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THE GUT MICROBIOME IN ATHLETES: MECHANISMS, TRAINING ADAPTATIONS, AND IMPLICATIONS FOR PERFORMANCE — A COMPREHENSIVE REVIEW

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Abstract

Background

The gut microbiota is increasingly seen as a key regulator of functions relevant to athletic performance. Exercise alters microbial composition, while microbial metabolites influence metabolism, immunity, gut barrier integrity, and recovery. Despite rapid growth of research, findings are inconsistent, underscoring the need for clearer mechanisms. This review summarizes current evidence on the bidirectional relationship between training and the gut microbiota and its implications for performance.

Aim

To consolidate open-access research on links between gut microbiota, exercise physiology, and performance, focusing on metabolic pathways, gut–muscle communication, immune modulation, intestinal permeability, and training-specific effects.

Material and Methods

This narrative review draws on open-access literature up to 2025, identified through PubMed, PMC, and Google Scholar. Included studies comprise mechanistic animal work, observational data, randomized trials, and systematic reviews examining physical activity, microbiota composition, microbial metabolites, and performance in athletes.

Results

Endurance training induces microbial adaptations, including increases in taxa metabolizing lactate and generating propionate. Strength and HIIT training show more variable changes shaped by diet, training load, and metabolic health. Microbial metabolites—especially SCFAs—may enhance energy regulation, immune balance, and gut barrier function, though evidence remains fragmented and causality unclear.

Conclusion

The gut microbiota is a dynamic component of exercise adaptation. While diverse and SCFA-producing microbes appear beneficial for metabolism, inflammation control, and recovery, overall findings are heterogeneous. More interdisciplinary research is needed to clarify causal pathways and support personalized, microbiome-based strategies in sports nutrition and training.

Keywords:

gut microbiome; athletic performance; exercise physiology; short-chain fatty acids (SCFAs); gut–muscle axis; intestinal barrier; endurance training; HIIT; strength training; microbial diversity; sports nutrition

1. **Introduction**

The gut microbiome is a dynamic, comlex ecosystem consisting of bacteria, fungi, viruses, and archae, that reside primarily in the human digestive tract. The main phyla of bacteria include *Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria* and *Verrucomicrobia* [1]. They interact with each other and with the host, playing a pivotal role in digestion, vitamin synthesis, short-chain fatty acids (SCFAs) production, and affecting brain health, immune system and inflammatory response [2, 3].

The gut microbiome is primarily shaped by the mode of delivery at birth, and is typically affected by factors such as age, diet, exercise, sleep, stress, illness, and drugs use [4, 5, 6]. Dysbiosis, an imbalance of the gut microbiome composition, may impact the integrity of the intestinal barrier, and is a cause to diseases such as diabetes mellitus, obesity, arthritis, and cardiovascular and neurodegenerative diseases [2].

In recent years, research has increasingly highlighted the importance of the gut microbiome in the context of human physical activity. According to Mach and Fuster-Botella (2017), regular exercise may affect the composition of the gut microbiota, increasing its diversity, especially in the *Firmicutes* phylum [4]. This diversity is associated with nutrient absorption, and enhanced production of short-chain fatty acids, that can result in the improvement of the endurance performance of the host. Moderate exercise can reduce inflammation, by causing a rise in interleukin-6, whereas prolonged, high-intensity training is connected to temporary immunosuppression, oxidative stress, and increased risk of illnesses [7]. Furthermore, certain bacterial genus may metabolize exercise-related compounds, such as lactate, into substrates for subsequent energy production. A study by Scheiman et al. showed that Veillonella species use lactate, producing propionate, that can increase VO2 max and overall performance [8].

Moreover, the microbiome is modified by factors fundamental for athletes: type of training and diet. For example, a high-protein diet typically associated with strength training can impact the diversity of the gut microbiota [9]. Endurance athletes often consume a high-carbohydrate diet, which can positively influence fermentation efficiency of the gut microbiome through the impact on an abundance of *Prevotella* [10]. Exercise itself modulates microbial composition by affecting gut transit time, immune signaling, and mucus secretion [11]. Accumulating studies also indicate that the increase of bacterial fermentation products can reduce recovery time of the athletes [10, 12].

Despite growing interest, no universal model fully explains how exercise, diet, and microbiota converge to shape performance outcomes. Available evidence is fragmented and varies across disciplines. Thus, the purpose of this review is to synthesize current open-access research and evaluate the connection between the gut microbiome and metabolism, type of training and performance. Specifically, the review focuses on:

(1) biological foundations of microbiome function;
(2) mechanistic links between microbiota and exercise physiology;
(3) effects of different training modalities;
(4) distinctive features of elite athletes;
(5) dietary strategies modulating microbiome composition; and
(6) emerging biomarkers and future directions.

By consolidating these findings, this work aims to support the development of personalized nutrition and training approaches informed by the gut microbiome.

2. **Biological Foundations of the Gut Microbiome**

The gut microbiome is an integral component of human physiology, influencing metabolic, endocrine, and immune systems. One of its most important functions involves the fermentation of non-digestible carbohydrates from dietary fiber. The metabolites of that fermentation are short-chain fatty acids, such as acetate, propionate and butyrate. They are not only substrates for colonocytes, but also take part in maintaining the integrity of the gut barrier and regulate gut endocrine functions [13]. Studies show that SCFAs can also have an impact on satiety, by influencing the peptide YY and glucagon-like peptide-1 production [14]. Regular physical activity enhances microbial diversity, leading to the increase of the SCFAs production [15].

The gut microbiota also metabolises bile acids (BAs) produced in the liver. In the intestine, BAs regulate digestion and metabolism of lipids and glucose by activating nuclear receptors. They also impact the composition of the microbiota, through their antimicrobial features [16]. Moreover, secondary BAs present anti-inflammatory effect by mediating the reduction of inflammatory cytokine production [17].

2.1 Gut barrier and immune regulation

The intestinal barrier is crucial for preventing translocation of harmful molecules, especially during strenuous physical activity, and SCFAs play a key role in maintaining a healthy gut barrier. For example, butyrate is the main energy source for the intestinal epithelial cells (IEC) and it reduces the permeability of the IEC. Furthermore, butyrate affects the immune system, by decreasing the levels of pro-inflammatory cytokines and increasing the synthesis of antimicrobial peptides [14]. SCFAs also modulate mucosal secretory functions, thereby protecting the mucosa [13]. BAs maintain the integrity of the gut barrier by influencing the expression of tight junction proteins [18].

A compromised barrier and increased intestinal permeability—often referred to as “leaky gut”—can increase local and systemic inflammation and impair recovery [19]. Ultimately, reduced SCFAs production may elevate the risk of the injuries among athletes [20].

2.2 Circadian rhythms and exercise

Studies demonstrate that there is a bidirectional influence between the circadian clock and the gut microbiota. It is determined by the feeding time, dietary composition and activity cycles [21]. Disruptions, such as those caused by irregular sleeping patterns or travel (common in competitive athletes), may impact microbial diversity and lead to metabolic disfunction [22, 23, 24]. Synchronization between training, nutrition, and feeding/fasting phases with circadian rhythms may preserve microbial homeostasis and therefore optimize physiological responses of athletes [25].

2.3 Gut-muscle axis

Animal models research shows that the gut microbiota affects skeletal muscle metabolism and function [26]. Possible mechanisms include participating in inducing insulin growth factor 1, that promotes anabolism. SCFAs may stimulate mitochondrial energy production, contributing to the muscle gain [27]. Moreover, it has been shown that the dysbiosis leads to increased expression of the markers associated with muscle atrophy [28]. BAs may also influence muscle metabolism through inducing fibroblast growth factor 19 in the intestine [28].

3. Mechanisms Linking the Gut Microbiome With Exercise Physiology

3.1 Energy metabolism

Regular physical activity is linked to the abundance of the bacteria of the phylum *Firmicutes,* such as *Ruminococcus, Lachnospiraceae* and *Holdemanella. Ruminococcu*s produces the SCFA succinate, which is involved in intestinal gluconeogenesis and thereby impacts glucose homeostasis [29]. It is also connected to increased insulin sensitivity. *Lachnospiraceae* produces acetate, amongst others, which is shown to improve glucose metabolism. *Holdemanella* may reduce hyperglycemia by regulating the production of the GLP-1 hormone [30]. SCFAs also elevate the production of peptide YY [31], that modulates intestinal transit and impacts satiety, ultimately decreasing food intake. Intense aerobic exercises are also associated with an increase in the abundance of *Bacteroidetes*. *Bacteroidetes* participate in the metabolism of carbohydrates, utilizing them through Carbohydrate-Active Enzymes (CAZymes) [32].

SCFAs, mainly propionate and acetate, activate free fatty acid receptors, FFAR2 and FFAR3, that regulate lipid storage and maintain metabolic homeostasis. The activation of receptors promotes the usage of excess energy, instead of storing it. It has also been shown to reduce the insulin sensitivity of adipocytes, ultimately leading to elevated energy expenditure [33, 34, 35]. Studies also show the increase of Veillonella in the marathon runners' gut [8]. This species can utilize lactate into acetate and propionate, which are the energy sources, thereby improving the endurance of the host [36].

3.2 Immune modulation

High training loads, particularly in endurance athletes, are associated with transient immunosuppression [37]. Intense exercise may increase the risk of infection through many pathways. For example, it influences production of the cytokines, that regulate the immune system [38]. Excessive training load has been associated with a higher risk of upper respiratory tract infections [39]. However, higher microbiome diversity contributes to the modulation of the immune system of the host and decrease of the upper respiratory tract infection risk [40]. Furthermore, probiotic supplementation has demonstrated benefits in modulating immune responses and reducing infection incidence [41, 42]. The gut microbiota also influences the immune system by stimulating the IgA secretion and shaping the gut associated lymphoid tissues (GALT) [43].

3.3 Regulation of inflammation and oxidative stress

Strenuous physical activity induces the production of reactive oxygen species (ROS), that leads to oxidative damage and inflammation, and can subsequently reduce athletic performance. It also impacts the release of glucocorticoids, that decrease the production of anti-inflammatory cytokines [44, 45]. It has been shown that probiotic intervensions in athletes can reduce oxidative stress levels and improve inflammatory responses [46, 47]. Certain *Lactobacillus* species may decrease cytokines production and mitigate systemic inflammation [47]. SCFAs, mainly butyrate and propionate, inhibit the ROS production and expression of the pro-inflammatory cytokines [48, 49].

3.4 Gut barrier integrity during exercise

The integrity of gut barrier is crucial for maintaining an efficient immune system, prevetening systemic inflammation and absorbing energy and nutrients. While moderate exercise can have a positive effect on the gut barrier permeability, high-intensity endurance training can reduce splanchnic perfusion, causing ischemia and leading to increased permeability [50]. It can result in endotoxemia, as lipopolysaccharides (LPS) and bacteria start circulating in the bloodstream [51]. Subsequently, increased LPS blood concentration triggers systemic inflammatory response and impacts nutrients absorption and overall athletic performance [52].

A diverse microbiome, especially rich in butyrate-producing taxa, helps maintain barrier function. Butyrate is the main energy source for colonocytes, it influences their proliferation and apoptosis, thereby impacting the integrity of the gut barrier [49]. SCFAs also upregulate mucus production and reinforce intercellular tight junctions, which restrict transit of bacteries [53]. Bacteria such as *Holdemanella biformis* can regulate the expression of gut barrier integrity markers and thereby impact its permeability [30].

Maintaining the integrity of gut barrier is essential not only for health but also for preventing performance-limiting gastrointestinal symptoms commonly reported by athletes [44].

4. Effects of Different Training Modalities on the Gut Microbiome

4.1 Endurance training

Endurance training induces significant shifts in microbial composition. Zhao et al. (2018) observed that long-distance endurance running results in rapid changes in the gut microbiota, for example an increase of the *Actinobacteria* phylum, that participates in the metabolism of steroids [54]. Ampe et al. (2025) showed the enhancement of *Bacteroidota* and diminution of *Firmicutes* in elite female cyclists microbiome in comparison to the non-athlete control group [55]. Moreover, Petersen et al. (2017) reported the increased *Methanobrevibacter smithii* abundance in professional cyclist, compared to amateurs. *M. smithii* contributes to metabolic efficiency of the microbiota through carbohydrate metabolism [10]. Furthermore, Shalmon et al. (2024) observed that there are differences in the composition of gut microbiome between runners and cyclists, suggesting the occuring changes are sport-specific [56]. Uchida et al. (2023) found that aerobic exercise training impacts the diversity of murine gut microbiota, promoting the increase of *Erysipelotrichaceae* and *Alcaligenaceae* families, that may have a positive effect on endurance capacity [57].

Although it is difficult to determine universal impact the endurance training has on the gut microbiota, it has been shown that some of bacteria genera, such as *Lactobacillus* and *Bifidobacterium* are typically increased in respond to exercise [50]. Moreover, Grosicki et al. (2019) observed rapid changes in ultramarathoner's microbiome after the race, suggesting that the microbiome adapts acutely to physiological demands [58].

4.2 Strength training

Resistance training was historically assumed to have limited impact on the microbiome. Indeed, numerous studies have reported no significant alterations in the gut microbiome composition after strength training [59, 60]. However, Jang et al. (2019) demonstrated that strength-trained individuals exhibit distinct microbial patterns, such as increased abundance of *Sutterella, Clostridium,* and *Faecalibacterium* [61]. This suggests that muscular load—independently of cardiorespiratory stress—may shape microbial function. Prokopidis et al. (2023) observed that supplementation of probiotics improved muscle strength and enhanced muscle mass, suggesting bidirectional link between the gut microbiota and exercise [62].

4.3 High-intensity interval training (HIIT)

HIIT represents a unique physiological stressor combining anaerobic bursts with brief recovery cycles. Wang et al. (2025) observed that HIIT promotes enhancement of *Lactobacillus, Eisenbergiella,* and *Limosilactobacillus,* that may improve muscle strength, endurance capacity, and have a positive impact on cardiovascular health [63]. Nechalová et al. (2024) reported that a 12-week program led to a reduction of the *Firmicutes/Bacteroidetes* ratio and an increase in the abundance of *Akkermansia muciniphila*, and decrease of such SCFAs producers as *Erysipelatoclostridium ramosum, Coprococcus comes,* and *Butyrivibrio fibrisolvens* [64].
However, many studies show that HIIT does not alter the composition of the gut microbiota, although it does improve glucose metabolism, insulin sensitivity and SCFAs production [65, 66, 67]. This suggests the changes in the microbiome diversity may be the result of the overall metabolic health improvement. For example, Couvert et al. (2024) documented the correlation between the reduction of abdominal fat and occuring changes in the gut microbiota diversity in obese men after 12-week cycling or running HIIT programs [68].

4.4 Team sports

Team-sport athletes typically undergo varied training combining strength, endurance, sprinting, and tactical drills—likely explaining the complexity of their microbial profiles. Clarke et al. (2014) demonstrated that professional rugby players possess highly diverse gut microbiota compared with non-athletes [69]. These differences were attributed partly to high caloric and protein intake but also to the metabolic demands of the sport. Another research, carried out by Petri et al. (2024) highlighted the differences in the gut microbiota composition between elite soccer players and sedentary men [70]. Both groups were similar in terms of age and BMI and were following the Mediterranean diet, which involved higher amounts of fiber and lower protein intake than in the previous studies. The study revealed that the compositiom of gut microbiome in athletes compared to sedentary individuals included an increase in the abundance of *Roseburia hominis, Ruminococcaceae,* and *Prevotella albensis,* and increase in butyrate production.

5. The microbiome of Elite Athletes

Elite athletes are at increased risk of systemic inflammation and developing respiratory infections due to cumulative stressors such as strenuous training, frequent travel, psychological stress, and strict dietary regimens. These factors may both challenge and enhance microbial diversity depending on context. Increasing evidence suggests that the gut microbiome

represents an additional layer of biological adaptation contributing to elite performance.
Scheiman et al. (2019) provided groundbreaking evidence that *Veillonella atypica*, increased in marathon runners, metabolizes exercise-induced lactate into propionate [8]. Transplantation of this bacterium into mice improved endurance capacity, suggesting a potential performance-enhancing mechanism. A study conducted by Hintikka et al. (2022) documented that elite athletes are characterised by lower phylogenetic diversity and reduced abundance of *Akkermansia* and *Ruminococcus torques* in comparison to control group [71]. Their study also showed a healthier lipid profile in elite athletes, as well as the positive correlation between Butyricicoccus abundance and HDL cholesterol levels.
Furthermore, a study by Li et al. (2023) revealed how the gut microbiota differs depending on the sport type, including wrestling, aerobics, and rowing, suggesting that microbiome adapts to specific training pattern [72].
In conclusion, current evidence indicates that the gut microbiome is a dynamic, adaptive system that both reflects and supports the physiological demands of elite athletic performance.

6. Microbiome as a Biomarker of Training Adaptation

Growing evidence suggests that the microbiome can serve as a biomarker of training adaptation and performance capacity, and correlates with training and recovery periods.
For example, Akazawa et al. (2023) found that training periodization alters the gut microbiota composition in Japanese elite athletes [73]. The training phase impacted the abundance of *Bacteroides, Blautia, Bifidobacterium,* and *Prevotella*. Moreover, according to the study, the alteration of *Bacteroides* abundance is linked to a change in VO_2max. Similarly, a research conducted by Carlone et al. (2025) showed how elite athletes gut microbiota changes depending on training, competition and recovery phases [74]. The main adaptations included fluctuations in the *Firmicutes/Bacteroidetes* ratio and increased abundance of *Rikenellaceae* in the recovery phase. Authors suggested that an analysis of the gut microbiota may be a useful tool in predicting recovery effectiveness and athletic performance.
As was mentioned earlier, a study by Uchida et al. (2023) showed that the abundance of certain bacterial families are associated with endurance performance [57]. This finding was also supported by the observation that transplantation of the gut microbiota from exercise-trained mice enhanced endurance performance of recipient.
Taken together, these studies indicate that the gut microbiome dynamically reflects training load and recovery status, making it a promising biomarker for assessing and predicting athletic adaptation and performance.

7. Dietary Interventions Modulating the Microbiome

7.1 Probiotics

Probiotics are live microorganisms—most commonly beneficial bacteria—that, when consumed in adequate amounts, provide health benefits to the host [75]. They support gut microbiota by introducing beneficial strains that enhance microbial balance, improve gut barrier function, reduce inflammation, and modulate immune responses [76]. Probiotics can also increase the abundance of health-promoting species and counteract disruptions caused by various stressors, including intense training, thereby contributing to overall gut health and metabolic stability. Their effects have been widely investigated in the context of sports performance. For example, a research by Lin et al. (2020) showed that *Bifidobacterium longum* subsp. *longum* Olympic No. 1 not only increased the abundance of the microbiota, but also enhanced aerobic endurance of the participants [77].

Similarly, Huang et al. (2020) reported that supplementation of *Lactobacillus plantarum* PS128 is linked to an increased endurance capacity [78]. The research also showed an increase in abundance of *Akkermansia*, *Lactobacillus*, *Bifidobacterium*, and *Butyricimonas*, as well as higher levels of SCFAs. However, PS128 supplementation did not improve VO_2max. A study conducted by Jäger et al. (2016) showed that *Bacillus oagulans* GBI-30 supplementation significantly improves recovery and reduces muscle damage following intense exercise [79]. It is also involved in maintaining performance during strenuous training. Additionally, there are numerus animal studies aiming to establish whether probiotic supplementation impacts an endurance capacity and overall physical performance. For instance, Soares et al. (2019) found that *Saccharomyces boulardii* increases VO_2max and improves aerobic performance in rats [80].

7.2 Synbiotics

Synbiotics, a combination of probiotics and prebiotics, are designed to confer synergistic health benefits by simultaneously introducing beneficial microorganisms and providing substrates that support their growth and activity [81, 82, 83]. Evidence from human studies indicates that synbiotic supplementation can modulate selected markers of gut and immune function, such as reducing the incidence of upper-respiratory tract infections in physically active individuals and influencing inflammatory and oxidative stress parameters in clinical populations. Some data from athletic settings also suggest that certain synbiotic formulations may contribute to improved training adaptations—for example, enhancing muscle strength in competitive athletes—although mechanistic pathways such as changes in short-chain fatty acids, intestinal permeability, or nutrient absorption have not been consistently demonstrated [84, 85]. Overall, while synbiotics show potential to benefit the gut–muscle axis and support aspects of performance and recovery [86], current findings remain heterogeneous, and further well-controlled studies are needed to confirm their specific physiological and ergogenic effects.

7.3 Dietary patterns

Given that diet can shape the gut microbiota and the microbiota may, in turn, impact athletic performance, supporting one's gut microbes should be regarded as an effective performance-optimizing approach for athletes [87]. Athletes frequently adopt nutritional strategies focused on performance: high protein intake, carbohydrate loading, supplementation, and often low dietary fiber — a combination that may lead to unintended consequences for microbial diversity [88]. A comprehensive review dedicated to athletes concluded that while regular exercise has the potential to benefit gut microbial activity and metabolic output, common sport-centric dietary practices (high protein, low fiber, simple carbohydrate load, food avoidance) may counteract these benefits [89]. Specifically, such diets may reduce microbial diversity, suppress SCFA-producing bacteria, and shift microbial metabolism toward proteolytic fermentation, with production of potentially harmful metabolites [9].

Dietary fiber provides fundamental substrates for microbial fermentation in the colon [90]. Studies show that high-fiber diet increases the diversity of gut microbiota and therefore impacts SCFAs production. SCFAs are associated with pathways involved in muscle function and energy metabolism, and emerging evidence suggests they may influence glycogen metabolism, which could potentially affect athletic performance [91].

Protein is indispensable for muscle repair, adaptation to training, and overall recovery. For athletes, recommendations often range between 1.2 and 2.0 g/kg/day depending on training type [90]. However, when high protein intake is not balanced with sufficient dietary fiber (or fermentable carbohydrate), it may lead to a shift in microbial metabolism: from carbohydrate fermentation to proteolytic fermentation in the colon [92]. Proteolytic fermentation can generate metabolites such as ammonia, hydrogen sulfide, phenols, indoles, and other nitrogenous compounds — some of which may damage the gut mucosa, impair barrier integrity, increase colonic pH, and favor growth of less beneficial (or even harmful) bacteria. In a study of bodybuilders consuming a very high-protein, low-fiber diet, the relative abundance of SCFA- and lactic acid–producing bacteria decreased, despite regular probiotic supplementation [93]. However, dietary strategies for athletes should not only consider protein quantity, but also the quality and balance of macronutrients — ensuring that protein is complemented by sufficient fermentable carbohydrates.

A well-structured dietary pattern that balances fiber-rich carbohydrates with adequate, but not excessive, protein intake therefore appears essential for maintaining a resilient gut microbiota that can effectively support athletes' health, recovery, and overall performance.

8. Future Directions

Although research on the gut microbiome in athletes has progressed considerably, many aspects of this relationship remain insufficiently understood. A key challenge for future work is the development of unified research protocols. Studies should employ comparable approaches to stool sampling, sequencing methodologies, dietary assessment, and monitoring of training loads so that results from different laboratories can be meaningfully contrasted and combined. Equally important is the need for experimental and mechanistic studies that can determine how particular microorganisms and their metabolites—such as short-chain fatty acids or bile acids—shape physiological processes relevant to sport, including endurance capacity, muscular adaptations, post-exercise recovery, and overall metabolic regulation. Achieving this will require the use of comprehensive multi-omics strategies that integrate microbial composition with metabolic outputs, gene expression, and protein function.

Another promising avenue involves examining how microbiome responses differ according to sport discipline and sex, as emerging evidence suggests that training-specific demands and biological differences create unique microbial patterns. Longitudinal studies that track athletes over extended periods—through preparation phases, competition seasons, travel, and recovery—would offer valuable insight into how the microbiota fluctuates in response to both acute stress and chronic workload.

Given the strong influence of diet on microbial ecology, nutritional factors should remain a central theme in upcoming investigations. Researchers should explore how various macronutrient profiles, fiber intake, and microbiome-directed supplementation strategies, including probiotics, prebiotics, and synbiotics, interact with athletic training to influence performance and health. Attention should also be paid to meal timing and circadian alignment, as these factors may help stabilize microbial rhythms and support optimal physiological functioning.

Finally, the potential clinical implications of microbiome disturbances in athletes warrant deeper exploration. Increasing evidence links alterations in microbial balance with heightened intestinal permeability, systemic inflammation, weakened immunity, and possibly even greater injury risk. Understanding these associations more clearly could enable the creation of personalized interventions aimed at preserving athlete health, improving adaptation to training, and reducing susceptibility to illness or injury.

9. Conclusions

Current evidence demonstrates that the gut microbiome plays a crucial role in modulating physiological pathways relevant to athletic performance, including energy metabolism, immune function, inflammation, oxidative stress, and gut barrier integrity. Exercise-induced changes in microbial composition—particularly increases in beneficial SCFA-producing taxa—may enhance metabolic efficiency and recovery while reducing susceptibility to illness. However, the magnitude and direction of microbiota alterations vary substantially across individuals, sport disciplines, and environmental factors such as diet, stress, and circadian disruption. Endurance athletes exhibit the most consistent microbial adaptations, including expansion of lactate-metabolizing species linked to improved performance. Conversely, strength training and HIIT produce inconsistent microbial shifts, often mediated by dietary intake or metabolic status rather than exercise alone. While elite athletes show distinct microbial profiles, these may not universally translate into enhanced diversity or uniform health benefits. Overall, the relationship between training modalities, microbial ecology, and performance outcomes is complex and multifactorial. A definitive mechanistic model linking gut microbiota and athletic performance has not yet been established.

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