



Fall 2024

**Biochemistry and Molecular Biology
Brown Bag Series**

**Madhavi Kadakia,
Vice Provost for Research and Innovation**

**Michael Craig,
Research Associate Professor**

*“Epigenetic response to traditional combined
training and high-intensity tactical training: a two-
arm, randomized comparative efficacy trial”*

Tuesday, October 22, 2024

11:00 AM

Location 105 Biological Sciences Building

Lab: Madhavi Kadakia, Ph.D.



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<https://science-math.wright.edu/biochemistry-and-molecular-biology>

Abstract:

The Precision High-Intensity Training through Epigenetics (PHITE) clinical trial (NCT03380923) trial was performed to define the molecular and epigenetic responses and functional adaptations occurring in response to traditional (TRAD) and high-intensity tactical training (HITT). Ninety participants completed 12 weeks of TRAD or HITT training (3 d/wk, supervised) followed by 4 weeks of detraining. Physiologic, epigenetic, performance, body composition, and *ex vivo* tissue-level outcomes were assessed in untrained and trained states at multiple timepoints after exercise and in the detrained state. Both TRAD and HITT prescriptions yielded minimal clinically important differences (MCID) in cardiorespiratory function (CRF) and functional muscle quality (fMQ), with ~90% of participants showing improvement in CRF or fMQ and ~40% showing improvement in both. Muscle-derived and circulating microRNAs have been linked to both exercise adaptation and athletic performance, suggesting their potential utility as biomarkers of fitness. Differential gene expression (DGE) analysis of small RNA sequencing data revealed an immediate (0hr post-exercise) release of exosomal miRNAs in response to exercise and downregulation at 24h post-exercise, while a general upregulation of muscle-derived miRNAs was not observed until 24h post-exercise. Males and females showed largely distinct profiles of differentially expressed miRNA in response to exercise. A miRNA signature of detraining was clearly evident in muscle. In parallel, 205 miRNAs with significant associations to MCID response or training state were identified using multidimensional modeling of miRNA read count data and associated metadata. Of these, 33 miRNAs were also present in the DGE pipeline and thus characterized as robust biomarkers of the exercise response. Taken together, our data provide critical insights into the kinetics and interindividual heterogeneity of the circulating and muscle miRNA response to TRAD and HITT exercise.