Exercise-Related Epigenetic Changes in Human Blood: Insights from Active and Sedentary Subjects

[1]Proia, P., [2]Volpes, S., [2]Cardinale, P.S., [3]Rappa, F., [3]Palladino, L., [3]Barone, R., [3] Cappello, F., [1]Pagliaro, A., [1]Alioto, A., [4]Boatta, A., [4]Messina, G., [2]Naselli F.

[1]Department of Psychology, Educational Science and Human Movement, Sport and Exercise Sciences Research Unit, University of Palermo, Italy

[2]Department of Biological, Chemical and Pharmaceutical Sciences and Technologies, University of Palermo, Palermo, Italy

[3]Department of Biomedicine, Neurosciences and Advanced Diagnostics (BiND), University of Palermo, 90127 Palermo, Italy

[4]Department of Human Sciences and Promotion of the Quality of Life San Raffaele University Rome (Italy)

Physical activity (PA) is well-established as a pivotal factor influencing overall health and disease risk; however, its molecular underpinnings remain an active area of research. Emerging evidence suggests that epigenetic mechanisms—such as DNA methylation, histone modifications, and non-coding RNA regulation—play a crucial role in mediating the health benefits associated with regular exercise. This study aimed to investigate how physical activity modulates epigenetic patterns in humans, focusing on a comparative analysis between physically active and sedentary individuals.

The research was conducted on ten adult participants divided into two groups: five athletes engaged in regular, structured training programs, and five sedentary controls. Peripheral blood samples were collected from all participants to assess systemic epigenetic changes, given the blood's accessibility and its reflection of whole-body physiological states. Epigenetic profiling was performed utilizing Methylation-Sensitive Arbitrarily-Primed PCR (MeSAP-PCR) to assess the possible genomewide changes in DNA methylation and Methylation-sensitive restriction endonuclease-PCR (MSRE-PCR) to study gene promoter methylation status of gene associated with oxidative metabolism, mitochondrial function and anti-inflammatory pathways.

Preliminary results revealed distinct epigenetic signatures between the two groups.Regular physical activity has been associated with favorable epigenetic modifications, including changes in global DNA methylation patterns. In cohorts of individuals engaged in consistent exercise training, studies have observed a trend toward global DNA hypermethylation. This epigenetic adaptation is believed to contribute to enhanced genomic stability, reduced expression of pro-inflammatory genes, and improved cellular function. Furthermore, athletes exhibited hypomethylation at promoter regions of genes associated with oxidative metabolism, mitochondrial function, and anti-inflammatory pathways, suggesting an epigenetic upregulation conducive to enhanced physiological performance and health. Conversely, sedentary individuals displayed hypermethylation in similar gene regions, potentially reflecting a suppressed expression profile linked to reduced metabolic efficiency.

These findings support the hypothesis that long-term exercise not only influences specific gene expression but may also play a protective role in maintaining genome integrity and

promoting healthy aging. The data underscore the potential of exercise as a non-pharmacological epigenetic modulator, capable of reprogramming gene expression patterns relevant to healthspan and disease prevention. Further research involving larger cohorts and longitudinal designs is warranted to elucidate causative relationships and quantify the durability of these epigenetic changes over time.

In conclusion, this study advances our understanding of the molecular basis of exercise benefits, highlighting epigenetic modifications as a key mechanism through which physical activity influences gene regulation. These insights pave the way for personalized exercise interventions targeting epigenetic pathways, ultimately contributing to optimized health outcomes.

References

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