Examining the impact of acute blood flow restricted aerobic exercise on PGC-1α mRNA
expression in young healthy males: A randomized cross-over trial

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Statistical Analysis

Descriptive statistics will be used for baseline participant characteristics. Testing for carryover effects for the primary outcome will be conducted in accordance with the statistical procedures outlined by Wellek and Blettner (Wellek and Blettner 2012). To compare the effect of exercise on mRNA expression within each experimental session and also to compare group means for baseline mRNA expression and changes in mRNA expression between CTL and BFR, paired t-tests will be performed on linear data using the $2^{-\Delta Cq}$ (BL vs. +3 h) and $2^{-\Delta\Delta Cq}$ (CTL vs. BFR) methods (Schmittgen and Livak 2008) with TBP as a housekeeping gene. Average heart rate, lactate, RPM, and ratings of perceived exertion (RPE) during CTL and BFR will be compared using paired t-tests. Corresponding effect sizes for a within-subjects design (G*Power) will be interpreted as small ($d = 0.2$), medium ($d = 0.5$), and large ($d = 0.8$ (Cohen, 1988, pp 284-288). Protein content (+3 hours – PRE; +0 hours - PRE), NIRS, and EMG data from BFR and CTL will be analyzed using with a two-way repeated measures ANOVA (condition x time). Leg specific RPE will be also analyzed using a two-way repeated measures ANOVA (condition x biopsy status). Any significant interaction or main effects will be subsequently analyzed using Bonferroni *post-hoc* analyses. Corresponding effect sizes will be interpreted using partial eta (η) squared values (small = 0.0099; medium = 0.588; large = 0.1379) (Cohen, 1988, pp 284-288). All statistical analysis will be performed using SPSS Version 25 (IBM) and GraphPad Prism Version 8.0. Statistical significance will be set at $p < 0.05$, and all data will be presented as means ± SD.

A priori sample size calculations were calculated for the primary outcome, between-group differences in fold change for PGC-1α mRNA. Power calculations using G*Power revealed that a sample size of 12 was required to detect a statistically significant large effect size ($d = 0.9$, a conservative estimate based on the findings of Christiansen and colleagues (Christiansen et al. 2018)) between BFR and CTL with 80% power ($d = 0.9$, α err prob = 0.05, 1-ß prob = 0.8).

References

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