The Relationship Between Exercise and Sport and Epigenetics

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ABSTRACT

Physical exercise training elicits multiple physiological adaptations, including enhanced cardiorespiratory endurance capacity, increased skeletal muscle hypertrophy, and improved arterial compliance, which mediates blood pressure regulation. The intersection of exercise physiology and epigenetic mechanisms has emerged as a prominent focus of scientific investigation. Epigenetics encompasses regulatory mechanisms that modulate gene expression without alterations to the DNA sequence, and these mechanisms demonstrate substantial plasticity in response to environmental stimuli, particularly exercise. Empirical evidence indicates that systematic physical activity modifies gene activation patterns through epigenetic processes, including DNA methylation, post-translational histone modifications, and non-coding RNAs. Such epigenetic alterations influence various critical physiological processes, including myogenesis, cellular energy metabolism, inflammatory response regulation, and cellular senescence. Distinct exercise modalities, including aerobic training, resistance exercise, and high-intensity interval protocols, induce specific epigenetic signatures that enhance physiological performance and adaptive capacity. Chronic exercise adaptation may facilitate the maintenance of such epigenetic modifications, potentially contributing to sustained health benefits throughout the lifespan. These findings demonstrate that exercise functions as a powerful modulator of both physical performance and genetic regulation.

Keywords: Exercise, sports, health, epigenetics.

INTRODUCTION

Exercise represents a fundamental lifestyle intervention that significantly influences human physiological homeostasis, mediating improvements across multiple biological systems, from muscular development and immunological function to energy metabolism and cardiovascular health. Recent investigations have demonstrated that exercise-induced adaptations extend beyond physiological parameters to encompass genetic regulation through epigenetic mechanisms. Such mechanisms elucidate how environmental stimuli—specifically exercise—modulate gene expression without alterations to the underlying DNA sequence. Epigenetics, the study of heritable changes in gene expression without alterations in DNA sequence, elucidates how environmental stimuli, such as exercise, regulate gene activity. Specifically, exercise has been shown to influence gene expression through mechanisms including DNA methylation, histone modifications, and small RNA regulation. While the shared human genome, comprising approximately 20,000 genes, provides a foundational blueprint, inter-individual genomic variation, including copy number variations, tandem repeats, and single nucleotide polymorphisms (occurring at >1% frequency), contributes to phenotypic diversity. A range of human phenotypes, such as muscle strength, skeletal structure, tendon elasticity, and cardiopulmonary capacity, influence athletic performance, each resulting from complex interactions among anatomical, biochemical, and physiological systems (Goldstein & Cavalleri 2005). Although the positive influence of physical exercise on epigenetic mechanisms and health is conceptually established, the precise nature of such relationships

remains a subject of investigation. Epigenetics addresses heritable changes in gene expression or cellular phenotype independent of DNA sequence alterations; thus, the individual epigenome governs gene activation and silencing (Lu et al., 2006).

Epigenetics is defined as the study of heritable changes in phenotype or gene expression induced by molecular mechanisms other than changes in DNA sequence (Bird, 2007). The concept of epigenetics has evolved, encompassing mechanisms that regulate gene expression independently of the DNA nucleotide sequence. Generally, non-genetic changes in gene expression and chromatin state are tightly regulated by DNA cytosine methylation, microRNA-mediated transcriptional regulation, and histone post-translational modifications (Golberg et al., 2007). A critical metabolic adaptation induced by regular exercise is mitochondrial biogenesis, which involves the coordinated action of peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1α), nuclear respiratory factor 1 (NRF1), and mitochondrial transcription factor A (TFAM) (Holloszy et al., 1984). Most importantly, exercise facilitates the adaptation of gene expression to environmental demands. By inducing epigenetic modifications in genes regulating muscle development, energy metabolism, and immune response, exercise potentially contributes to long-term health optimization. Studies have demonstrated exercise-induced changes in promoter methylation of genes crucial for energy and glucose homeostasis, including PGC-1α, pyruvate dehydrogenase kinase kinase isoenzyme 4 (PDK4), and peroxisome proliferator-activated receptor δ (PPAR-δ) (Barres et al 2012). This study will examine the effects of exercise on genetic expression at the epigenetic level, the genetic changes induced by diverse exercise modalities, and the relationship between sustained exercise and enduring genetic adaptations. This comprehensive analysis provides valuable insights into how exercise shapes both physical performance and the epigenetic landscape of individuals.

Epigenetic Effects of Exercise and Sport on Genetic Expression

Epigenetics investigates the mechanisms by which environmental factors modulate gene expression without altering the underlying DNA sequence. These regulatory processes typically involve DNA methylation, histone modifications, and RNA-mediated mechanisms. Physical exercise is recognized as a potent modulator of such epigenetic mechanisms, capable of either augmenting or attenuating the activity of specific genes. Consequently, exercise influences diverse physiological processes, including muscle development, energy metabolism, inflammation, and aging. The health and wellness benefits derived from regular aerobic and resistance exercise training encompass a reduction in the risk and severity of cardiovascular, metabolic, and pulmonary diseases, obesity, and certain cancers (Na HK and Oliynyk, 2011). Empirical evidence supports the role of exercise as a key driver of the epigenetic adaptations. For instance, Mahoney et al. (2005) demonstrated that regular physical activity induces alterations in histone proteins, leading to differential gene expression. Subsequent research has shown that exercise-induced acetylation results in an immediate increase in histone H3 protein within skeletal muscle. Human studies have implicated histone deacetylases (HDACs) and class IIa histone deacetylases (HDAC IIa) as critical regulators of post-exercise gene expression (Ratthaff et al., 2007). While calcium-dependent mechanisms were historically considered the primary drivers of gene expression modulation, contemporary research has revealed that histone protein modifications, mediated by calcium-dependent pathways, augment the expression of oxidative genes and kinases. These pathways involve calcium-calmodulin kinase-dependent proteins (CaMKI, II, IV), protein kinase D, AMP-activated protein kinase (AMPK), and salt-inducible kinase (SIK1)-related AMPK kinases. Exercise is a recognized activator of such kinases within skeletal muscle, with certain kinases identified as regulators of HDACs and HDAC IIa activity (Zeng et al. 2012).

Table 1. Genetic polymorphisms associated with sports performance

Gene	Name	Associated phenotypes	Polymorphism ID
ACE	Angiotensin I converting enzyme	I-allele, endurance performance; D-allele, strength performance	rs4646994 (Aluminum Diameter)
ACTN3	α-actinin-3	577Ter (T) allele, endurance performance; Arg577 (C) allele, strength performance	rs1815739 T>T
ADRB2	β-2 adrenoreceptor	16 Arg (A) and Gln27 (C) alleles, endurance performance	rs1042713 G>A; rs1042714 C>G
BDKRB2	Bradykinin receptor B2	T-allele, durability performance	rs1799722 T>T
COL5A1	Collagen, type V, α1	CC genotype, protection from exercise-related muscle cramps during ultra-marathon; T-allele, endurance performance	rs12722 C>T
CRP	C-reactive protein, associated with pentraxin	A-allele, endurance performance	rs1205 A>G
GABPB1	GA binding protein transcription factor, β subunit 1 (nuclear respiratory factor 2)	G-allele, durability performance	rs7181866 A>G
PPARA	Peroxisome proliferator-activated receptor α	G-allele, endurance performance; C-allele, strength performance	rs4253778 G>C
PPARGC1A	Peroxisome proliferator-activated receptor γ coactivator 1 α	G-allele, durability performance	rs8192678 G>A

Gene	Name	Associated phenotypes	Polymorphism ID
VEGFA	Vascular endothelial growth factor A	C-allele, endurance performance	rs2010963 G>C
ADRA2A	α-2A-adrenergic receptor	Plays a central role in the regulation of systemic sympathetic activity and thus cardiovascular responses such as heart rate and blood pressure	*Dra* I identifies a restriction fragment length polymorphism in the 3_-untranslated region (6,7-/6,3-kb polymorphism
AMPD1	Adenosine monophosphate deaminase 1	GG homozygotes, elite power athlete status, faster acceleration and sprint times	rs17602729 G>A
EPAS1	Endothelial PAS domain protein 1	The AA genotype at rs1867785 is underrepresented in sprint/power athletes; the TT genotype at rs11689011 is underrepresented in sprint/power athletes	rs1867785; rs11689011
NFATC4	Activated T cell nuclear factor calcineurin-dependent 4	G-allele, elite endurance athlete status	rs2229309 G>C
NOS3	Nitric oxide synthase 3	GG genotype is slower than other genotypes	rs1799983 T>A>G
AGT	Angiotensinogen	235Thr (C) allele, power performance	rs699 T>C
IL6	Interleukin-6	Power performance, power performance	rs1800795 Ç>G
TRHR	Thyrotropin-releasing hormone receptor	C-allele, muscle mass	rs16892496 A>C
VDR	Vitamin D receptor	A-allele, power performance	rs1544410 A>G

Gene	Name	Associated phenotypes	Polymorphism ID
PPARGC1B	Peroxisome proliferator-activated receptor γ coactivator 1 α	C-allele, power athlete status	rs10060424 T>A,C
PPARG	Peroxisome proliferator-activated receptor γ	G-allele is a short-term and very intense exertion with anaerobic energy production.	rs1801282 C>G
HIF1A	Hypoxia-induced factor 1α	The T-allele has a higher frequency in weightlifters and strength-oriented athletes	rs11549465 T>T
PTPRK	Protein tyrosine phosphatase receptor type K	C-allele, sprint test performance	rs55743914 T>T
TERT	Telomerase reverse transcriptase	G-allele, runners	rs33954691 G>A
RDH13	Retinol dehydrogenase 13	G-allele, increased proportion of fast-twitch muscle fibers	rs4806637 A>G
CBLN2	Cerebellin 2 precursor	G-allele, runners	rs8093502 T>T
CPNE5	Kopina V	G-allele, runners	rs3213537 T>T
CNTN4	Encodes contactin 4	A-allele overrepresented in soccer players	rs62247016 A>T
LINC00305, LINC01924	Long intergenic non-protein-coding RNA 305, 1924	Functional role in the development of atherosclerosis by inducing the production of inflammatory cytokines in monocytes and regulating apoptosis via miR-136	rs2850711 A>T

Gene	Name	Associated phenotypes	Polymorphism ID
AGTR1	Angiotensin II receptor type 1	C-allele, essential hypertension. A-allele, down-regulated by miR-155	rs5186 A>C
MIR499A	MicroRNA 499a	GG genotype, myocardial infarction and ischemic stroke. rs3746444 polymorphism impairs regulation of blood pressure and anti-apoptotic effect in cardiomyocytes	rs3746444 A>G
MIR4513	MicroRNA 4513	Blood pressure, total lipids, total cholesterol, low-density lipoprotein cholesterol, blood glucose. TT genotype, coronary artery disease. T-allele, reduction in Mir-4513	rs2168518 T>T
MIR149	MicroRNA 149	Coronary artery disease	rs2292832 T>C
MIR27A	MicroRNA 27a	C-allele, increased miR expression with negative effect on adipogenesis. CC genotype, protective role against T2DM. G-allele, increased risk of early cardiovascular autonomic neuropathy	rs895819 T>A,C,G
CREB1	CAMP responsive element binding protein 1	A-allele, a smaller decrease in heart rate during submaximal exercise testing after training; a larger exercise-induced temperature increase	rs2253206 A>G,T
CPT2	Carnitine palmitoyltransferase 2	Small alleles, CPT2 deficiency	rs1799821 G>A; rs1799822 A>G
PYGM	Muscle-associated glycogen phosphorylase	Cut variant, exercise intolerance, cramps and contractures during exercise and stressful situations	rs116987552 G>A

Gene	Name	Associated phenotypes	Polymorphism ID
CNTF	Ciliary neurotrophic factor	GG genotype, athlete phenotype	rs1800169 G>A
ACVR1B	Activin A receptor type 1B	Dynamic knee flexion and extension, isometric strength	rs11612312 T>C; rs2854464 A>C,G
NGF	Nerve growth factor	CC genotype, more anxious females; TT genotype, more anxious males, less anxious females	rs6330 C>T
BDNF	Brain-derived neurotrophic factor	CC genotype runners faster than A-allele carriers	rs6265 G>A
NGFR	Nerve growth factor receptor	Vagal autonomic dysregulation	rs2072446 T>T
MSTN	Myostatin	Peak power during muscle contractions	rs1805086 A>G
SCN9A	Sodium voltage-gated channel alpha subunit 9	AA genotype, increased pain perception	rs1805086 A>G
COMT	Catechol-O-methyltransferase	A-allele, higher dopamine levels; lower pain threshold; sensitivity to stress	s4680 G>A

(Naureen et al., 2020).

Furthermore, exercise, through the enhancement of muscle hypertrophy and aerobic capacity, exerts systemic effects on diabetes and other metabolic disorders. Augmentation of type I muscle fiber density, facilitated by aerobic activity, promotes glucose and lipid metabolism, representing a critical mechanism in the prevention and management of metabolic diseases. Exercise-mediated modulation of promoter methylation and gene activation is well-documented. Specifically, moderate to high-intensity exercise induces immediate reductions in the methylation of active promoters, including peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1α), mitochondrial transcription factor A (TFAM), pyruvate dehydrogenase kinase isoenzyme 4, and MEF2A, and delayed methylation of peroxisome proliferator-activated receptor δ (PPARδ) promoters 3 hours post-exercise. Such exercise-induced alterations manifest as cytosolic changes in both human and murine models, mediated by fluctuations in intracellular calcium (Ca2+) and adenosine monophosphate (AMP), both of which are central to the activation of signaling cascades (Ntanasis-Stathopoulos et al., 2013).

DNA Methylation: Studies have demonstrated that exercise can modulate DNA methylation patterns in muscle cells, thereby influencing muscle adaptation and overall metabolic homeostasis through the regulation of gene expression. For example, resistance training often results in decreased methylation of genes associated with muscle hypertrophy, facilitating increased muscle protein synthesis.

Histone Modifications: Post-translational modifications of histone proteins, which determine chromatin accessibility and consequently gene expression, are also subject to exercise-induced modulation. Exercise can induce histone modifications, such as acetylation and methylation, which accelerate muscle adaptation. For instance, intense training may lead to increased histone acetylation in muscle cells, enhancing the expression of genes involved in muscle development and endurance.

Impact of Various Types of Exercise on Genetic Changes

Heritability significantly influences physical fitness, with estimates suggesting a genetic component of up to 50% (Buçç, 1992). In contexts where selection criteria involve high performance across multiple tasks, a trade-off may exist, wherein enhanced performance in one domain could impede performance in another. Data from international decathletes support this hypothesis; performance in events reliant on explosive power and fast-twitch muscle fibers (100m run, shot put, long jump, 110m hurdles) is negatively correlated with performance in the 1500m race, which demands endurance and slow-twitch muscle fiber activity (Van Damme et al., 2002). These findings suggest that athletes may possess inherent predispositions towards superior performance in either sprint/power or endurance domains.

A significant challenge lies in elucidating the genetic underpinnings that predispose athletes to excel in specific sports (e.g., sprinting versus marathon running). Identifying genes associated with athletic performance is complex, as each causal gene likely contributes only a small fraction to the overall heritability. The "one gene as a silver bullet" approach has, therefore, proven inconclusive, especially given that the 2005 human gene map identified 165 autosomal gene entries and quantitative trait loci (QTL) related to physical performance and health-related phenotypes, with an additional five on the X chromosome. Furthermore, 17 mitochondrial genes have been identified, with sequence variants impacting fitness and performance phenotypes (Dudaklar, 2008). The considerable genetic diversity observed between endurance athletes and sprinters likely reflects natural selection. For instance, α-actinin-3 (ACTN3), a highly conserved actin-binding protein within the contractile apparatus of mammalian fast skeletal muscle fibers, is almost exclusively found in elite strength athletes. Conversely, the R577X polymorphism (a premature stop codon polymorphism) resulting in ACTN3 deficiency is more prevalent among elite endurance athletes, such as marathon runners and rowers (MacArthur et al., 2007).

Elucidating the impact of individual genes on heterogeneous phenotypes presents significant challenges. While rare, well-defined extreme phenotypes can be readily linked to rare gene mutations, associating common polymorphisms, such as the ACE I/D polymorphism, with diverse sports disciplines or continuous variables like left ventricular mass (LV), maximal oxygen uptake (VO2max), or bone mineral density (BMD) is considerably more complex. The I allele has a frequency of approximately 50%, and athletic performance,

along with the aforementioned continuous variables, is influenced by numerous environmental and biological factors, including exercise, gender, age, and race. Consequently, robust statistical power, often requiring large sample sizes (several hundred participants), is necessary to draw definitive conclusions in such studies. Genome-wide linkage analysis studies, which examine the association between hundreds of polymorphisms and a specific disease phenotype (e.g., obesity or type 2 diabetes), offer a potential approach. A recent genome-wide linkage scan study estimated the heritability of athlete status at 60% (De Moor et al., 2007).

Several independent investigations have established that the absence of alpha-actinin-3 protein is detrimental to sprint and power performance in both athletes and the general population (Yang et al., 2003). Specifically, Yang et al. (2003) were the first to demonstrate highly significant associations between ACTN3 genotype and athletic performance. They found that 50% (53/107) of elite white sprint athletes possessed the RR genotype, compared to 30% (130/436) of healthy white control participants and 31% (60/194) of elite endurance athletes. Elite endurance athletes exhibited a slightly higher frequency of the XX genotype (24%) than controls (18%). These findings suggest that the presence of the ACTN3 protein (associated with the 577R allele) may confer an advantage in activities requiring sprinting or power. Conversely, ACTN3 deficiency (associated with the 577X allele) may offer some benefit to endurance athletes. The results are corroborated by multiple human association studies demonstrating a positive correlation between the 577X allele and elite endurance athlete performance (Niemi et al., 2005).

Distinct exercise modalities (e.g., aerobic exercise, resistance training, high-intensity interval training [HIIT]) elicit varied epigenetic modifications across different biological systems. This suggests that each exercise type may induce distinct genetic adaptations. The I allele of the ACE gene is theoretically linked to reduced circulating angiotensin II levels, leading to decreased vascular resistance, potentially facilitating cardiac output during strenuous exercise (Jones et al., 2002). The I allele may also enhance muscle efficiency, a critical factor in long-distance running performance (Williams et al., 2000), suggesting a higher frequency of this allele in elite endurance athletes, as frequently reported (Collins et al., 2004). Conversely, the D allele is observed with greater frequency among individuals participating in power-oriented sports (Nazarov et al., 2001). These findings were recently corroborated in a study involving 39 Portuguese Olympic swimming hopefuls, categorized into two homogeneous groups: short-distance swimmers (SDS; 50-200m, predominantly anaerobic events) and middle-distance swimmers (MDS; 400-1500m, mixed anaerobic and aerobic events). Additionally, a group of 32 non-elite swimmers was analyzed, and a control group ($N = 100$) was selected from the Portuguese population. The authors observed a significantly higher DD genotype frequency ($P = 0.029$) and D allele frequency ($P = 0.021$) in elite short-distance swimmers (SDS) compared to the control group (Costa et al., 2009). Their results are consistent with previous observations demonstrating an association between the D allele and elite short-distance swimmer status (Tsianos et al., 2004), as well as an association between the D allele and sports emphasizing strength and power.

Aerobic Exercise (Endurance Exercise): Aerobic exercise is typically undertaken to enhance cardiovascular function and energy metabolism. This exercise modality has been demonstrated to stimulate mitochondrial biogenesis and induce epigenetic reprogramming of genes governing energy metabolism. Specifically, aerobic exercise may promote the activity of genes regulating mitochondrial function, such as PGC-1α, by reducing DNA methylation.

Resistance Exercise (Weight Lifting): Resistance exercise is associated with skeletal muscle hypertrophy and strength gains. This form of exercise elicits epigenetic regulation of genes involved in muscle protein synthesis and repair. Notably, decreased DNA methylation and altered histone modifications have been observed in genes related to muscle growth, such as IGF-1, leading to increased gene expression. Resistance training may also attenuate muscular inflammation by suppressing the activity of specific genes associated with inflammatory processes.

High-Intensity Interval Training (HIIT): High-intensity interval training (HIIT) is characterized by brief periods of high-intensity exercise, exerting a potent effect on metabolic adaptations. HIIT induces epigenetic changes, including DNA methylation and histone modifications, in genes regulating lipid oxidation and glucose metabolism. Furthermore, it can enhance the activity of genes that improve cardiovascular health and increase insulin sensitivity.

Long-Term Sport Engagement and Genetics

Genetics, the scientific discipline focused on heredity and variation in living organisms, encompasses the study of gene function, genome structure, chromatin organization, recombination rates, mutational processes, and evolutionary history. The overarching goal is to provide a comprehensive understanding of the human genome and its intricate relationship with human biology, physiology, and disease. Over the past two decades, accumulating evidence has supported associations between single nucleotide polymorphisms (SNPs) and both the predisposition to injuries in sports participation and athletic performance outcomes (Lippi et al., 2010). Sport performance is underpinned by complex interactions among interconnected genes and their variants, which regulate key performance indicators and ultimately shape the overall athletic phenotype. Consequently, a polygenic model of inheritance is considered more relevant for explaining sports performance (Buxens et al., 2011). Furthermore, individual polymorphisms may not independently exert a measurable effect on performance; however, the presence of other polymorphisms can lead to amplified phenotypic effects through gene-gene interactions (epistasis). Therefore, combinations of polymorphisms may have a more substantial impact on the overall athletic phenotype than single polymorphisms, a factor that should be considered when predicting sports performance and tailoring training regimens (Flueck et al., 2010).

The ACE gene, located on chromosome 17q23.3, encodes angiotensin-converting enzyme (ACE), which catalyzes the conversion of angiotensin I to angiotensin II, a physiologically active peptide. Angiotensin II is a potent vasopressor and aldosterone-stimulating peptide that regulates blood pressure and fluid-electrolyte balance. ACE, therefore, plays a crucial role in the renin-angiotensin system. Numerous studies have linked an insertion/deletion (I/D) polymorphism, involving a 287 base-pair Alu repeat element within intron 16 of the ACE gene, to individual variability in exercise-related phenotypes, particularly those related to muscle (skeletal). In addition to its role in blood pressure regulation, ACE is expressed in skeletal muscle, where it can influence muscle function and biomechanical properties (Gordon et al., 2001). The ACE D allele is associated with higher circulating and tissue concentrations of ACE, resulting in increased angiotensin II levels; this allele is hypothesized to be advantageous for performance in strength- or power-oriented sports, such as weightlifting (Jones et al., 2002).

Long-term exercise can have profound effects on the persistence and continuity of genetic adaptations. Sustained exercise stabilizes epigenetic modifications, enhancing the body's metabolic flexibility, which can be maintained throughout life. Through epigenetic pathways, long-term exercise can optimize cardiovascular health, muscular endurance, and overall metabolic function. While many studies have reported a positive association between the ACE I/D polymorphism and enhanced long-term endurance and strength performance, some studies have failed to find such a correlation. Such discrepancies may be attributable to the inclusion of mixed sport disciplines (resulting in phenotypic heterogeneity), limitations in sample size, and other confounding factors, including ethnicity and geography. For example, a study investigating Kenyan athletes found no association between ACE I/D alleles and athletic performance, suggesting the influence of ethnic and geographic factors (Scott et al., 2005).

Aging and Epigenetic Aging: The aging process is accompanied by epigenetic changes, which contribute to age-related diseases. However, regular long-term exercise can decelerate epigenetic aging. Research indicates that regular physical activity can alter the methylation patterns of genes associated with aging. Specifically, anti-inflammatory genes may be activated, while genes associated with inflammation are suppressed.

Inherited Epigenetic Effects: Certain epigenetic changes are heritable, meaning that long-term exercise can impact not only the individual but also subsequent generations. In particular, epigenetic modifications related to metabolic health can be transmitted to the offspring of athletic parents. Therefore, exercise habits can influence not only an individual's health but also the health of future generations.

CONCLUSION

Exercise extends beyond enhancing physical performance; it profoundly influences our genetic expression through epigenetic mechanisms. While distinct exercise modalities trigger specific genetic adaptations, long-term engagement in sports and exercise possesses the potential to reprogram our genetic makeup, promoting

sustained health. Numerous health-related studies have corroborated such effects (Kaya & Algin, 2022; Algin, Yesilbas & Kantek, 2024; Pekgor et al., 2024; Algin, 2024). These findings underscore the significance of exercise for overall health and present novel opportunities for developing personalized exercise programs in the future. In conclusion, epigenetic mechanisms provide a framework for understanding the impact of sports and exercise on gene expression. Exercise modulates the activity of genes, without altering the underlying DNA sequence, thereby playing a crucial role in biological processes such as muscle development, metabolism, inflammation, and aging. While different types of exercise induce distinct epigenetic changes, long-term exercise can perpetuate such modifications, potentially extending healthy lifespan. Epigenetics reveals that exercise exerts potent and enduring effects not only on physical performance but also on our fundamental genetic constitution.

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