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The Role of DNA Methylation in Regulating Skeletal Muscle Adaptation to Exercise: A Literature Review

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Abstract

Introduction: The skeletal muscle tissue has a remarkable degree of plasticity. In the case of exercise training, the skeletal muscle adapts to match the specific stress imposed by the training modality. Aerobic exercise training promotes oxidative metabolism, angiogenesis, and fiber type switching from type IIb to IIa. Conversely, resistance exercise training promotes muscle protein synthesis and a hypertrophic response of the skeletal muscle. Regardless of training modality, the tissular adaptation of the skeletal muscle is a consequence of underlying changes in gene expression. Changes in promoter DNA methylation regulate genes' activation, or silencing, by influencing euchromatin and heterochromatin organization, respectively, determining chromatin accessibility to transcriptional machinery. It surmises that dynamic DNA methylation mechanisms would regulate acute exercise-responsive genes in skeletal muscle. In the context of exercise training, alterations in DNA methylation of gene promoters could support long-term changes in gene expression or restrict the responsiveness of acute exercise genes.

Methods: This literature review involves a comprehensive search of peer-reviewed articles published after the year 2000 in databases including UBC Library, PubMed, Google Scholar, and Web of Science. Articles selected for inclusion were screened based on relevance to the topic and quality of evidence. Data extraction was focused on identifying key findings related to DNA methylation changes in skeletal muscle following exercise interventions.

Results: Resistance training alters DNA methylation in skeletal muscle, enhancing genes for muscle growth and strength. Aerobic training reduces DNA methylation, boosting genes for mitochondrial biogenesis, glucose metabolism, and muscle endurance.

Discussion: The discussion highlights that aerobic and resistance training induce long-term epigenetic modifications in skeletal muscle, creating a "memory" enhancing muscle adaptability and performance in future exercises. These findings improve our understanding of the epigenetic and molecular mechanisms that regulate muscle hypertrophy and adaptation, which could eventually contribute to the development of therapeutic strategies for muscle-wasting diseases and metabolic disorders. This emphasizes the potential for personalized exercise regimens to optimize health outcomes.

Conclusion: This literature review emphasizes the pivotal role of DNA methylation in skeletal muscle adaptation to exercise, highlighting the distinct epigenetic modifications induced by aerobic and resistance training that enhance muscle function and metabolic health.

Keywords: DNA methylation; skeletal muscle; aerobic exercise; resistance exercise; exercise training; CpG island

Introduction

Skeletal Muscle: Skeletal muscle, comprising approximately 40% of the total body weight in humans, is one of the most dynamic and adaptable tissues in the body [1]. Skeletal muscle contains 50 -75% of all body proteins and significantly contributes to overall protein turnover [1]. The composition of skeletal muscle includes 75% water, 20% protein, and 5% other substances such as inorganic salts, minerals, fats, and carbohydrates [1]. Muscle mass is influenced by the balance between protein synthesis and degradation, which are sensitive to various factors including nutritional status, hormonal balance, physical activity, and health conditions [1]. Skeletal muscle is integral to a multitude of physiological functions including locomotion, thermoregulation, and glucose homeostasis [2]. In addition to these roles, skeletal muscle is also essential for posture maintenance and protection of internal organs [3].

Structurally, skeletal muscle is composed of muscle fibers, which are long, cylindrical cells containing multiple nuclei. These fibers are grouped into bundles known as fascicles, which are surrounded by connective tissue [1]. Skeletal muscle fibers can be classified into three primary

types based on their contraction speed and metabolic properties: Type I (slow-twitch), Type IIa (fast-twitch oxidative), and Type IIb (fast-twitch glycolytic) [3].

Type I fibers are characterized by their high oxidative capacity and endurance, utilizing aerobic metabolism to produce energy. They contain a high density of mitochondria and myoglobin, which supports sustained activity such as long-distance running [2]. In contrast, Type II fibers are adapted for rapid and forceful contractions. Type IIa fibers combine oxidative and glycolytic metabolism, making them suitable for activities requiring both endurance and strength, while Type IIb fibers rely primarily on anaerobic glycolysis, making them ideal for short, intense bursts of activity [3].

Metabolically, these fiber types differ significantly. Type I fibers are rich in enzymes for aerobic respiration and have a high capillary density, facilitating efficient oxygen delivery and utilization. Type IIa fibers, on the other hand, are characterized by a relatively high mitochondrial content and moderate glycolytic enzyme activity, allowing for sustained energy production under both aerobic and anaerobic conditions [3]. Type IIb fibers possess a greater concentration of glycolytic enzymes and a lower mitochondrial density, enabling rapid ATP production through glycolysis but resulting in quicker fatigue [2].

Skeletal muscle demonstrates remarkable plasticity, particularly in response to exercise. Exercise-induced adaptations include fiber type switching, increased mitochondrial density, and enhanced lipid and glucose metabolism [4]. For instance, endurance training can induce a transition from Type IIb to Type IIa fibers, enhancing oxidative capacity and fatigue resistance [5]. This plasticity is also evident in the increased mitochondrial volume observed after endurance training, which improves the muscle's oxidative metabolism [6]. Additionally, exercise enhances lipid utilization and glucose uptake, contributing to improved metabolic health [5]. Satellite cells play a crucial role in this process by proliferating and differentiating to repair or form new muscle fibers, thereby facilitating muscle regeneration and adaptation [7].

Aerobic exercise, characterized by activities such as running and cycling, relies predominantly on aerobic metabolism and involves sustained, rhythmic contractions of large muscle groups [2]. Aerobic training, over the long term, enhances cardiovascular and muscular endurance through increased mitochondrial density and capillary networks [4]. Resistance exercise, including weightlifting and resistance band exercises, involves short bursts of high-intensity contractions, primarily engaging anaerobic energy systems. Long-term resistance training leads to increased muscle mass and strength through muscle hypertrophy, the enlargement of muscle fibers [5].

Muscle hypertrophy occurs as a result of increased protein synthesis within muscle fibers, leading to greater muscle cross-sectional area and enhanced force production [6]. The extent of hypertrophy varies between muscle fiber types; Type II fibers typically exhibit a more pronounced hypertrophic response compared to Type I fibers due to their greater capacity for protein synthesis and larger initial size [5].

DNA Methylation: DNA methylation is a crucial epigenetic modification involving adding a methyl group to the DNA molecule, typically at the 5' position of cytosine rings within CpG dinucleotides. This modification plays a significant role in regulating gene expression and maintaining genomic stability. CpG islands, regions rich in cytosine and guanine nucleotides, are often located near gene promoters and serve as key sites for methylation, which can significantly influence gene transcription [8].

The methylation of CpG islands often leads to gene silencing. Methyl groups inhibit the binding of transcription factors and other proteins essential for gene activation. This silencing effect is mediated through the recruitment of methyl-CpG-binding domain proteins (MBDs). These proteins attract additional molecules, such as histone deacetylases (HDACs) and chromatin-remodeling complexes, which remove acetyl groups from histones and promote histone methylation. This results in tighter packing of the chromatin into a condensed, transcriptionally inactive state known as heterochromatin. In contrast, regions of the genome that lack methylation are typically associated with a more open chromatin state, referred to as euchromatin, which is accessible for transcription and gene expression [8].

Key enzymes responsible for DNA methylation are DNA methyltransferases [DNMTs], including DNMT1, DNMT3a, and DNMT3b. DNMT1 primarily maintains methylation patterns after DNA replication, ensuring that methylation marks are accurately propagated during cell division. DNMT3a and DNMT3b, however, are involved in de novo methylation, establishing new methylation patterns during early development and in response to environmental factors [9].

A common misconception is that the structure of DNA and its associated chromatin is static. However, it is now well-understood that chromatin is highly dynamic. This dynamism allows for the regulation of gene expression in response to various physiological signals, including exercise. The reversible nature of DNA methylation and other epigenetic modifications facilitates this dynamic behavior, allowing for the addition or removal of these modifications in response to environmental and developmental cues, thereby altering chromatin structure and gene expression patterns [10].

DNA demethylation dynamics refer to the intricate processes that remove methyl groups from DNA, thus reversing DNA methylation. This demethylation is crucial for regulating gene expression, embryonic development, and cellular differentiation. It occurs through passive and active mechanisms: passive demethylation happens during DNA replication when maintenance methylation is inhibited, while active demethylation involves specific enzymatic pathways, such as those mediated by the TET (ten-eleven translocation)

family of enzymes. TET enzymes oxidize 5-methylcytosine to form intermediates like 5-hydroxymethylcytosine, which are further processed and eventually replaced with unmethylated cytosine. This dynamic balance of methylation and demethylation is essential for maintaining cellular function and genomic stability, and its dysregulation is associated with various diseases [11].

DNA methylation is a reversible process that is critical in regulating chromatin state and gene expression. This epigenetic modification, mediated by DNMT enzymes, influences whether regions of the genome are in a transcriptionally active euchromatin state or a repressive heterochromatin state.

Given the dynamic nature of skeletal muscle and its ability to adapt to various forms of exercise, understanding the mechanisms of DNA methylation and its effects on chromatin dynamics is essential for elucidating how gene expression is regulated in response to various physiological stimuli, including exercise. This review aims to investigate the specific role of DNA methylation in regulating skeletal muscle adaptation to different exercise modalities, including aerobic and resistance training. By examining the existing literature, this study seeks to explore how changes in DNA methylation contribute to the long-term and acute adaptations observed in skeletal muscle in response to exercise. The following sections will examine the effects of resistance and aerobic exercise on DNA methylation, exploring how these changes influence muscle function and metabolic health.

Methods

A review was conducted to investigate the role of DNA methylation in regulating skeletal muscle adaptation to exercise. A search was performed among peer-reviewed articles published after the year 2000 in databases including UBC Library, PubMed, Google Scholar, and Web of Science using keywords such as "DNA methylation," "skeletal muscle," "aerobic exercise," "resistance exercise," "exercise training," and "CpG island." Not all papers were included. The inclusion criteria were studies published in peer-reviewed journals focusing on DNA methylation changes in skeletal muscle in response to aerobic and/or resistance exercise, involving human participants or animal models, and available in English. Exclusion criteria were review articles, meta-analyses, case studies, studies that did not specifically examine DNA methylation changes in skeletal muscle, and articles not accessible in full text.

To ensure the inclusion of high-quality evidence, articles were further assessed based on their methodological rigor and study design. Studies were prioritized if they utilized randomized controlled trials (RCTs), longitudinal designs, or robust experimental models with appropriate controls. Additional criteria for determining quality included sample size adequacy, clear definition of exercise interventions, accurate and reproducible methods for assessing DNA methylation, and thorough reporting of results, including statistical significance and effect sizes. Studies that did not meet these quality standards were excluded to maintain the reliability and relevance of the findings presented in this review.

Data extraction from the selected studies was carried out using a standardized form to ensure consistency and comprehensiveness. The extracted data included details about the authors and publication year, the type of exercise intervention (aerobic or resistance), the duration and intensity of the exercise regimen, the methods used to assess DNA methylation, and the specific genes and loci analyzed for methylation changes. This systematic approach ensured that the review comprehensively covered the existing literature on how DNA methylation influences skeletal muscle adaptation to different types of exercise.

Results

Effects of Resistance Training on DNA Methylation: Resistance training is defined as high-intensity interval training, such as weightlifting, that leads to significant changes in the DNA methylation landscape of skeletal muscle. These changes are critical for muscle hypertrophy and increased strength associated with this type of exercise. Studies have demonstrated that resistance training induces site-specific alterations in DNA methylation, particularly in gene promoters related to muscle growth, repair, differentiation, and metabolism [10, 12]. These epigenetic modifications are associated with changes in gene expression, with hypomethylation often correlating with increased transcription of genes involved in increased muscle size and strength [10]. For instance, acute exercise has been shown to induce hypomethylation in promoter regions of key genes such as PGC-1α, PDK4, and PPAR-δ, coinciding with their increased expression [13]. Importantly, some genes exhibit retained hypomethylation even after detraining, suggesting an epigenetic memory mechanism in skeletal muscle [10]. These findings highlight the importance of DNA methylation in regulating the adaptive response of skeletal muscle to resistance exercise.

One notable example of resistance training affecting DNA methylation is the modulation of the myostatin gene (MSTN). Myostatin is a negative regulator of muscle growth, and its expression is tightly controlled by DNA methylation. Resistance training has been shown to decrease the methylation of the MSTN promoter region, resulting in reduced myostatin expression [10]. This demethylation promotes muscle growth by lifting the inhibitory effects of myostatin on muscle cell proliferation and differentiation. The reduction in MSTN promoter methylation was observed in acute and chronic resistance training groups, highlighting the immediate and long-term epigenetic adaptations to this form of exercise [14].

Resistance training also influences the methylation status of genes involved in metabolic pathways. For example, PGC-1α (peroxisome proliferator-activated receptor gamma coactivator 1-alpha), a key regulator of

mitochondrial biogenesis and oxidative metabolism, exhibits altered methylation patterns in response to resistance exercise [15]. The promoter region of PGC-1α tends to become hypomethylated following resistance training, facilitating its expression [16]. This change supports enhanced mitochondrial function and energy metabolism in muscle cells, contributing to improved muscle endurance and metabolic health [13].

Another significant area of impact is the regulation of inflammatory and stress response genes. Resistance training modulates the methylation of genes such as IL-6 and TNF-α, which are involved in the inflammatory response. Hypermethylation of these gene promoters can reduce their expression, thereby mitigating chronic inflammation and promoting a more favorable environment for muscle repair and growth. This epigenetic regulation helps in balancing the inflammatory response, ensuring that it is sufficient to support muscle adaptation without causing excessive tissue damage [17].

Impacts of Aerobic Training on DNA Methylation: Aerobic training has been widely recognized for its benefits on cardiovascular health, metabolic function, and overall physical well-being [1]. Several studies have demonstrated that aerobic exercise can lead to significant changes in DNA methylation in skeletal muscle [7]. For instance, exercise training has been shown to reduce global DNA methylation levels, which is associated with the activation of metabolic genes that are otherwise repressed [18]. This hypomethylation can enhance the expression of genes involved in mitochondrial biogenesis, glucose metabolism, and muscle fiber type specification [18].

Research has identified specific genes that undergo methylation changes in response to aerobic training. In one study, 13 increased and 90 decreased differentially methylated cytosines [DMCs] were identified following 8 weeks of aerobic training [18]. Among the genes with decreased methylation were those involved in metabolic pathways, such as CNGA1, FCGR2A, KIF21A, and MEIS1, which play roles in glucose metabolism, immune response, and cellular signaling [18].

The reduction in DNA methylation observed in genes such as CNGA1 and FCGR2A suggests an increased gene expression that can enhance metabolic processes critical for improved muscle function and endurance [18]. CNGA1 is involved in cyclic nucleotide-gated channels, influencing cellular signaling and muscle contraction [18]. FCGR2A plays a role in immune function and inflammation, which are crucial during the muscle adaptation process post-exercise [18].

Aerobic exercise is known to promote mitochondrial biogenesis, the process by which new mitochondria are formed within cells, enhancing the oxidative capacity of skeletal muscle [2]. This process is partly regulated by DNA methylation changes. Genes such as PGC-1α, a key regulator of mitochondrial biogenesis, can be epigenetically modified by exercise, leading to increased gene expression and mitochondrial content [18].

Aerobic training can induce fiber type switching from fast-twitch glycolytic fibers (Type II) to slow-twitch oxidative fibers (Type I), which are more efficient in utilizing oxygen for energy production [5]. This switch is accompanied by changes in DNA methylation in genes regulating muscle fiber type. For example, the hypomethylation of genes involved in oxidative metabolism can enhance the oxidative capacity and endurance of skeletal muscle [18].

Improvements in insulin sensitivity following aerobic exercise are also linked to changes in DNA methylation. Training enhances insulin-stimulated glucose uptake by skeletal muscle, a process that is regulated by genes whose expression is influenced by methylation status [18]. For instance, exercise-induced hypomethylation of the GLUT4 gene, which encodes a glucose transporter, can increase its expression and improve glucose disposal in muscle cells [18].

Molecular Mechanisms of DNA Methylation in Metabolic Gene Regulation: In response to exercise, the methylation of metabolism-associated genes is dynamically regulated by a balance between DNMTs and demethyltransferases, such as TET enzymes [13]. DNMTs, particularly DNMT3a and DNMT3b, catalyze the addition of methyl groups to cytosine residues within CpG islands, typically silencing genes linked to metabolic pathways. In the context of exercise, downregulation of DNMT3a activity has been shown to contribute to hypomethylation at promoter regions of key metabolic genes such as PGC-1α and PDK4, which are pivotal for mitochondrial biogenesis and fatty acid oxidation [13]. This hypomethylation enhances gene transcription, thus increasing the capacity for oxidative metabolism in skeletal muscle. Conversely, TET enzymes, including TET1 and TET2, mediate active DNA, initiating the process of removing methyl marks. This demethylation is crucial for the reactivation of genes that had been repressed under basal conditions. Exercise-induced TET activity promotes the expression of genes regulating glucose uptake, lipid metabolism, and energy homeostasis, thereby fine-tuning the epigenetic landscape to optimize the metabolic response to exercise [11]. Together, these molecular mechanisms facilitate an adaptive enhancement of metabolic function in response to both acute and long-term exercise stimuli [11].

Discussion

Long-term epigenetic memory in skeletal muscle refers to the sustained changes in DNA methylation patterns resulting from previous exercise stimuli. Studies indicate that these epigenetic modifications can persist even after periods of detraining, meaning the muscle retains a "memory" of past exercise at the molecular level [18]. This retained hypomethylation or hypermethylation in specific

gene promoters can influence gene expression, making the muscle more responsive to subsequent training. For instance, genes involved in muscle growth, repair, and metabolism may remain hypomethylated, facilitating quicker and more efficient adaptations during future exercise sessions. Consequently, this epigenetic memory enhances the muscle's overall adaptability and performance, providing a molecular basis for the long-term benefits of regular exercise [18].

Understanding the epigenetic modifications induced by aerobic and resistance training can aid in the development of targeted therapies for muscle-wasting diseases, such as sarcopenia and cachexia [19]. By manipulating DNA methylation patterns, it may be possible to enhance muscle growth and function in individuals suffering from these conditions [10]. Additionally, aerobic and resistance training-induced epigenetic changes could be harnessed to improve metabolic health, offering new strategies for managing obesity, type 2 diabetes, and other metabolic disorders [18, 20, 21]. This knowledge also emphasizes the importance of incorporating resistance training into rehabilitation programs for older adults and patients recovering from chronic illnesses, to promote muscle strength, functional independence, and overall health.

Although both training types induce DNA methylation changes that improve muscle function and metabolic health, it is evident that both forms of exercise induce specific and distinct epigenetic modifications which should be considered for more personalized clinical implications. Aerobic exercise primarily reduces global DNA methylation, promoting the activation of genes involved in mitochondrial biogenesis, glucose metabolism, and muscle fiber type specification [18]. This leads to improved oxidative capacity, insulin sensitivity, and endurance, facilitated by the hypomethylation of key metabolic genes such as PGC-1α and GLUT4 [18]. On the other hand, resistance training induces site-specific hypomethylation, particularly in gene promoters related to muscle growth and differentiation, such as PGC-1α, MSTN, and inflammatory response genes like IL-6 and TNF-α [10]. These changes support muscle hypertrophy, strength gains, and a favorable inflammatory environment for muscle repair [14]. Importantly, both types of exercise can induce long-term epigenetic adaptations, reflecting an epigenetic memory that enhances muscle responsiveness to future exercise stimuli [10, 18].

Conclusions

This literature review underscores the critical role of DNA methylation in skeletal muscle adaptation to exercise. Aerobic exercise primarily reduces global DNA methylation, enhancing mitochondrial and metabolic gene expression, while resistance exercise induces site-specific hypomethylation, promoting muscle growth and differentiation. These epigenetic modifications significantly contribute to muscle function and metabolic health.

The importance of this study lies in its elucidation of the molecular mechanisms through which exercise influences gene expression and muscle adaptation, providing a deeper understanding of how physical activity can be harnessed to improve muscle function and metabolic health. These insights have significant implications for the development of targeted exercise interventions and therapies aimed at preventing and managing muscle-wasting diseases, metabolic disorders, and enhancing overall health and performance.

Future research should focus on longitudinal studies to further explore the long-term effects of exercise-induced DNA methylation changes and their impact on health outcomes. Additionally, investigating the interplay between different types of exercise, nutritional status, and other environmental factors on epigenetic modifications could provide a more comprehensive understanding of how to optimize exercise prescriptions for personalized health benefits. Ultimately, this knowledge will contribute to the advancement of precision medicine in exercise science, enabling more effective and individualized approaches to health and fitness.

List of Abbreviations

CpG: cytosine-phosphate-guanine
DMC: differentially methylated cytosine
DNA: deoxyribonucleic acid
DNMT: DNA methyltransferase
GLUT4: glucose transporter type 4
HDACs: histone deacetylases
MBD: methyl-CpG-binding domain
MSTN: myostatin
NOS: Newcastle-Ottawa scale
PGC-1α: peroxisome proliferator-activated receptor gamma coactivator 1-alpha
SMD: standardized mean difference
TET: ten-eleven translocation

Conflicts of Interest

The authors declare no conflicts of interest related to this study.

Ethics Approval and/or Participant Consent

This literature review involved the analysis of previously published studies and did not require ethical approval or participant consent.

Authors' Contributions

RA: Focused on the exercise training aspects, including the review and synthesis of the literature on aerobic and resistance training impacts on skeletal muscle. RA contributed to the analysis of how exercise influences DNA methylation and was involved in drafting sections discussing exercise-induced epigenetic modifications especially aerobic exercise and worked on the discussion and conclusion sections of the manuscript.
PS: Contributed to the research and analysis of DNA methylation mechanisms, including the review of relevant

literature and interpretation of epigenetic data. PS was responsible for drafting sections of the manuscript related to DNA methylation and its role in skeletal muscle adaptation. Additionally, PS drafted the section on the impact of resistance training on DNA methylation and worked on the discussion and conclusion sections of the manuscript.

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References

[1] Frontera WR, Ochala J. Skeletal Muscle: A Brief Review of Structure and Function. Calcif Tissue Int. 2015 Mar;96(3):183–95. https://doi.org/10.1007/s00223-014-9915-y
[2] Hoppeler H, Flück M. Plasticity of Skeletal Muscle Mitochondria: Structure and Function: Medicine & Science in Sports & Exercise. 2003 Jan;35(1):95–104. https://doi.org/10.1097/00005768-200301000-00016
[3] Lieber RL, Ward SR. Skeletal muscle design to meet functional demands. Phil Trans R Soc B. 2011 May 27;366(1570):1466–76. https://doi.org/10.1098/rstb.2010.0316
[4] Mukund K, Subramaniam S. Skeletal muscle: A review of molecular structure and function, in health and disease. WIREs Mechanisms of Disease. 2020 Jan;12(1):e1462. https://doi.org/10.1002/wsbm.1462
[5] Smith JAB, Murach KA, Dyar KA, Zierath JR. Exercise metabolism and adaptation in skeletal muscle. Nat Rev Mol Cell Biol. 2023 Sep;24(9):607–32. https://doi.org/10.1038/s41580-023-00606-x
[6] Zhou Y, Zhang X, Baker JS, Davison GW, Yan X. Redox signaling and skeletal muscle adaptation during aerobic exercise. iScience. 2024 May;27(5):109643. https://doi.org/10.1016/j.isci.2024.109643
[7] Grefte S, Kuijpers-Jagtman AM, Torensma R, Von den Hoff JW. Skeletal muscle development and regeneration. Stem Cells Dev. 2007;16(5):857-68. http://doi:10.1089/scd.2007.0058.
[8] Bird A. DNA methylation patterns and epigenetic memory. Genes Dev. 2002 Jan 1;16(1):6–21. https://doi.org/10.1101/gad.947102
[9] Jeltsch A, Jurkowska RZ. New concepts in DNA methylation. Trends in Biochemical Sciences. 2014 Jul;39(7):310–8. https://doi.org/10.1016/j.tibs.2014.05.002
[10] Turner, D.C., Seaborne, R.A. & Sharples, A.P. Comparative Transcriptome and Methylome Analysis in Human Skeletal Muscle Anabolism, Hypertrophy and Epigenetic Memory. 2019; https://doi.org/10.1038/s41598-019-40787-0
[11] Bhutani N, Burns DM, Blau HM. DNA Demethylation Dynamics. Cell. 2011 Sep;146(6):866–72. https://doi.org/10.1016/j.cell.2011.08.042
[12] Kanzleiter T, Jähnert M, Schulze G, Selbig J, Hallahan N, Schwenk RW, et al. Exercise training alters DNA methylation patterns in genes related to muscle growth and differentiation in mice. American Journal of Physiology-Endocrinology and Metabolism. 2015 May 15;308(10):E912–20. https://doi.org/10.1152/ajpendo.00289.2014
[13] Barrès R, Yan J, Egan B, Treebak JT, Rasmussen M, Fritz T, et al. Acute Exercise Remodels Promoter Methylation in Human Skeletal Muscle. Cell Metabolism. 2012 Mar;15(3):405–11. https://doi.org/10.1016/j.cmet.2012.01.001
[14] Kazemi F. The correlation of resistance exercise-induced myostatin with insulin resistance and plasma cytokines in healthy young men. J Endocrinol Invest. 2016 Apr;39(4):383–8. https://doi.org/10.1007/s40618-015-0373-9
[15] Narkar VA. PGC1α promoter methylation and nucleosome repositioning: Insights into exercise and metabolic regulation in skeletal muscle. Endocrinology (Philadelphia). 2017;158(7):2084-2085. https://doi.org/10.1210/en.2017-00439.
[16] Lee S, Garcia L, Leon AD, Bustos RZ, Campos B, Krentzel JA, Mandarino L, Coletta DK. 167-OR: Exercise training alters peroxisome proliferator-activated receptor gamma coactivator 1 alpha (PGC-1 alpha) DNA methylation in human skeletal muscle. Diabetes. 2020;69 (Supplement_1). https://doi.org/10.2337/db20-167-OR
[17] Horsburgh S, Robson-Ansley P, Adams R, Smith C. Exercise and inflammation-related epigenetic modifications: Focus on DNA methylation. Exercise Immunology Review. 2015;21:26-41. https://go.exlibris.link/9XXBFCCy
[18] Garcia LA, Zapata-Bustos R, Day SE, Campos B, Hamzaoui Y, Wu L, et al. Can Exercise Training Alter Human Skeletal Muscle DNA Methylation? Metabolites. 2022 Mar 2;12(3):222. https://doi.org/10.3390/metabo12030222

[19] Howlett KF, McGee SL. Epigenetic regulation of skeletal muscle metabolism. Clinical Science. 2016 Jul 1;130(13):1051–63. https://doi.org/10.1042/cs20160115

[20] LeBrasseur NK, Walsh K, Arany Z. Metabolic benefits of resistance training and fast glycolytic skeletal muscle. American Journal of Physiology-Endocrinology and Metabolism. 2011 Jan;300(1): E3–10. https://doi.org/10.1152/ajpendo.00512.2010

[21] Strasser B, Schobersberger W. Evidence for Resistance Training as a Treatment Therapy in Obesity. Journal of Obesity. 2011;2011:1–9. https://doi.org/10.1155/2011/482564

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