

Gut Microbiota in Athletes: Implications for Physical Performance and Recovery

Karina Reczek ¹ 
Anna Zalewska ¹ 
Weronika Hariasz ² 
Marta Drobik ¹ 
Katarzyna Gądek ¹ 
Marek Borowiec ¹ 
Agnieszka Gontkowska ² 
Adam Lichodij ¹ 

¹ Medical Faculty, Wrocław Medical University, Wrocław, Poland

² Medical Faculty, University of Opole, Opole, Poland

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Corresponding author

Weronika Hariasz
131880@student.uni.opole.pl

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Abstract

The gut microbiota represents a potentially important component of athletic adaptation, functioning as a specialized metabolic organ that interacts with host physiology through the gut-muscle axis. This review aims to analyze the role of the gut microbiota in modulating physical performance and post-exercise recovery in athletes, with particular emphasis on microbial metabolites and diet-dependent mechanisms. A narrative literature review was conducted based on studies indexed in PubMed and Scopus (2013–2026). The analysis included experimental, clinical and animal studies focusing on gut microbiota composition, short-chain fatty acids (SCFAs), exercise physiology and sports nutrition. The unique microbial ecosystem of athletes may contribute to physical performance through the production of SCFAs, such as acetate and propionate, which can

influence skeletal muscle metabolism via AMPK and GLUT4 signalling pathways. Animal studies suggest that intestinal microbes are important for maintaining skeletal muscle mass, neuromuscular integrity and exercise capacity. Additionally, the gut microbiota may contribute to post-exercise recovery by enhancing intestinal barrier function, modulating immune responses and reducing oxidative stress and systemic inflammation. These effects are strongly influenced by dietary composition, particularly the balance between protein and fibre intake, which determines microbial homeostasis and metabolite production. Current evidence supports an association between gut microbiota, exercise performance and recovery, although direct causal evidence in athletes remains limited. Its modulation through targeted nutritional strategies and gut-training protocols represents a promising direction for personalized sports nutrition in competitive athletes.

Introduction

The human gut microbiota is defined as a complex and dynamic community of microorganisms that inhabit the gastrointestinal (GI) tract (Afzaal et al. 2022; Rinninella et al. 2019). Often characterized as a “metabolically active organ”, this ecosystem is critical for maintaining host homeostasis through its metabolic, protective, and structural functions (Ahlawat et al. 2021; Dogra et al. 2020). As a key regulator of digestion, it enables the extraction and synthesis of nutrients and metabolites, such as bile acids, amino acids and short-chain fatty acids (SCFAs), which are essential for systemic energy balance (Afzaal et al. 2022; Khosravi, Mazmanian 2013). Furthermore, it maintains intestinal barrier integrity and plays a fundamental role in the development and modulation of the immune system (Brestoff, Artis 2013; Khosravi, Mazmanian 2013; Tomkovich, Jobin 2016).

The composition of the gut microbiota exhibits high inter-individual variability, influenced by factors such as age, lifestyle and dietary choices (Ma et al. 2026; Rinninella et al. 2019). A healthy gut is typically dominated by the phyla *Firmicutes* and *Bacteroidetes* and characterized by high microbial richness and diversity, which are considered hallmark features of a stable microbial ecosystem (Afzaal et al. 2022; Ma et al. 2026). Recent research identifies physical activity as a significant driver of microbial shifts, with athletes representing a unique model for studying these interactions due to their distinct lifestyle and training demands (Clarke et al. 2014). This bidirectional relationship has given rise to the concept of the gut–muscle axis, a signalling network where microbial metabolites may influence skeletal muscle function and exercise adaptation, while physical activity reciprocally shapes microbial composition and diversity (Przewłocka et al. 2020).

Despite growing interest in this relationship, several research gaps remain. Most human studies are observational and include relatively small and heterogeneous groups of athletes, making it difficult to separate the effects of exercise from those of diet, training modality, body composition and other lifestyle factors. Moreover, several proposed mechanisms of the gut-muscle axis have been demonstrated mainly in animal models, while direct causal evidence in

trained humans remains limited. Understanding this axis is crucial for optimizing health and performance in competitive sports. This review synthesizes current evidence regarding the gut microbiota in athletes. Firstly, the characteristic features of the athletic gut microbiome and the role of diet (protein, fibre and carbohydrates) are examined. Secondly, the mechanisms through which microbial metabolites, particularly SCFAs, influence skeletal muscle metabolism, energy substrate utilization and physical performance are discussed, including evidence derived from germ-free (GF) animal models. Finally, the contribution of the gut microbiota to post-exercise recovery processes, such as immune modulation, intestinal barrier function and the regulation of oxidative stress, is evaluated. Particular attention is given to distinguishing observations obtained in humans from mechanistic evidence derived from animal studies.

Research Objective

The objective of this review is to synthesize current evidence regarding the role of the gut microbiota in athletic performance and recovery, with particular emphasis on the gut–muscle axis, microbial metabolites such as SCFAs, and the influence of dietary factors on microbial composition and function in athletes.

Methodology

This narrative review was based on a literature search conducted using the PubMed and Scopus databases. The search included studies published between 2013 and 2026 focusing on gut microbiota, physical activity, athletes, SCFAs and exercise recovery.

The search used combinations of relevant terms connected by the Boolean operators ‘and’ or ‘or’ and included: “gut microbiota” or “gut microbiome”, together with “athlete”, “exercise” or “physical activity”, and terms related to the main topics of the review, including “physical performance”, “recovery”, “short-chain fatty acids” or “SCFA”, “skeletal muscle”, “diet”, “fibre”, “protein”, “carbohydrate” and “probiotics”.

Original research articles, review articles, and relevant experimental studies in humans and animals were included. Non-English publications, conference abstracts and opinion papers were excluded.

Studies were considered relevant when they addressed athletes or physically active individuals, exercise interventions or experimental mechanisms related to the gut-muscle axis and reported outcomes concerning gut microbiota composition or function, microbial metabolites, physical performance, skeletal muscle metabolism, post-exercise recovery, intestinal barrier function, inflammation or sports nutrition. Both acute and chronic exercise studies were considered.

Studies were selected based on relevance to the topic after screening titles, abstracts and full texts. Additional relevant articles were identified by screening the reference lists of relevant articles.

Because the present article was designed as a narrative rather than a systematic review, the literature-selection process was not conducted according to a PRISMA protocol and numerical records of publications identified and excluded at each stage were not prospectively collected. No formal risk-of-bias tool was applied. However, the study design and the distinction between human and animal evidence were considered when interpreting the findings.

The findings were synthesized narratively.

Gut Microbiota: Characteristics and Shaping Factors in Athletes

Athletes represent a distinct population whose gut microbiota is notably rich and complex, reflecting the unique physiological demands associated with elite athletic performance. Current evidence demonstrates that physical activity is a significant driver of inter-individual microbial variation, clearly distinguishing athletes from sedentary individuals. However, these differences should be interpreted cautiously because athletes and sedentary individuals also differ in diet, energy intake, body composition and other lifestyle factors. This distinction is apparent not only in composition, such as higher microbial diversity and increased abundance of *Akkermansia muciniphila* observed in professional rugby players (Clarke et al. 2014), but also at the functional level. Metagenomic and metabolomic analyses reveal that the athletic microbiota possesses an enriched metabolic potential, particularly in pathways related to amino acid biosynthesis and carbohydrate metabolism (Barton et al. 2018).

However, the “athlete microbiome” is not a uniform entity; rather, its structure is significantly stratified by the specific requirements of different sport disciplines and training modalities (Jang et al. 2019; O’Donovan et al. 2020; Petersen et al. 2017). For instance, bodybuilders exhibit a distinct profile characterized by a higher abundance of *Faecalibacterium* and *Sutterella*, alongside a lower abundance of *Bifidobacterium* (Jang et al. 2019). In contrast, competitive cyclists show a strong dose-response relationship between exercise volume and the abundance of *Prevotella*, with professional-level athletes further distinguished by the high transcriptional activity of *Methanobrevibacter smithii* (Petersen et al. 2017). These patterns are further reinforced by Sports Classification Groups (SCGs), where high-dynamic sports are associated with an enrichment of *Faecalibacterium prausnitzii*, while sports with high static components are associated with distinct host metabolic markers, such as increased urinary lactate (O’Donovan et al. 2020).

The functional specialization of the athletic gut is most evident in its acute response to extreme physical stress. This is exemplified by a post-race increase in *Veillonella* abundance in marathoners runners, which is hypothesized to facilitate the conversion of exercise-induced lactate into propionate via the methylmalonyl-CoA pathway (Scheiman et al. 2019). Importantly, the increase in *Veillonella* was observed in humans, whereas the improvement in exercise capacity following administration of *V. atypica* or propionate was demonstrated experimentally in mice. Therefore, these findings provide mechanistic support but do not establish an ergogenic effect in human athletes. Crucially, many of these stable and specialized microbial signatures appear to be the result of long-term, sustained adaptation. While cardiorespiratory training can induce transient shifts in sedentary individuals, these changes often return to baseline, and resistance training alone may show no significant impact over short durations. This suggests that the robust gut ecosystem observed in elite athletes likely emerges from chronic training rather than short-term exercise cycles (Bycura et al. 2021).

In addition to the effects of exercise, diet plays a significant role in shaping the human gut microbiota. The two factors are closely linked: in general athletes consume diets with higher energy content than sedentary individuals and are often recommended a macronutrient profile high in carbohydrates and protein, with lower fat intake (Kerksick et al. 2018). Dietary composition and energy availability are key determinants of the athletic gut community structure, where an optimized nutritional profile can contribute up to 7–22% of daily caloric turnover through microbial metabolism, while insufficient intake may lead to detrimental shifts in microbiota maturity and diversity (Mohr et al. 2020).

While protein intake and exercise are important modulators of gut microbial diversity, their benefits appear to be contingent on overall nutritional status. Specifically, high-protein diets may negatively impact microbial diversity and reduce beneficial SCFA-producing bacteria when carbohydrate and fibre intake is insufficient (Jang et al. 2019). These effects may also depend on protein source, total dietary composition and the availability of fermentable carbohydrates. This protein-induced shift is primarily driven by the fermentation of unabsorbed dietary protein in the colon, a process that favours the growth of proteolytic taxa such as *Clostridium*, *Bacillus* and *Staphylococcus* (Szurkowska et al. 2021). While protein catabolism can yield beneficial metabolites like indole, it also produces potentially toxic compounds, including ammonia, sulfides and p-cresol, which may compromise gut epithelial integrity (Blachier et al. 2019).

The impact of such diets is exemplified by a study on endurance runners, where 10-week protein supplementation resulted in an increased abundance of *Bacteroidetes* alongside a decrease in health-associated taxa, including *Roseburia spp.*, *Blautia spp.* and *Bifidobacterium longum* (Moreno-Pérez et al. 2018). However, these microbial changes were not shown to cause impaired athletic performance. The detrimental effects of high protein intake appear to be significantly

attenuated by adequate fibre consumption. Evidence suggests that when fibre intake meets or exceeds recommended levels (e.g. ≥ 25 g/day), the abundance of commensal bacteria such as *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* can be preserved despite high protein consumption (Jang et al. 2019).

This potential buffering role of fibre is supported by observations across different athletic populations. For example, resistance athletes with low fibre intake have been shown to exhibit reduced levels of SCFA-producing bacteria, whereas professional rugby players with high fibre intake (median ~ 39 g/day) maintain high diversity and a balanced community structure (Clarke et al. 2014; Jang et al. 2019). Consequently, maintaining a balance between protein quantity and microbiota-accessible carbohydrates (MACs) is essential to prevent dysbiosis and maintain intestinal health in athletes.

Beyond energy provision, carbohydrates serve as essential substrates for the gut microbiota, which possesses enzymatic capabilities to disassemble complex fibres that escape human digestion (El Kaoutari et al. 2013; Holscher 2017). In endurance athletes, chronic high-fibre intake typically favours an enrichment of the *Prevotella* genus, a profile associated with enhanced metabolic capacity, although its health implications may be strain-specific (Chen et al. 2024). However, athletes often face a “nutritional paradox”: while complex carbohydrates are vital for microbial health, many limit fibre intake to ensure rapid gastric emptying and minimize GI distress during competition (Holscher 2017; Thomas et al. 2016). Such long-term fibre restriction may compromise microbial diversity and the production of SCFAs (Clark, Mach 2016; Jang et al. 2019). Nevertheless, the risk of GI distress associated with high carbohydrate intake can be mitigated through “gut-training” protocols, which improve the intestinal tolerance of extreme nutritional loads in elite athletes (King et al. 2022). It should be noted that the available evidence for gut-training primarily concerns gastrointestinal tolerance and carbohydrate absorption rather than direct modification of the gut microbiota. Furthermore, the production of beneficial SCFAs is not solely dependent on isolated fibre intake; emerging evidence suggests a synergistic effect where the interaction between specific MACs, such as L-arabinose and simple sugars like sucrose, significantly enhances the metabolic output of acetate and propionate producers (Tomioka et al. 2022).

The Role of Gut Microbiota in Physical Performance and Athletic Adaptation

The gut microbiota significantly influences host energy metabolism through the production of bioactive metabolites, primarily SCFAs, which are estimated to contribute approximately 10% of the host’s daily caloric requirements (Alruways

2023; Sales, Reimer 2023). These metabolites, mainly acetate, propionate and butyrate, are produced in the colon via the microbial fermentation of indigestible carbohydrates, such as dietary fibre and resistant starch (Alruways 2023; Fusco et al. 2023; Martin-Gallausiaux et al. 2021; Wang et al. 2024). Within this metabolic profile, acetate typically accounts for the largest proportion (approximately 60%), while propionate and butyrate each constitute about 20% (Martin-Gallausiaux et al. 2021; Ottria et al. 2026; Sales, Reimer 2023).

Beyond direct caloric provision, SCFAs act as signalling molecules and metabolic regulators within skeletal muscle. Most direct evidence for these mechanisms, however, comes from experimental models. They activate AMPK, a key regulator of cellular energy homeostasis, which promotes the efficient metabolism of glucose and lipids, thereby optimizing energy availability during physical activity (Cerdá et al. 2016). Furthermore, by binding to G protein-coupled receptors (GPR41 and GPR43), SCFAs stimulate the secretion of glucagon-like peptide-1 (GLP-1) and peptide YY (PYY). These hormones regulate energy expenditure and insulin sensitivity, and their activation may influence pathways relevant to post-exercise glycogen resynthesis and metabolic recovery (Hernández et al. 2019; Martin-Gallausiaux et al. 2021; Sasidharan Pillai et al. 2024).

Emerging evidence indicates that these microbial pathways directly modulate skeletal muscle substrate utilization, a key determinant of physical performance. In rodent models, SCFAs enhance glycogen storage capacity in skeletal muscle by upregulating the expression of glucose transporter type 4 (GLUT4), thereby facilitating increased glucose uptake and glycogen resynthesis (Maruta et al. 2016). Given that muscle glycogen depletion is a primary limiting factor during prolonged exercise, this mechanism suggests a potential for improved endurance capacity, although human data remain limited.

Beyond glycogen modulation, specific bacterial taxa utilize host-derived metabolites to sustain physical exertion. For instance, *Veillonella* possesses the unique capacity to convert circulating lactate (originating from working muscles) into propionate via the methylmalonyl-CoA pathway, a mechanism proposed to enhance endurance capacity in rodent models, though its quantitative significance in humans requires further investigation (Scheiman et al. 2019). In a related line of evidence, microbially produced acetate, derived from dietary fibre fermentation, has been shown to serve as a direct energy substrate for skeletal muscle during prolonged activity. Crucially, depletion of these microbial metabolites, whether through antibiotic treatment or a low-fibre diet, markedly reduced exercise capacity, an effect that was specifically reversed by acetate infusion (Okamoto et al. 2019). These effects were demonstrated in mice and require confirmation in human athletes.

The role of the gut microbiota in maintaining exercise capacity and skeletal muscle homeostasis is further supported by GF and antibiotic-treated animal models. GF mice exhibit significantly lower exercise capacity and impaired

physiological adaptation compared to conventionally colonized counterparts. Colonization with butyrogenic bacteria such as *Eubacterium rectale* enhanced endurance by optimizing energy availability (including upregulation of GLUT4) and improving the clearance of fatigue-associated metabolites like ammonia (Huang et al. 2019). Additionally, the gut microbiota is a determinant of skeletal muscle mass and physical strength. GF models display significant muscle atrophy and impaired grip strength, which are linked to downregulation of key neuromuscular junction proteins (e.g. Rapsyn, Lrp4) and reduced systemic availability of essential amino acids. Importantly, microbiota transplantation reversed these deficits, restoring muscle mass and oxidative metabolic capacity (Lahiri et al. 2019). These findings support a mechanistic gut-muscle relationship but cannot be directly extrapolated to competitive athletes. In line with these findings, transient depletion of the gut microbiota using antibiotics increases muscle fatigability and reduces running performance in mice, without affecting muscle mass or mitochondrial biogenesis. Instead, these performance deficits correlate directly with disrupted systemic glucose homeostasis and reduced muscle glycogen reserves, both of which are restored following natural microbial reseedng (Nay et al. 2019).

Overall, human studies currently provide mainly associative evidence, whereas stronger causal evidence for specific microbiota-muscle mechanisms comes from animal models. Further controlled human studies are required to determine whether targeted microbiota modification can produce meaningful improvements in athletic performance.

Table 1. Main effects of gut microbiota on physical performance and recovery in athletes

Gut microbiota-related mechanism	Potential effect in athletes
SCFAs production	Improved energy metabolism and glycogen resynthesis
AMPK and GLUT4 activation	Enhanced glucose uptake and exercise efficiency
Regulation of intestinal barrier integrity	Reduced endotoxemia and systemic inflammation
Modulation of immune function	Improved recovery and reduced infection risk
Regulation of oxidative stress	Protection against muscle damage
Lactate metabolism by <i>Veillonella spp.</i>	Potential support of endurance performance

Source: own work.

Gut Microbiota in Post-Exercise Recovery Processes

Post-exercise recovery is a key component of the body’s adaptation to training loads and involves the repair of damaged muscle structures, regulation of the

immune response, and restoration of redox balance. In recent years, a growing body of research has suggested that the gut microbiota may play an important role in modulating these processes by influencing immune function, regulating inflammatory pathways and interacting with mechanisms related to oxidative stress (Barton et al. 2018; Carlone et al. 2025; Clark, Mach 2016; Mach, Fuster-Botella 2017; O'Brien et al. 2022). Consequently, the gut microbiota is increasingly recognized as a factor that may affect the efficiency of post-exercise recovery and the body's ability to adapt to prolonged training stress (Hughes 2020; Marttinen et al. 2020; O'Brien et al. 2022).

Proper functioning of the immune system is one of the key determinants of recovery processes following physical exercise. Intense physical activity can lead to temporary disturbances in immune function, commonly described as the "open window" phenomenon, during which susceptibility to infections may increase (Nieman, Wentz 2019; Walsh 2018). This mechanism is associated, among other factors, with changes in the activity of immune cells and a transient rise in inflammatory mediators following strenuous exercise.

The gut microbiota plays an important role in regulating the host immune response. Intestinal microorganisms can influence the activity of immune cells such as T lymphocytes, macrophages and natural killer (NK) cells, all of which are involved in tissue repair processes occurring after exercise (Belkaid, Harrison 2017; Jäger et al. 2019). Regulation of these immune cells facilitates the removal of damaged cellular structures and the initiation of tissue repair mechanisms.

Another important aspect of the interaction between the gut microbiota and the immune system is its role in maintaining intestinal barrier function. Intense physical exertion may increase intestinal permeability and promote the translocation of bacterial endotoxins into the bloodstream, which can contribute to the development of systemic inflammation (Costa et al. 2017; Takami et al. 2024). However, studies suggest that a balanced gut microbiota may help counteract this effect by strengthening epithelial integrity and modulating immune responses (Carlone et al. 2025; Varghese et al. 2024).

Inflammation itself is a natural component of muscle recovery after exercise, as the microdamage to muscle fibres caused by training initiates repair processes. Nevertheless, excessive or prolonged inflammation may delay recovery and increase the risk of overtraining (Peake et al. 2017). An increasing number of studies indicate that the gut microbiota may contribute to the regulation of inflammatory responses through modulation of pro- and anti-inflammatory cytokine production. Intestinal microorganisms can influence the activity of regulatory T cells and anti-inflammatory macrophages, which play a key role in resolving inflammation (Belkaid, Harrison 2017). Through these mechanisms, the gut microbiota may contribute to a more rapid return to physiological

homeostasis following physical exertion, although direct evidence in athletes remains limited.

Furthermore, research suggests that the composition of the gut microbiota may influence levels of inflammatory markers associated with exercise-induced inflammatory response, such as interleukin-6 and tumour necrosis factor- α (O'Brien et al. 2022; Scheiman et al. 2019). However, changes in inflammatory markers alone do not establish a causal microbiota-mediated improvement in recovery.

Intense physical activity increases the production of reactive oxygen species (ROS), which may contribute to oxidative stress and cellular damage within skeletal muscle tissue. Excessive oxidative stress can lead to mitochondrial damage, protein degradation and impaired muscle cell function (Kunst et al. 2023).

Growing evidence indicates that the gut microbiota may influence the regulation of the body's redox balance by producing metabolites with antioxidant properties and by modulating the activity of enzymes responsible for neutralizing ROS (Marttinen et al. 2020; Monda et al. 2017). In addition, microbial metabolites may interact with signalling pathways involved in skeletal muscle metabolism, including AMPK and mTOR pathways, which regulate muscle protein synthesis and the adaptive response of muscles to physical exercise (Lahiri et al. 2019). Many of these mechanisms, however, remain primarily supported by preclinical evidence.

Exercise-induced muscle damage is one of the primary factors limiting recovery capacity in athletes. Clinical studies have shown that modulation of the gut microbiota through dietary interventions or probiotic supplementation may reduce markers of muscle damage and alleviate post-exercise muscle soreness (Shirkoochi et al. 2025). Nevertheless, the effects reported in probiotic studies are heterogeneous and appear to depend on the bacterial strain, dose, study population and measured outcome.

These mechanisms may be linked to the influence of the gut microbiota on maintaining intestinal barrier integrity and regulating inflammatory processes in the body (Costa et al. 2017; Varghese et al. 2024). Moreover, emerging evidence suggests that the gut microbiota may also affect mitochondrial function in muscle cells and influence cellular metabolism associated with regenerative processes (Lahiri et al. 2019).

It should also be emphasized that beneficial effects of probiotic supplementation do not necessarily demonstrate a sustained modification of the resident gut microbiota. Therefore, probiotic effects and microbiome remodelling should not be considered equivalent.

The major mechanisms involved in the gut-muscle axis are summarized in Figure 1.

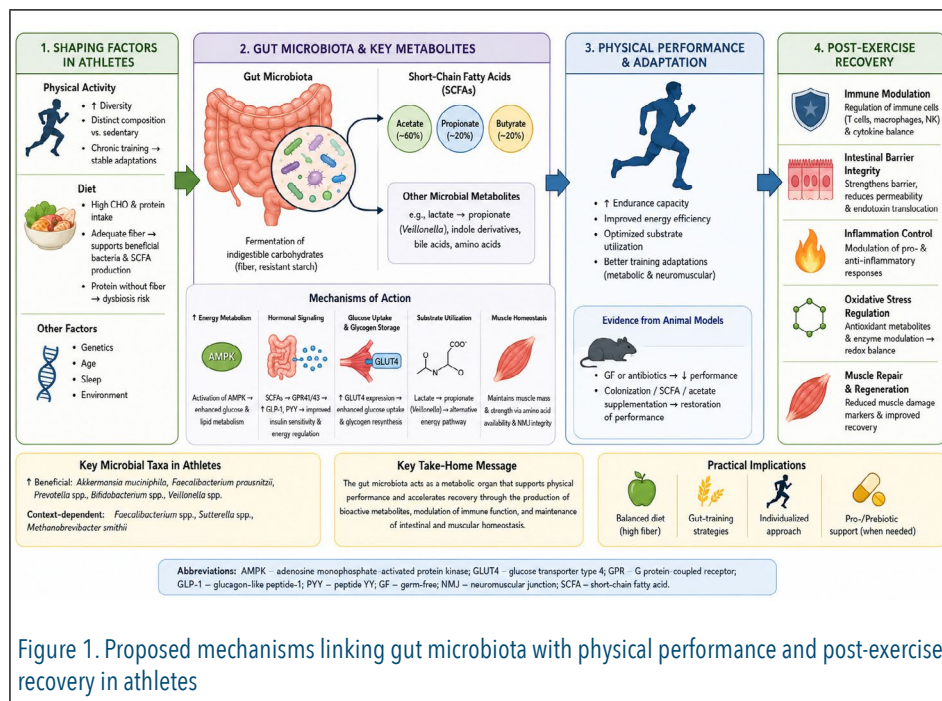


Figure 1. Proposed mechanisms linking gut microbiota with physical performance and post-exercise recovery in athletes

Source: own work.

Discussion

Although current evidence strongly suggests an association between gut microbiota composition and exercise performance, much of the available evidence remains observational and does not establish direct causality. Furthermore, substantial heterogeneity between studies, including differences in dietary protocols, training status and microbiome analysis techniques, makes direct comparison of results challenging.

An important limitation of the current literature is the difficulty in separating the effect of exercise from that of diet and other characteristics of an athletic lifestyle. Athletes frequently differ from sedentary controls in energy intake, macronutrient composition, fibre intake, supplement use, body composition and training load. Consequently, microbial differences observed between these populations cannot be attributed exclusively to physical activity.

The interpretation of mechanistic findings also requires caution. Experimental studies using GF animals, antibiotic-induced microbiota depletion or administration of selected microorganisms provide important evidence for potential causal pathways involving SCFAs, glucose metabolism, muscle glycogen and skeletal muscle function. However, these findings do not necessarily predict the magnitude or clinical relevance of the same mechanisms in trained humans.

Human intervention studies remain relatively limited and do not consistently demonstrate that short-term exercise or nutritional interventions produce persistent changes in gut microbiota or improvements in performance. Similarly, evidence regarding probiotics is promising but heterogeneous, and no universal microbial profile or microbiome-targeted intervention can currently be recommended to enhance athletic performance.

Therefore, further well-controlled longitudinal human studies are required to better determine the mechanistic role of gut microbiota in exercise adaptation and post-exercise recovery. To provide a clearer overview of the available evidence and its methodological limitations, representative human and animal studies investigating the relationship between gut microbiota, exercise performance and recovery are summarized in Table 2.

Table 2. Representative studies examining gut microbiota in relation to exercise performance and recovery

Study	Study design/ population	Main finding	Limitation
Clarke et al. 2014	Cross-sectional study; professional rugby players and controls	Athletes showed greater gut microbial diversity and differences in selected taxa	Cross-sectional design and substantial dietary differences between athletes and controls limit causal interpretation
Jang et al. 2019	Observational study; bodybuilders, distance runners, and sedentary controls	Sport-specific dietary patterns were associated with differences in the relative abundance of selected bacterial taxa	Small sample and difficulty separating the effects of diet from those of exercise type
Bycura et al. 2021	Human exercise intervention; cardiorespiratory and resistance training	Cardiorespiratory training induced initial microbiota changes that were not sustained, whereas resistance training produced no detectable overall changes in gut microbiota	Relatively short intervention and participants were not elite athletes
Scheiman et al. 2019	Human observational cohorts combined with experimental mouse studies	<i>Veillonella</i> abundance increased after endurance exercise in humans, whereas <i>V. atypica</i> and propionate increased treadmill running time in mice	The causal performance-enhancing effect was demonstrated in mice, not in human athletes

Study	Study design/ population	Main finding	Limitation
Okamoto et al. 2019	Experimental mouse study	Microbiota depletion and a diet low in microbio- ta-accessible carbohydrates reduced endurance capacity, while acetate administration restored exercise capacity	Preclinical evidence; translation to human athletic performance remains uncertain
Lahiri et al. 2019	Germ-free and colonized mouse models	Gut microbiota influenced skeletal muscle mass, met- abolic function, and neuro- muscular-related pathways	Mechanistic animal evidence with limited direct applicability to human athletes
Shirkoohi et al. 2025	Systematic review and meta-analysis of clinical trials of probiotic supple- mentation	Pooled analyses showed reduced creatine kinase concentrations and a modest improvement in VO ₂ max following probiotic supple- mentation	Considerable hetero- geneity was present, and the certainty of evidence for several outcomes was moder- ate to low

Source: own work.

Limitations

Despite growing interest in the relationship between the gut microbiota and athletic performance, several limitations remain. A substantial proportion of available evidence derives from animal studies, while human studies are often characterized by small sample sizes and heterogeneous methodologies. Additionally, differences in diet, training status and microbiome analysis techniques limit direct comparison between studies.

The present review also has methodological limitations related to its narrative design. The literature search was not conducted according to a systematic-review protocol, the number of records identified and excluded at individual stages was not prospectively recorded, and formal risk-of-bias tools were not applied. Therefore, some degree of selection bias cannot be excluded.

Future Perspectives

Future research should focus on the development of personalized microbiome-targeted nutritional strategies for athletes, including individualized probiotic interventions and precision sports nutrition approaches. Additionally, integration of multi-omics technologies may improve understanding of the mechanistic relationship between gut microbiota composition, exercise adaptation and recovery processes.

Emphasis should be placed on well-controlled longitudinal human studies that account for dietary intake, training load, sex, body composition and other major confounding factors. Future interventions should also assess whether microbiome changes are directly associated with objective improvements in performance or recovery.

Conclusions

In recent years, the gut microbiota has become an important focus of research in the field of exercise physiology. An increasing body of evidence suggests that intestinal microorganisms may influence processes relevant to athletes, including energy metabolism, immune system function and post-exercise recovery (Martinen et al. 2020; Patel et al. 2024). It has also been demonstrated that regular physical activity can modify the composition of the gut microbiota, increasing its diversity and promoting the growth of bacteria that produce SCFAs, which support intestinal barrier integrity and exert anti-inflammatory effects (Chen et al. 2024; Varghese et al. 2024).

Studies further indicate that the gut microbiota of athletes differs from that of sedentary individuals, which may have implications for metabolic and recovery processes (Carlone et al. 2025). However, these differences do not establish that a specific microbial profile directly improves athletic performance. At the same time, intense physical exertion may lead to temporary disturbances in gut microbiota balance and increased intestinal permeability, which may promote inflammatory responses and negatively affect post-exercise recovery (Xia et al. 2024).

For this reason, strategies aimed at modulating the gut microbiota, such as targeted dietary interventions and supplementation with probiotics or prebiotics, have attracted growing scientific interest. Some studies suggest that such approaches may support intestinal barrier function and help limit inflammatory processes associated with intense physical exercise (Aparicio-Pascual et al. 2025). Nevertheless, the evidence for direct improvements in performance and recovery remains heterogeneous.

Despite the increasing number of studies, many mechanisms underlying the interaction between the gut microbiota and physical performance remain insufficiently understood. Future research should focus on the application of advanced microbiome analysis techniques, such as metagenomics and metabolomics, which may provide deeper insight into the role of the gut microbiota in exercise adaptation and recovery processes in athletes (Zhao et al. 2026).

Overall, the gut microbiota should currently be considered a potentially relevant component of the interaction between diet, exercise, and recovery rather than an established independent determinant of athletic performance. Further controlled human studies are needed before specific microbiome-targeted strategies can be routinely recommended to athletes.

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Author Contributions

Conceptualization: A.Z., W.H.

Writing – original draft preparation: W.H., A.Z., M.D., K.G., M.B., K.R., A.G., A.L.

Writing – review and editing: W.H., A.Z., M.D., K.G., M.B., K.R., A.G., A.L.

Supervision: W.H., A.Z.

Project administration: W.H., A.Z.

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Declaration of Generative AI Use

During the preparation of this manuscript, the authors used ChatGPT-5 powered by OpenAI solely to improve language clarity and assist in the preparation of Figure 1 based on concepts and mechanisms identified by the authors from the reviewed literature. The tool was not used to generate original scientific content, interpret study findings, or draw conclusions. All generated material was reviewed and edited by the authors, who take full responsibility for the content of this publication.

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