2B), pyruvate dehydrogenase E1 component subunit alpha (PDH-E1α), proteasome subunit beta type-4 (PSMB4), proteasome subunit beta type-6 (PSMB6) and proteasome subunit beta type-7 (PSMB7), and the three up-regulated proteins were α-actin, creatine kinase M-type (M-CK) and myosin regulatory light chain 2 (MLC2), while adenylate kinase isoenzyme 1 (AK1) was a new protein spot. Notably, 5-HTR2B is related to the neuromuscular excitability, PSMB4, PSMB6 and PSMB7 are involved in protein degradation, α-actin and MLC2 are related to skeletal muscle contraction, while PDH-E1α, M-CK and AK1 are connected with energy metabolism. These findings indicate that the adaptive response of skeletal muscle after long-term high-intensity exercise may be related to the decrease of muscle protein degradation, as well as the enhancement of neuromuscular excitability, muscle contraction and ATP production.

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