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The Role of Gut Microbiome Modulation in Athletic Performance, Recovery, and Quality of Training: A Narrative Review

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Abstract

Background: Growing evidence suggests that the gut microbiota influences exercise performance through the production of metabolites that regulate numerous physiological processes. Short-chain fatty acids (SCFAs), including butyrate, acetate, and propionate, contribute to energy metabolism, immune regulation, skeletal muscle function, and post-exercise recovery. Gut microbiota composition also affects intestinal barrier integrity and may reduce exercise-induced gastrointestinal syndrome (EIGS).

Aim: To summarize current evidence regarding the role of the gut microbiota in athletic performance, recovery, training quality, and gastrointestinal health, and to evaluate nutritional strategies targeting the gut microbiome in athletes.

Material and methods: A narrative review of peer-reviewed literature published mainly between 2016 and 2025 was conducted using PubMed, Scopus, and Google Scholar. Original studies, systematic reviews, meta-analyses, and position statements investigating the gut microbiota, physical performance, recovery, probiotics, prebiotics, dietary interventions, and EIGS were included.

Results: Current evidence indicates that SCFA-producing bacteria enhance mitochondrial function, ATP production, glycogen storage, and anti-inflammatory responses. Probiotic strains and fiber-rich diets may improve recovery, immune function, intestinal barrier integrity, and exercise capacity. *Veillonella atypica* may enhance endurance by converting exercise-induced lactate into propionate, whereas prolonged high-protein, low-fiber diets may adversely affect gut microbiota composition.

Conclusions: Targeted modulation of the gut microbiota through appropriate nutrition and selected probiotic supplementation may improve athletic performance, recovery, intestinal health, and training quality. Further well-designed clinical studies are needed to develop personalized microbiome-based nutritional strategies for athletes.

Keywords: gut microbiota, sport, physical performance, recovery, probiotics, prebiotics, short-chain fatty acids (SCFAs), gut–muscle axis, gut–brain axis, sports nutrition

Introduction

An increasing body of evidence indicates that the gut microbiome plays a crucial role not only in maintaining health but also in shaping exercise capacity, post-exercise recovery, and physiological adaptations to training.[\(1,2\)](#)

The gut microbiome is a complex ecosystem of microorganisms inhabiting the human gastrointestinal tract, comprising approximately 10^{14} – 10^{15} microbial cells.[\(3\)](#) It consists

primarily of bacteria but also includes archaea, fungi, viruses, and protozoa.[\(4\)](#) The dominant bacterial phyla are Firmicutes (Bacillota) and Bacteroidetes (Bacteroidota), which play essential roles in nutrient metabolism, short-chain fatty acid (SCFA) production, and the maintenance of intestinal barrier integrity.

Studies have demonstrated that athletes and individuals who engage in regular physical activity exhibit greater gut microbial diversity than sedentary individuals.[\(5\)](#) They also show a higher abundance of beneficial bacterial taxa, including *Akkermansia* spp. and *Prevotella* spp. This microbial profile is associated with enhanced metabolic activity and may contribute to improved exercise performance and recovery.[\(6\)](#)

Intense and prolonged physical exercise may lead to the development of exercise-induced gastrointestinal syndrome (EIGS). EIGS comprises a series of physiological responses to exercise that impair normal gastrointestinal function. These responses occur through two principal pathways. The first is the circulatory–gastrointestinal pathway, in which blood flow is redistributed toward active skeletal muscles and peripheral tissues to support muscular metabolism and thermoregulation, resulting in reduced perfusion of the splanchnic organs. The second is the neuroendocrine–gastrointestinal pathway, characterized by increased sympathetic nervous system activity, leading to disturbances in gastrointestinal motility and function.[\(7\)](#)

Splanchnic hypoperfusion results in intestinal ischemia, which damages the intestinal epithelium and disrupts the function of cells responsible for maintaining intestinal barrier integrity. Consequently, intestinal permeability increases due to the disruption of tight junction proteins, including claudins and occludins.[\(7\)](#)

Damage to the intestinal barrier activates local inflammatory responses mediated by NF- κ B and pro-inflammatory cytokines such as IL-1 β , TNF- α , and IFN- γ , further exacerbating barrier dysfunction.[\(7\)](#) Increased intestinal permeability facilitates the translocation of bacteria and bacterial endotoxins, including lipopolysaccharide (LPS), into the systemic circulation, thereby promoting both local and systemic inflammation.[\(8\)](#)

These alterations may manifest clinically as nausea, diarrhea, abdominal pain and cramping, and impaired nutrient absorption.[\(7\)](#) Such symptoms not only reduce athletes' comfort but, more importantly, compromise their ability to maintain the planned training intensity and

successfully accomplish training objectives. Therefore, preserving intestinal barrier integrity and maintaining a balanced gut microbiome are essential for sustaining high-quality training.

In light of these observations, the aim of the present review is to evaluate the impact of the gut microbiome on athletic performance and post-exercise recovery. Athletes experiencing gastrointestinal dysfunction are often unable to fully execute their training programs, which directly affects the quality of sports preparation.

Methodology

This narrative review was prepared based on a comprehensive analysis of the current scientific literature concerning the relationship between the gut microbiota and athletic performance. The literature search was conducted using the PubMed, Scopus, and Google Scholar databases. Original research articles, systematic reviews, meta-analyses, and position statements published primarily between 2016 and 2025 were considered. The following keywords and their combinations were used: gut microbiota, gut microbiome, exercise, physical performance, athletes, probiotics, prebiotics, short-chain fatty acids, gut–muscle axis, gut–brain axis, and exercise-induced gastrointestinal syndrome (EIGS). Preference was given to peer-reviewed publications published in English that addressed the effects of gut microbiota on exercise performance, recovery, immune function, gastrointestinal health, and nutritional interventions. Studies not directly related to physically active individuals or athletes, conference abstracts, and publications lacking sufficient methodological quality were excluded. The collected evidence was synthesized narratively to summarize the current understanding of the role of the gut microbiota in sports performance and to identify potential directions for future research.

Gut microbiota, short-chain fatty acids, and exercise performance

Growing evidence suggests that the gut microbiota influences exercise performance through the production of metabolites that regulate numerous physiological processes.[\(9\)](#)

Particular attention has been given to bacteria such as *Faecalibacterium prausnitzii*, *Roseburia hominis*, members of the genera *Eubacterium* and the family *Lachnospiraceae*, as well as

Akkermansia muciniphila. Through the fermentation of dietary fiber, these microorganisms produce short-chain fatty acids (SCFAs), primarily **butyrate, acetate, and propionate**. Physically active individuals have been shown to harbor a greater abundance of SCFA-producing bacteria than sedentary individuals.[\(10\)](#)

SCFAs influence skeletal muscle metabolism through several mechanisms.

Acetate, which readily enters the systemic circulation, can be taken up by skeletal muscles and utilized for ATP production, particularly during prolonged exercise. In addition, acetate enhances glucose uptake and promotes glycogen synthesis in skeletal muscle, thereby improving energy availability.[\(11\)](#)

Among the SCFAs, **butyrate** appears to play a particularly important role. It protects against oxidative stress and muscle loss by stimulating mitochondrial function and biogenesis while increasing the proportion of oxidative (type I) muscle fibers. Mechanistically, butyrate activates AMP-activated protein kinase (AMPK) and the peroxisome proliferator-activated receptor gamma coactivator-1 alpha (PGC-1 α) signaling pathway, resulting in enhanced mitochondrial biogenesis. A greater mitochondrial density improves aerobic ATP production, increases fatty acid oxidation, and reduces oxidative stress, collectively contributing to improved endurance performance.[\(11\)](#)

Lactobacillus spp. produce lactic acid (lactate), which can be utilized by other gut bacteria that produce butyrate. During this process, lactate is converted into acetyl-CoA, a key precursor for butyrate synthesis. Consequently, *Lactobacillus* spp. indirectly promote the production of short-chain fatty acids (SCFAs), which may beneficially influence energy metabolism and exercise performance. [\(12\)](#)

In addition to their effects on skeletal muscle, butyrate, propionate, and acetate contribute to **energy harvest** from dietary substrates. In individuals consuming a high-fiber diet (approximately 60 g/day), SCFAs may provide up to 10% of daily energy requirements, representing an additional source of metabolic fuel during prolonged endurance exercise.[\(10\)](#)

The gut–brain axis

Beyond their metabolic functions, gut microbiota-derived metabolites also influence central nervous system function through the **gut–brain axis**.[\(13\)](#)

Microbial metabolites such as SCFAs, together with neurotransmitters including serotonin and dopamine produced or regulated by intestinal microorganisms, communicate with the brain through both the circulation and the vagus nerve. These signaling molecules modulate cognitive function, mood, stress responsiveness, and the perception of fatigue. Furthermore, they contribute to psychological well-being by attenuating systemic inflammation and preserving blood–brain barrier integrity.

A healthy gut microbiota may also suppress excessive activation of the **hypothalamic–pituitary–adrenal (HPA) axis**, resulting in lower cortisol concentrations and reduced stress and anxiety. Consequently, athletes may demonstrate improved concentration, greater psychological resilience, and more efficient recovery following strenuous exercise.[\(14\)](#)

Anti-inflammatory effects of beneficial bacteria

Several probiotic strains, including *Bifidobacterium longum* BL986, *Lactiplantibacillus plantarum* PS128, *Bacillus coagulans*, *Bacillus subtilis* DE111, and *Limosilactobacillus fermentum* VRI-033, have been shown to reduce circulating concentrations of the pro-inflammatory cytokines **TNF- α** and/or **IL-6**, which typically increase after intense exercise. Some of these strains also enhance the production of the anti-inflammatory cytokine **IL-10**, thereby contributing to the attenuation of chronic low-grade inflammation.[\(11\)](#)

Moreover, higher SCFA production has been associated with greater aerobic capacity (VO_2peak) and an increased abundance of butyrate-producing bacteria.[\(10\)](#)

SCFAs also promote the differentiation of regulatory T cells (Tregs), thereby maintaining immune tolerance and suppressing excessive inflammatory responses. Regular physical activity further increases the abundance of SCFA-producing bacteria while reducing the prevalence of

pro-inflammatory taxa such as **Proteobacteria**. Consequently, lipopolysaccharide (LPS) production decreases, intestinal barrier function improves, and systemic inflammation is attenuated. [\(15\)](#)

Through the **gut–muscle axis**, a healthy gut microbiota may therefore reduce circulating LPS and pro-inflammatory cytokines while enhancing anti-inflammatory signaling, ultimately promoting muscle function and facilitating training adaptations. [\(14\)](#)

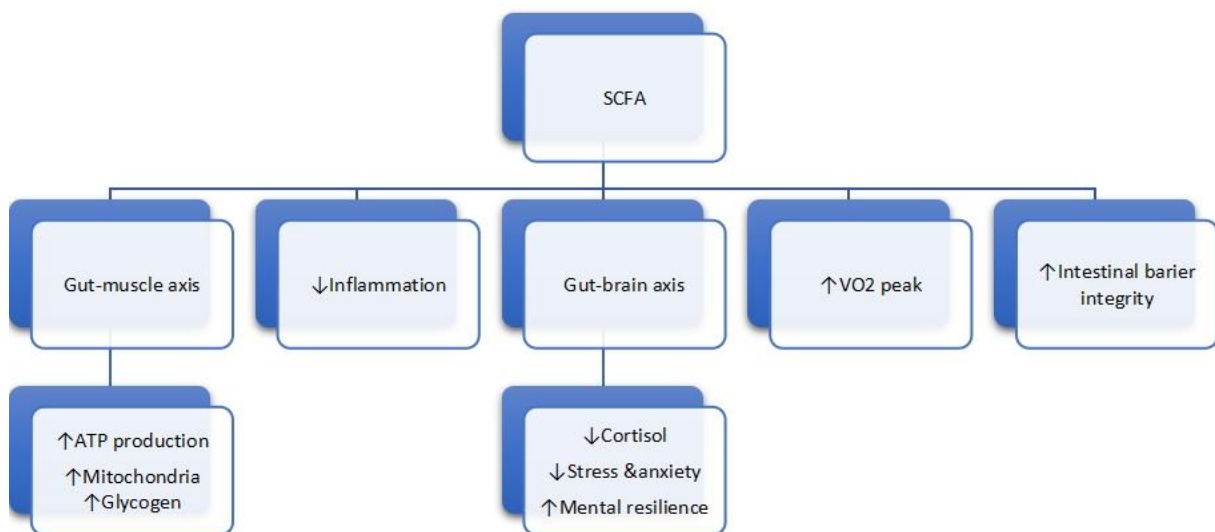


Figure 1. The role of SCFAs- summary

Lactobacillus and exercise recovery

Members of the genus *Lactobacillus* have attracted considerable attention because of their beneficial effects on inflammation, recovery, and exercise performance.

In triathletes, supplementation with *Lactobacillus plantarum* reduced circulating concentrations of TNF- α , IL-6, and IL-8 while simultaneously increasing IL-10 levels and plasma concentrations of branched-chain amino acids (BCAAs). By attenuating exercise-induced inflammation, probiotic supplementation may improve training tolerance and help athletes maintain a high level of physical performance.

Lactobacillus species suppress the activation of the transcription factor **NF- κ B** and reduce the production of pro-inflammatory cytokines while enhancing anti-inflammatory cytokine secretion. These immunomodulatory effects promote skeletal muscle repair following exercise, reduce muscle soreness, and alleviate fatigue.

Furthermore, supplementation with *Lactobacillus plantarum* has been reported to improve iron utilization, potentially accelerating erythropoiesis and enhancing aerobic capacity and endurance performance.

Gut bacteria, including members of the genera *Clostridium*, *Bacillus*, and *Streptococcus*, as well as representatives of the phylum Proteobacteria, also participate in amino acid metabolism and may increase amino acid bioavailability to the host. For example, supplementation with *Bacillus coagulans* has been shown to increase serum amino acid concentrations following milk protein ingestion.[\(15\)](#)

Veillonella atypica—a performance-enhancing bacterium

Among gut microorganisms associated with athletic performance, *Veillonella atypica* has received particular attention. The abundance of this bacterium increases following intense physical exercise. Unlike most gut bacteria, *V. atypica* utilizes lactate produced by exercising skeletal muscles and converts it into SCFAs, primarily **propionate**.[\(10,16\)](#)

Both the abundance of *Veillonella* species and the expression of genes involved in the metabolic pathway converting lactate into propionate increase after exercise. [\(10,16,17\)](#)

Animal studies have demonstrated that intestinal colonization with *Veillonella atypica* prolongs running time to exhaustion by approximately **13%** compared with control animals. Remarkably, direct administration of propionate into the intestinal lumen produced a similar

improvement in endurance capacity, suggesting that propionate is the principal mediator of this effect.[\(10,16,17\)](#)

These findings indicate that lactate released by working muscles may be utilized by the gut microbiota for propionate synthesis. The resulting propionate subsequently enters the systemic circulation, where it may contribute to improved endurance performance.[\(10,16\)](#)

Furthermore, animals colonized with *Veillonella atypica* exhibited lower circulating concentrations of pro-inflammatory cytokines following exercise than control animals. These observations suggest that an appropriately balanced gut microbiota may attenuate exercise-induced inflammation, thereby promoting more efficient post-exercise recovery.[\(16\)](#)

Modulation of the gut microbiota as a strategy to enhance athletic performance

An increasing body of evidence suggests that modulation of the gut microbiota may represent a practical strategy for optimizing sports performance. Interventions involving **probiotics, prebiotics, synbiotics, and postbiotics** can alter both the composition and metabolic activity of the gut microbiota, leading to improvements in immune function, intestinal barrier integrity, energy metabolism, and recovery processes. Consequently, these interventions may reduce inflammation, enhance nutrient utilization, and improve the body's capacity to adapt to exercise-induced stress.[\(5,14,15,18\)](#)

Probiotics, immunity, and psychological resilience

A well-balanced gut microbiota plays a pivotal role in maintaining immune homeostasis. Supplementation with selected strains *Lactobacillus* and *Bifidobacterium* strains has been shown to reduce the incidence of gastrointestinal symptoms as well as upper respiratory tract infections in athletes.[\(1,18\)](#) Since respiratory infections frequently interrupt training programs, reducing their occurrence may contribute to greater training continuity and improved athletic preparation.

Several *Lactobacillus* species have also been reported to stimulate immunoglobulin A (IgA) secretion, thereby enhancing mucosal immunity and modulating immune responses.[\(14\)](#)

Interestingly, supplementation with *Bifidobacterium lactis* CBP001010, *Lactobacillus rhamnosus* CNCM I-4036, *Bifidobacterium longum* ES1, and fructooligosaccharides has been associated with improved sleep quality and reduced perceived stress and anxiety in professional soccer players.

Similarly, *Bifidobacterium longum* R0175 has been shown to reduce anxiety and circulating free cortisol concentrations, whereas animal studies have demonstrated that *Lactobacillus helveticus* decreases anxiety-like behavior and lowers adrenocorticotrophic hormone (ACTH) levels. [\(19\)](#) These mechanisms may be particularly relevant for athletes, as reduced chronic stress facilitates recovery, improves concentration, and supports consistent training quality.

Diet and gut microbiota composition

Diet is one of the most important determinants of gut microbiota composition.

A diet rich in dietary fiber provides substrates for bacterial fermentation, promoting the growth of beneficial SCFA-producing bacteria such as *Akkermansia*, *Roseburia*, and *Faecalibacterium*. As discussed above, SCFAs exert numerous beneficial effects on exercise performance, recovery, and adaptation to training.[\(14\)](#)

In strength and endurance sports, protein supports the repair of micro-injuries occurring during training and helps maintain muscle mass [\(20\)](#). A high-protein diet is frequently used by athletes [\(6\)](#) it is crucial to examine their impact on the microbiome.

Excessive protein intake can lead to amino acid fermentation in the colon, resulting in the generation of undesirable metabolites such as phenol, hydrogen sulfide, amines, and urea. These compounds can increase the permeability of the intestinal barrier, exacerbate inflammation, and damage intestinal epithelial cells. Additionally, intense physical exertion itself increases urea concentrations [\(19\)](#).

High protein intake also increases the abundance of protein-fermenting bacteria such as *Clostridium*, *Bacillus*, *Staphylococcus*, and other species belonging to the Proteobacteria family [\(6\)](#). Therefore, a high-protein diet must be properly balanced. Consuming a diet rich in vegetables, fiber, and/or starch alongside animal protein appears to reduce the negative impact of amino acid byproducts fermented by the microbiome [\(19,21\)](#)

This is particularly important to remember because athletes—especially before competitions or intense exertion—often temporarily adopt diets low in fiber and resistant starch to reduce the risk of gastrointestinal discomfort. However, prolonged adherence to such practices can lead to reduced microbiota diversity and limited production of short-chain fatty acids (SCFAs) [\(19\)](#).

Polyphenols and gut microbiota

Polyphenols are bioactive compounds naturally present in fruits, vegetables, cocoa, tea, and coffee. [\(22\)](#) These compounds positively influence gut microbiota composition by promoting the growth of beneficial microorganisms, including *Lactiplantibacillus*, *Bifidobacterium*, *Roseburia*, *Faecalibacterium*, and *Akkermansia muciniphila*, while simultaneously inhibiting the proliferation of potentially pathogenic bacteria.

Importantly, polyphenols are themselves metabolized by the gut microbiota. Their microbial metabolites—including phenylpropionic acid (PPA), hydroxyphenylacetic acid (HPAA), and 4-hydroxyphenylacetic acid (4-HPAA)—possess antioxidant and anti-inflammatory properties and contribute to the maintenance of intestinal barrier integrity.[\(23\)](#)

Discussion

One of the major challenges in this field is the considerable interindividual variability in responses to dietary interventions and probiotic supplementation.

The effectiveness of nutritional and probiotic strategies depends largely on each individual's gut microbiota composition, genetic background, and metabolic characteristics. Consequently, identical dietary or probiotic interventions may produce markedly different outcomes among

athletes. These observations underscore the need for more personalized approaches to microbiome-targeted nutritional strategies in sports medicine.[\(14\)](#)

In addition, a notable gap remains in the current literature. The effects of physical activity on the gut microbiome appear to vary depending on the type of exercise performed (e.g., endurance versus resistance training). Although accumulating evidence suggests that regular physical activity exerts beneficial effects on gut microbiome health, including increased microbial diversity and enhanced production of short-chain fatty acids (SCFAs), comprehensive studies are still lacking. Further research is needed to fully elucidate how different exercise modalities and intensities influence gut microbiome composition and function. [\(5,15\)](#)

The future of sports nutrition research is moving toward personalized nutritional strategies. In this context, **nutrigenomics**—the field that investigates the interactions between nutrition and the genome [\(24\)](#)—may play a pivotal role. Advances in nutrigenomics have the potential to optimize dietary interventions according to an individual's genetic profile and metabolic characteristics, thereby improving exercise performance, training adaptations, and overall athletic potential.[\(14\)](#)

Conclusions

Current evidence indicates that the **gut–muscle axis** is an important regulator of exercise performance, recovery, and physiological adaptation to physical training. Particular attention has been directed toward SCFA-producing bacteria, including *Faecalibacterium prausnitzii*, *Roseburia hominis*, *Akkermansia muciniphila*, and *Veillonella atypica*. Through the production of butyrate, propionate, and acetate, these microorganisms support skeletal muscle energy metabolism, exert anti-inflammatory effects, preserve intestinal barrier integrity, and facilitate post-exercise recovery.

Appropriate modulation of the gut microbiota through a well-balanced diet, together with targeted probiotic and prebiotic supplementation, may attenuate the adverse consequences of intensive training, including exercise-induced gastrointestinal syndrome (EIGS), increased intestinal permeability, and chronic low-grade inflammation.

Maintaining gut health should therefore be considered an integral component of athletic preparation. Optimizing gut microbiota composition has the potential to improve training continuity, enhance recovery, promote physiological adaptation to exercise, and ultimately support superior athletic performance.

However, it should be emphasized that several important knowledge gaps remain. Considerable interindividual variability means that the effectiveness of dietary and probiotic interventions is highly individualized. Future research is expected to focus on the development of personalized nutrition and supplementation strategies that take into account an athlete's gut microbiota composition, genetic background, and metabolic profile. Such approaches may further optimize athletic performance and improve training outcomes.

Disclosure

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