Basal Molecular Profiles for Predicting Physical Performance Enhancements After Endurance Training

Patel, Krish (School: Casady School)

Understanding the transcriptomic association of athletic performance, including VO2max, is critical for elucidating the interplay between molecular biology and exercise outcomes. Predicting long-term exercise-induced physical performance using quantitative transcriptomic data remains a challenging yet highly desirable goal. In this study, transcriptomic data, encompassing both baseline and acute exercise (0-week) gene expression profiles, was leveraged to develop machine learning-based regression models that predict long-term (12-week) improvements in multiple physical tests, including VO2max, squat weight, and the power test. Transcriptomic and performance data were collected from the PHITE cohort (n = 85), with a subset (n = 57) that incorporated gene expression fold-change profiles at 3 and 24 hours after acute exercise. Baseline expression of key genes, including TTC7A and COL6A1, were associated with VO2max enhancement, enabling predictive models with notable cross-validation (CV) accuracy (R^2 = 0.537 for VO2max; R^2 = 0.437 for power test; R^2 = 0.409 for squat weight). By adding 22 baseline samples and fold-change gene expression, the predictive power of the VO2max model was further improved (CV R^2 = 0.625). A similar approach also improved the power test prediction model (CV R^2 = 0.448). These findings highlight the utility of transcriptomic data, both basal and after acute exercise, in conjunction with regression models to accurately predict long-term exercise-induced VO2max performance. The results underscore the dynamic relationship between the transcriptome and individual variability in athletic trainability over extended training periods, highlighting the promising utility of predictive models in understanding and optimizing long-term physical performance.

Awards Won: