

Transcriptome responses in human skeletal muscle to acute and regular aerobic exercise: a meta-analysis

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Inactivity is strongly associated with the development of type 2 diabetes mellitus, cardiovascular diseases, depression, cachexia, and sarcopenia. Regular aerobic exercise is broadly used as a key intervention to prevent and treat these diseases. In our study we aimed to identify and compare (i) the transcriptome responses to acute and regular aerobic exercise in human skeletal muscle and (ii) the biological effects and transcription factors (TFs) associated with these transcriptome changes. We used the robust rank aggregation method to analyze 27 transcriptome datasets for the m. vastus lateralis of healthy humans subjected to acute and/or regular aerobic exercise. We found 493 and 815 differentially expressed genes (DEGs) (mainly up-regulated) for the acute and regular exercise, respectively. Gene Ontology analysis found that acute exercise was associated with regulation of transcription, angiogenesis and response to various stimuli, while regular exercises – with extracellular matrix (ECM) organization and angiogenesis. Surprisingly, only a few genes encoding mitochondrial proteins were up-regulated after acute and regular exercise (18 and 27 out of 1097, respectively). Promoters of DEGs induced by acute exercise were strongly enriched by the TFs belonging to the ATF/CREB/AP-1 superfamily. In turn, promoters of DEGs induced by regular exercise were strongly enriched by the TFs RELB, JUND, ETV4. Summing up, acute exercise mainly induces the expression of genes encoding TFs and other regulators of gene expression. By contrast, regular aerobic exercise up-regulates genes encoding ECM proteins and many ECM regulators, as well as angiogenesis-related genes. Exercise-induced up-regulation of the mitochondrial proteins is not regulated at the mRNA level. This work was supported by the RFBR (no. 19-315-90135).