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Titel des Beitrags: Advances in exercise, fitness, and performance genomics in 2010.

Abstract:
This review of the exercise genomics literature emphasizes the strongest articles published in 2010 as defined by sample size, quality of phenotype measurements, quality of the exercise program or physical activity exposure, study design, adjustment for multiple testing, quality of genotyping, and other related study characteristics. One study on voluntary running wheel behavior was performed in 448 mice from 41 inbred strains. Several quantitative trait loci for running distance, speed, and duration were identified. Several studies on the alpha-3 actinin (ACTN3) R577X nonsense polymorphism and the angiotensin-converting enzyme (ACE) I/D polymorphism were reported with no clear evidence for a joint effect, but the studies were generally underpowered. Skeletal muscle RNA abundance at baseline for 29 transcripts and 11 single nucleotide polymorphisms (SNPs) were both found to be predictive of the VO2max response to exercise training in one report from multiple laboratories. None of the 50 loci associated with adiposity traits are known to influence physical activity behavior. However, physical activity seems to reduce the obesity-promoting effects of at least 12 of these loci. Evidence continues to be strong for a role of gene-exercise interaction effects on the improvement in insulin sensitivity after exposure to regular exercise. SNPs in the cAMP-responsive element binding position 1 (CREB1) gene were associated with training-induced HR...
response, in the C-reactive protein (CRP) gene with training-induced changes in left ventricular mass, and in the methylenetetrahydrofolate reductase (MTHFR) gene with carotid stiffness in low-fit individuals. We conclude that progress is being made but that high-quality research designs and replication studies with large sample sizes are urgently needed.