

Sex-specific epigenetic adaptations to endurance exercise

S. Landen,¹ S. Voisin,¹ S. Lamon² and N. Eynon,¹ ¹Institute for Health and Sport, Victoria University, Melbourne, VIC 3011, Australia and ²Institute for Physical Activity and Nutrition, School of Exercise and Nutrition Sciences, Deakin University, Geelong, VIC 3216, Australia.

Males and females are adapting to exercise training differently, and epigenetics is emerging as a potential mechanism underpinning those differences. Epigenetic modifications are structural adaptations of chromosomal regions that bring about altered gene expression and include mechanisms such as DNA methylation and microRNAs (miRNAs). While exercise training is known to remodel the skeletal muscle epigenome, it is still unknown whether it does so differently in men and women, leading to sex-specific physiological adaptations. In the Gene Skeletal Muscle Adaptive Response to Training (SMART) study, we investigated DNA methylation and miRNA expression changes following an acute bout and four weeks of high-intensity interval training (HIIT) in 25 healthy men; the same analysis on 20 women is ongoing. Using a linear model adjusted for age, we found that epigenetic patterns can predict baseline fitness levels with high accuracy (adjusted R² = 0.96), and we identified 3111 differentially methylated loci after 4 weeks of HIIT (FDR < 0.005) in men. The comparison of male and female epigenetic profiles following exercise may uncover different genes that are contributing to the exercise response in the sexes.