

Gut Microbiome and Sports Performance: The Symbiotic Relationship

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ABSTRACT: The gut microbiome is a biome of organisms shaped by diet and environment. Humans provide food and shelter to gut microbes, which in turn help with digestion and nutrient absorption. In this review, I discuss the symbiotic relationship between exercise and the increasingly studied gut microbiome. This paper covers: (1) an overview of the gut microbiome, (2) the microbiome's effects on athletic performance, (3) exercise's influence on the microbiome, and (4) future directions and limitations. A diverse microbiome can improve endurance and reduce fatigue, whereas exercise can increase short-chain fatty acid (SCFA) levels and microbial diversity. There is a cooperative relationship between physical activity and the gut microbiome. Increased microbiota diversity benefits sports performance, but misunderstandings persist regarding probiotics. Probiotics are currently viewed as a universal supplement to boost energy and activity. However, this review demonstrates that standardized probiotics are not beneficial because each individual's microbiome is unique. Therefore, this review proposes a transition beyond palliative care to personalized supplementation enabled by omics-based technologies.

KEYWORDS: Medical and Health Sciences, Gut-Muscle Axis, Short-Chain Fatty Acids, Omics-based Precision Nutrition, Microbial Diversity, Probiotics, Athletic Performance.

■ Introduction

The gut microbiome is a growing subject in research, functioning as a unique microbial ecosystem essential for digestion, immunity, and vitamin synthesis. It is largely influenced by diet, antibiotics, and the environment.¹ The gut microbiota comprises four phyla,² which aid in fermentation and metabolite production.² “Gut-on-a-chip” technology helps clarify the microbiome's role: it actively guides the immune system toward tolerance.⁴ Specifically, these microfluidic models simulate the physical environment of the human intestine, including fluid flow and mechanical stretching that mimics peristalsis (contractions and relaxations of the digestive tract muscle to move food, waste, and water forward). This is relevant because it allows researchers to observe how the intestinal barrier reacts to the physical stress of exercise in a controlled setting, showing how a healthy microbiome maintains tight junctions between cells to prevent systemic inflammation.⁵ Gut bacteria prevent inflammatory molecules from crossing the gut barrier and triggering immune responses. By stabilizing this barrier, the gut not only aids digestion but also helps maintain and regulate the immune system.

In this paper, we discuss how the gut microbiome is increasingly recognized as a key factor in athletic performance and health, the symbiotic relationship between exercise and the gut microbiome, and how this relationship can be leveraged to improve athletic performance. The gut microbiome is becoming an increasingly major component of an athlete's capacity. The “gut-muscle axis” suggests that microbial health directly impacts physical output. This axis represents a bidirectional pathway where microbial metabolites influence skeletal muscle function. At the molecular level, this axis functions via the systemic circulation of short-chain fatty acids (SCFAs), which

act as signaling molecules that cross the gut-blood barrier to reach muscle tissue.⁶ This systemic connection is vital for athletes, because impaired gut motility and poor nutrient absorption—which stem from a lack of stable microbiota—can lead to reduced energy. In the context of this review, an “athlete” is defined using the McKinney *et al.* classification, which categorizes individuals based on their training volume (≥ 10 hours/week) and commitment to formal competition. This encompasses a wide range of athletes, from professionals to recreational athletes, who engage in structured, high-intensity physical activity.⁷ Furthermore, the microbiome can protect against physiological stress. High-performance training can cause inflammation, often referred to as a “leaky gut,” in which the intestinal barrier is compromised, leading to muscle fatigue and longer recovery times. Instead, a diverse microbiome can strengthen the intestinal barrier, thereby reducing these symptoms.⁸ Physical activity increases microbial diversity and SCFA production, regardless of diet.⁹ These SCFAs, such as butyrate, act as a critical histone deacetylase inhibitor, which downregulates pro-inflammatory pathways and ensures the intestinal epithelium can withstand the “leaky gut” stress of high-intensity training. This interaction demonstrates that a diverse microbiome is a requirement for peak efficiency. Other bacterial species can recycle waste products into fuel.¹⁰ Therefore, the gut microbiome ensures that nutrients are converted with maximum efficiency.

Despite the numerous benefits of a robust microbiome, probiotics are currently used inconsistently and ineffectively due to the lack of a personalized approach. The goal of this review is to synthesize the current understanding of the gut microbiome and its two-way relationship with sports performance (Figure 1). This paper moves beyond symptom management

and suggests a proactive, molecularly optimized approach. I will evaluate precision nutrition, in which dietitians shift from generalized probiotic use to individualized, omics-based prescriptions.¹¹ By identifying specific genetic markers, dietitians can maximize each athlete's metabolic uniqueness.

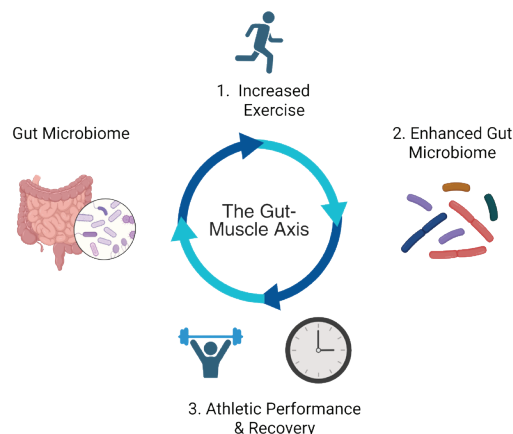


Figure 1: The Gut-Muscle Axis: A Positive Feedback Cycle for Athletes. With increased physical activity, such as running or training, the gut microbial diversity increases. This is indicated by increased production of Short-Chain Fatty Acids (SCFA), including butyrate and propionate. These SCFAs support nutrient absorption, muscle repair, endurance, and reduced inflammation, allowing athletes to continue exercising and further reinforcing the diverse microbial ecosystem. Created using Biorender.

Overview of Gut Microbiome:

The gut microbiome refers to the microbiota (the community of microorganisms) within the gastrointestinal tract (GI).¹² These microbiota aid digestion and nutrient absorption. This leads to fermentation that produces important metabolites, such as SCFAs, lactate, and branched-chain fatty acids. These are essential for athletes.² The gut microbiome comprises trillions of microorganisms in the digestive tract.¹³ The human gut microbiota contains four phyla: Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria.² Specifically, Bacteroidetes and Firmicutes are the two dominant phyla, accounting for over 90% of the gut's bacteria.¹⁴ When examining these phyla within athletic populations, it is important to distinguish between “elite” athletes—those competing at national or international levels—and “recreational” athletes—those who do not meet the 10-hour-per-week training threshold described in the previous McKinney *et al.* definition. This distinction is necessary because exercise volume creates a distinct performance microbiome that may not be present in sedentary or moderately active individuals.¹⁵ In athletic populations, greater diversity of these phyla and a specific increase in the genus *Akkermansia* have been linked to improved metabolic markers.⁴ Many are not host-associated but are distinct microbial species. This microbiome supports various functions, including digestion, nutrient absorption, immune function, regulation of inflammation, and gut-brain communication.¹³

To specifically evaluate the resilience of an athlete's digestive tract under physical strain, researchers created a “human gut-on-a-chip.”¹⁶ This miniature device mimicked a human intestine. The chip contained human gut cells and good bacteria, simulating a real digestive system. During this study, they examined gut bacteria, immune cells, and muscle-like

movement without harming real-life humans or animals.¹⁶ In the experiment, the transcriptomes of VSL #3, a mixture of 8 probiotic strains (*Lactobacillus casei*, *Lactobacillus plantarum*, *Lactobacillus acidophilus*, *Lactobacillus delbrueckii subspecies bulgaricus*, *Bifidobacterium longum*, *Bifidobacterium breve*, *Bifidobacterium infantis*, and *Streptococcus thermophilus*), were analyzed to observe their interaction with the host. The probiotics were co-cultured with human gut microbes. After transcriptomic analysis, gene expression patterns in healthy human ileal tissue were identified.¹⁶ The ileum contains more gut microbes than nearby regions and plays a key role in immune function. This shows that the microbiome instructed the immune system to be more tolerant.

Building on this tolerance, commensal bacteria promote the development of anti-inflammatory immune cells, such as regulatory T cells, which then secrete signals, including Interleukin-10 (IL-10), a potent anti-inflammatory cytokine that dampens inflammatory responses.¹⁶ Therefore, due to the microbiome's direct influence, there is a less inflammatory state. Kim *et al.* found that the inflammatory toxin lipopolysaccharide (LPS) failed to breach the gut barrier in the model.¹⁶ LPS is a pro-inflammatory endotoxin found in the cell walls of Gram-negative bacteria that can trigger systemic inflammation if it enters the bloodstream. The microbiome maintains tight junctions between gut cells by producing SCFAs, thereby strengthening the physical barrier.¹⁶ This barrier prevents pro-inflammatory molecules, such as LPS, from entering the bloodstream and triggering the body's immune system. The gut microbiota regulates the balance between pro-inflammatory cytokines, such as Tumor Necrosis Factor alpha and Interleukin-6 (IL-6), and anti-inflammatory cytokines like IL-10 and Transforming Growth Factor-beta, thereby affecting inflammation and the autoimmune system.¹⁷

The functional impact of this regulation is further clarified by Schirmer *et al.*, who identified a link between the gut and the immune system's inflammatory response: the gut microbiota composition determines the secretion of specific cytokines (chemical signals) into the bloodstream, depending on the bacteria present.¹⁸ During this process, they used *in vitro* simulation with human immune cells (monocytes and lymphocytes) and exposed them to three separate bacterial challenges (*Lipopolysaccharide*, *Bacteroides fragilis*, and *Staphylococcus aureus*). Then, after the immune cells interacted with the bacteria for a specific period, they measured the concentration of cytokines produced. The results demonstrated that each bacterium had a distinct response.¹⁸ Specifically, certain bacteria induced high levels of Interleukin-1 beta (pro-inflammatory), while others favored an IL-10 response, proving that the host immune profile is highly dependent on individual microbial presence.¹⁸

The clinical efficacy of these interactions has been demonstrated in trials. For instance, a randomized, double-blind trial showed that daily supplementation with *Lactobacillus helveticus* significantly reduced the duration of Upper Respiratory Tract Infections in athletes by modulating T-cell activity. This effect is likely driven by the strain's ability to enhance Interferon-gamma secretion and stimulate T-cell activation, thereby

buttressing the first line of defense against viral pathogens during post-exercise immunosuppression.¹⁹

Complementing this defense, clinical trials on healthy, physically active adults using *Bifidobacterium animalis* subsp. *Lactis* have shown a reduction in circulating systemic inflammation markers, such as C-reactive protein and IL-6. These findings reinforce the gut microbiome's role in maintaining gut barrier integrity by specifically upregulating tight junction proteins, such as occludin and zonulin. These actions prevent the translocation of endotoxins, which typically trigger systemic inflammation, in highly active individuals undergoing heat or mechanical stress on the gastrointestinal tract.²⁰

Gut Microbiome's Role in Athletic Performance:

The gut microbiome plays a key role in sports. A more diverse microbiome often enables higher performance (Figure 2). To illustrate the necessity of these microbes, one study compared germ-free (axenic) animals with conventionally raised animals.¹² The germ-free (GF) animals had less body fat, reduced gut motility, and showed multiple behavioral differences.¹² These axenic animals were completely free of living microorganisms. In Kuziel and Rakoff-Nahoum's experiment, the microbiome caused specific innate and adaptive immune responses.¹² The germ-free mice had a lower basal metabolic rate (BMR), which is neither positive nor negative. A lower BMR can lead to longer lifespans because it requires fewer calories. However, it can also increase the risk of faster weight gain and other health issues. This finding contradicts the initial results, as the experiment found the mice had gained less fat, even though a lower BMR can increase weight.

This study clarifies that when germ-free mice remain lean despite a low BMR, it means that, without a microbiome, an organism is an inefficient nutrient processor. It cannot efficiently use the energy from its diet, which is an immense disadvantage for high performance. While these axenic models primarily highlight fundamental metabolic pathways, the inability to process nutrients efficiently suggests that, without microbial aid, an athlete cannot effectively fuel the high caloric demands of training. The performance gap is further illustrated when comparing GF mice to specific pathogen-free (SPF) mice. SPF Mice possessed a diverse microbiota dominated by *Bacteroidetes* and *Firmicutes* and consistently showed greater endurance on the treadmill.²¹ This is due to the microbiota's ability to support skeletal muscle uptake of glucose and maintain antioxidant enzyme activity, which are severely limited in germ-free models.

Gut motility refers to the movement of food and waste through the digestive tract.²² Impaired motility reduces nutrient absorption. This fundamental link between the microbiome and metabolic efficiency has been demonstrated in human trials. Athletes supplemented with a high-dose blend of *Bifidobacterium* and *Lactobacillus* strains experienced an increased VO_2 max and an extended exercise duration before failure, demonstrating that optimized microbial activity directly translates into measurable aerobic gains.²³ Furthermore, professional cyclists who used a similar mixture of *Bifidobacterium animalis* and *Lactobacillus hevea* reported significantly less

nausea and vomiting, suggesting that the microbiome supports performance by maintaining the physical integrity of the GI tract under the stress of training.²⁴

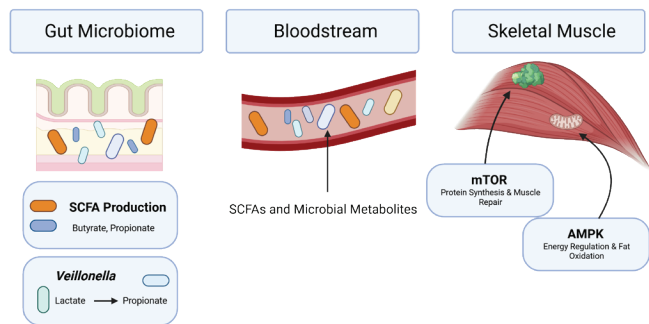


Figure 2: The Gut-Muscle Axis in Athletic Performance. The gut microbiome produces Short-Chain Fatty Acids, such as butyrate and propionate, which cross the intestinal barrier and enter circulation. Additionally, Veillonella, a Gram-negative bacterium found in the gut, metabolizes lactate, produced during exercise, into propionate. These metabolites enter the bloodstream and reach skeletal muscle, where they influence metabolic pathways, including mechanistic target of rapamycin-mediated protein synthesis and muscle repair, and adenosine monophosphate-activated protein kinase-mediated energy metabolism and fatty acid oxidation. Created using Biorender.

These findings indicate that athletes with a less diverse gut microbiome may experience poorer athletic performance. If reduced gut motility impairs nutrient absorption, maintaining microbial diversity will be critical for metabolic efficiency and energy availability during high-intensity training. Furthermore, a diverse microbiome strengthens the intestinal barrier, thereby reducing systemic inflammation that often leads to muscle fatigue and prolonged recovery times.²⁵

By connecting the nutrient-processing seen in animal models to the increased aerobic capacity in human trials, it is clear that a diverse microbiome optimizes energy conversion. This conversion is primarily driven by SCFAs—small, lipid-like carboxylic acids produced during the fermentation of non-digestible carbohydrates.²⁶ SCFAs not only provide a supplemental energy source but also act as signaling ligands that enter the bloodstream and bind to receptors in skeletal muscle to regulate fatty acid oxidation and glucose homeostasis.

This relationship between diversity and metabolic output is further supported by a study by Wiley Barton *et al.*, in which athletes had higher fecal metabolite levels—such as SCFAs, propionate, and butyrate—than control (sedentary) groups.²⁷ Metabolism performs four key functions for cells: generating ATP, converting nutrients, converting simpler structures into macromolecules, and aiding cellular functions.²⁸ Therefore, with better metabolic regulation, the cell grows only when necessary. Additionally, the enzyme mechanistic target of rapamycin (mTOR) catalyzes anabolic processes by regulating protein synthesis and degradation. In contrast, adenosine monophosphate-activated protein kinase (AMPK) catalyzes catabolic processes by breaking down fats and sugars (Figure 2).²⁸ The gut-muscle axis influences this balance because SCFAs such as butyrate can inhibit histone deacetylases, effectively upregulating the pathways required for muscle protein synthesis via mTOR. Simultaneously, propionate serves as a precursor for gluconeogenesis, helping maintain energy levels

and preventing the overactivation of AMPK, which can lead to muscle breakdown during prolonged endurance tasks.²⁹ When these processes are accelerated, athletes can more easily break down nutrients and build muscle. Barton *et al.* suggest that the high levels of SCFAs found in athletes act as primary mediators between the gut microbiome and cellular metabolic pathways.²⁷

Specifically, SCFAs such as butyrate and propionate travel through the bloodstream to skeletal muscle, modulating the balance between mTOR and AMPK. This is exemplified by specific bacteria, such as *Veillonella*, which metabolize exercise-induced lactate into propionate, thereby directly fueling endurance performance.¹⁰ This regulation provides a stable energy source and enables microbial metabolites to more efficiently activate mTOR for muscle repair while activating AMPK to optimize fat oxidation and energy production. As a result, the microbiome links nutrition and exercise, ensuring that ingested energy is converted into physical power. The synthesis of molecular signaling (mTOR/AMPK) and clinical performance outcomes (VO₂ max/fatigue resistance) confirms that the microbiome is a non-negotiable factor in athletic endurance. This indicates that metabolic speed in athletes is determined not solely by training but also by the gut microbiome. Ultimately, these findings shift from a solely external focus on sports performance to an internal focus on microbiome management, suggesting that an athlete's ability is supported by their microbial health.

How Exercise Influences the Gut Microbiome:

While the microbiome supports exercise, exercise has likewise been shown to alter the gut microbiome. Hsu *et al.* compared germ-free (GF) mice with specific pathogen-free (SPF) mice.³⁰ They had each group of mice perform exercises, including endurance swimming and treadmill running. In these tests, SPF mice exhibited greater exercise capacity and endurance than their GF counterparts.³⁰ This suggests that a diverse microbiota plays a prominent role in exercise and may be required for optimal performance.

In a study by Mika *et al.*, the authors investigated whether exercise (wheel running) at a juvenile stage (three weeks old) would produce a more diverse microbial community than initiating exercise during adulthood (ten weeks old).³¹ Rats were placed in cages with running wheels, providing voluntary wheel access. In their experiment, they found that initiating exercise during the juvenile stage was associated with increased Bacteroidetes and decreased Firmicutes.³¹ This Bacteroidetes-to-Firmicutes ratio is often associated with a lean phenotype and improved metabolic health. These microbial groups are crucial because they extract energy from food through fermentation, enabling efficient calorie absorption. The Mika study further reveals that early-life exercise specifically promotes the abundance of *Probiococcus* and *Lactobacillus* species, creating a microbial signature that enhances the host's metabolic plasticity into adulthood.³² Consequently, this combination overall indicates a lean phenotype, which is widely associated with regular exercise.

Furthermore, this metabolic shift can be linked with increased SCFA production. SCFAs are signaling molecule that triggers intracellular signaling cascades when bound to specific cells, such as by activating membrane receptors and directly modulating enzymes and transcription factors.³³ This is particularly important because SCFAs such as butyrate provide the primary energy source for colonocytes—specialized epithelial cells that line the lumen of the large intestine—therefore strengthening the gut barrier. This overall indicates that voluntary aerobic exercise positively influences gut health.

In a study by Clarke, S. F. *et al.*, 40 elite male professional rugby players were recruited.⁴ They collected fecal and blood samples and extracted DNA to use for the experiment. They found that the alpha-diversity of elite athletes, a measure of the variability of microbial species within a single fecal sample, was significantly higher than that of the high-BMI group and the control groups (sedentary individuals). Alpha diversity was assessed to quantify richness and evenness within the sample. The researchers concluded that higher alpha diversity is associated with better health outcomes.⁴

Adding to the list of benefits, Candace R. Longoria *et al.* established that exercise is among the few lifestyle factors that can independently increase SCFA levels.⁹ A nutritious diet can act as fuel, signaling to SCFA-producing bacteria. They found that physical activity can eliminate metabolic waste products, such as trimethylamine N-oxide (TMAO). After ingesting foods high in choline or Lecithin (red meat, eggs, dairy, etc.), certain bacteria in the body ferment them into a gas called Trimethylamine (TMA). This gas is transported to the liver, where an enzyme converts it to TMAO.⁹ Exercise reduces the abundance of high-TMA-producing bacteria, thereby reducing the amount of raw TMA gas secreted into the liver. Furthermore, exercise has been shown to downregulate FMO3 activity. This ensures that TMAO production would be slower and TMAO concentration would drop, regardless of diet changes.⁹

Parallel to these findings in elite athletes, there was also an increase in SCFA producers among non-athletes with increasing physical activity.³⁴ *Faecalibacterium*, a SCFA-producing bacterium, showed higher population levels in relatively active individuals.³⁵ This is critical because SCFAs can reduce inflammation through signaling pathways, regulate immune function, and modulate obesity.³⁶

Future Directions and Limitations:

Probiotics are microorganisms that modulate the microbiome and confer benefits on the host, thereby supporting gut health after antibiotic therapy.³⁷ Athletes often use them to improve markers of oxidative or inflammatory stress. However, probiotics have not been shown to improve performance.² In a group of 24 recreational runners, they were given probiotic supplements (*Lactobacillus acidophilus*, *Bifidobacterium bifidum*, and *Bifidobacterium animalis subsp lactis*) 28 days before a marathon. Compared with the control group (recreational runners who did not receive probiotic supplementation), the experimental group experienced less severe gastrointestinal symptoms and a modest decrease in average speed. Unfortunately, the finishing times did not differ significantly.² This

finding indicates that probiotics did not affect performance but rather helped minimize physical symptoms that would otherwise impair a runner's experience.

Since probiotic effects are highly strain-specific, their efficacy must be evaluated at both the strain and species levels rather than in a broad category.³⁸ Different strains have different effects on elite athletes. In a study testing *Lactobacillus rhamnosus* (*L. rhamnosus*) strain ATCC 53103 in marathon runners, Kekkonen *et al.* found that the probiotic had no effect on the total incidence or number of respiratory infections, nor did it reduce the number of GI symptom episodes.³⁹ However, the duration of GI episodes was reduced. These GI symptoms were defined as flatulence, abdominal pain, loose stools, or diarrhea, and participants reported their severity on a scale.³⁹ Conversely, Shing *et al.* had male runners use a multistrain probiotic supplement (*Lactobacillus acidophilus*, *L. rhamnosus*, *Lactobacillus casei*, *Lactobacillus plantarum*, *Lactobacillus fermentum*, *Bifidobacterium lactis*, *Bifidobacterium breve*, and *Streptococcus thermophilus*).⁴⁰ This study concluded that GI discomfort was minimally reduced, but supplementation significantly increased running time to fatigue.⁴⁰ These discoveries indicate that different probiotic strains affect athletes differently: *L. rhamnosus* had a negligible effect on marathon runners,³⁹ whereas multistrain supplementation had a significant effect on male runners.⁴⁰ Given that the *L. rhamnosus* strain does not exhibit a significant effect, combining multiple strains might improve athletic performance. This raises a critical question for future research: whether there is an optimal threshold for strain diversity or a point beyond which adding more strains no longer provides additional benefit.

In response to these challenges, precision nutrition, informed by omics technologies and gut microbiome research, offers a new approach to enhancing athletic performance through individualized interventions. Penggalih *et al.* found that precision nutrition can optimize athletic performance by using omics technologies (nutrigenomics, metabolomics, proteomics, and transcriptomics) to dive into an athlete's molecular and metabolic nuances.¹¹ By identifying specific genetic markers, doctors can create appropriate diets to potentially reduce injury risk or increase endurance. For example, metabolomics can help identify metabolic responses to exercise, aiding dietitians in developing recovery strategies.¹¹ As shown by Li *et al.*, the future of sports nutrition lies in sports-specific probiotic strategies.⁴¹ This evolution highlights a shift from generalized supplements to a sharper focus on the "gut-muscle axis," where specific microbial metabolites directly influence muscle recovery and energy availability. This research relies heavily on multi-omics, as stated in Penggalih *et al.*,¹¹ to bring together "responders" and "non-responders." By combining metagenomic screening with metabolomics, future studies can identify which probiotic strains would benefit an athlete. Ultimately, researchers should go beyond symptom management and work toward identifying molecular thresholds at which strain diversity and personalized nutrition plans ensure measurable improvements in athletic power and endurance.

To achieve this, future research may implement longitudinal monitoring frameworks that utilize wearable biosensors

and ingestible "smart pills" to track real-time microbial fluctuations during high-intensity phases.⁴² By mapping these fluctuations, researchers can identify windows of vulnerability in the gut barrier where targeted interventions may be more effective. Furthermore, interventional studies should transition from traditional randomized controlled trials to randomized, blinded, multiple-crossover clinical trial designs that prioritize the individual's unique baseline microbiome and metabolic responses over broad population averages.⁴³ This will ensure the data is accurate, and any benefits will not be hidden as they might be in a larger group. To incentivize this work, the scientific community should establish open-access "Performance Microbiome" biobanks.⁴⁴ These platforms can allow for the sharing of multi-omics data across institutions, encouraging the validation of strain-specific claims through large-scale meta-analyses and reducing the financial burden on individual researchers. Moreover, by encouraging and rewarding researchers for debunking, the field of microbial research will maintain its integrity.

However, knowledge of the gut microbiome is limited due to inconsistent research.⁴⁵ Many athletes suffer from gastrointestinal infections due to prolonged, intense exercise.⁴⁶ O'Brien believes that this inflammation is due to changes in the microbiome.⁴⁶ Although the use of probiotics is increasingly common, the American Gastroenterological Association states that assessing their benefits is difficult due to differences in methodologies, specimens, and participants.⁴⁵ For instance, although the *L. rhamnosus* strain had little effect on performance,³⁹ multiple-strain supplements have been shown to decrease fatigue time.⁴⁰ Additionally, Kekkonen *et al.* included participants of both genders, with a sample of 114 marathon runners,³⁹ whereas Shing *et al.* tested only 10 male runners.⁴⁰ This discrepancy underscores that athletes cannot rely on standardized probiotics, as few studies have demonstrated their benefits.

■ Conclusion

This review of the intersection of sports science and microbiology confirms that the human gut is not merely a digestive organ but an increasingly dominant component of an athlete's performance. As shown by the distinct physiological advantages of axenic versus conventionally raised animals, a diverse microbiota is crucial for efficient nutrient absorption and for regulating systemic inflammation.¹² The relationship is symbiotic: a diverse microbiome fuels endurance by producing metabolites such as SCFAs,¹⁰ while physical activity enhances microbial richness and flushes metabolic waste, such as TMAO.⁹ This is significant because it highlights how athletes should be more mindful of their gut microbiome through their diet and environment.

Despite this association, the current application of probiotic supplementation remains inconsistent. While single-strain probiotics were ineffective at improving runners' endurance,³⁹ the multi-strain formula provided fatigue-reducing benefits.⁴⁰ These disparities highlight that standardized supplementation is no longer a viable solution for future athletes. Instead, dietitians and researchers should prioritize precision nutrition over

symptom management. This can take the form of omics-based technologies, such as nutrigenomics and metabolomics, used to optimize athletic performance through molecular individualization.¹¹

Ultimately, while exercise has been shown to benefit gut health, further optimizing performance and endurance requires mapping and manipulating the microbiota at the molecular level. With this manipulation, athletes are not limited to generalized estimates; instead, they can use data and molecular studies to identify specific strains and effective doses. There needs to be an interdisciplinary effort among sports nutritionists, immunologists, and data specialists to translate omics into real-world solutions. This approach will ensure that research is inclusive and diverse, including underrepresented groups. Future research should focus on developing personalized probiotic supplementation tailored to the person's microbiome.

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