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The Role of the Gut Microbiome in Exercise Physiology and Athletic Performance: A Review of Evidence

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Abstract

Background

The human gut microbiome interacts with host metabolism, immunity, and neuroendocrine signaling. Evidence shows habitual exercise modulates microbial diversity and function, with athletes exhibiting distinct "athletic" profiles enriched in short-chain fatty acid (SCFA)–producing taxa and altered metabolism versus sedentary people.

Aim

Synthesize evidence on the bidirectional gut microbiome–exercise relationship, focusing on microbial links to exercise physiology, training adaptations, performance, and microbiome-targeted strategies for athlete health/performance.

Material and methods

Comprehensive review of Google Scholar, Scopus, PubMed for human/animal studies on: (1) exercise-induced microbiota changes; (2) microbiome–fitness/performance associations; (3) microbial metabolites (e.g., SCFAs, bile acids); (4) dietary/probiotic/prebiotic interventions in athletes/active individuals. Prioritized recent reviews, RCTs, longitudinal studies; no meta-analysis due to heterogeneity.

Results

Endurance exercise links to higher diversity, SCFA-producers, and carbohydrate/amino acid metabolism capacity; extreme training causes dysbiosis, permeability, inflammation. SCFAs mediate diet–microbiota–host effects on mitochondria, substrate use, insulin sensitivity; gut signals affect immunity, barrier, gut–brain axis (stress/mood/cognition). Fiber-rich diets, select probiotics/synbiotics reduce illness, GI issues, inflammation, and may boost endurance/recovery (strain/context-specific).

Conclusions

The gut microbiome represents a modifiable factor in exercise physiology and athletic performance. Well-periodized training combined with microbiome-supportive nutrition may promote metabolic efficiency, immune resilience, and psychological robustness, whereas chronic excessive training and suboptimal diets may have adverse effects. Further progress requires well-designed, sport- and sex-specific longitudinal studies integrating multi-omics approaches and standardized exercise and intervention protocols.

Keywords: gut microbiome; exercise; athletic performance; short-chain fatty acids; endurance training; resistance training; probiotics; prebiotics; athletes; gut–brain axis

AI statement: Artificial intelligence tools have not been used to produce or alter the scientific content of the paper. Publicly available AI-powered websites have been used to identify better wording for certain expressions and sentences to ensure a smooth reading experience, while having no impact on the interpretation of cited evidence.

1. Introduction

The human gut microbiome is a complex, dynamic ecosystem comprising trillions of microorganisms that interact with host metabolism, immune function, endocrine signaling, and neural pathways. [1,2,3] Over the past decade, rapid advances in high-throughput sequencing and metabolomics have revealed that gut microbiota composition and function are both a determinant and a correlate of human health and disease. [3,4] Among the environmental factors shaping the microbiome, diet has long been recognized as a dominant driver, but accumulating evidence now shows that physical activity and structured exercise are also potent modulators of gut ecology. [5,6]

In athletes, this interaction is especially important. Elite and highly trained individuals present extreme physiological phenotypes - enhanced cardiorespiratory fitness, muscle mass and strength, metabolic flexibility, and high training loads - that are accompanied by distinct gut microbial signatures compared with sedentary controls. [2,6,7] Cross-sectional studies in professional rugby players, endurance athletes, and other high-level competitors consistently report higher alpha diversity, enrichment of short-chain fatty acid (SCFA) - producing taxa, and greater functional capacity for energy harvest and xenobiotic metabolism. [7,8] These features are often accompanied by elevated fecal SCFAs, altered bile acid metabolism, and expanded gene repertoires for carbohydrate and amino-acid utilization. [9,10,11]

At the same time, exercise is fundamentally a stressor. While moderate, well-periodized training exerts anti-inflammatory and cardiometabolic benefits, excessive or poorly recovered high-intensity and ultra-endurance exercise can increase gut permeability, endotoxemia, and dysbiosis, with downstream effects on immune competence, gastrointestinal (GI) function, and recovery. [3,6,12] Observational data in ultra-marathon runners, long-distance triathletes, and elite endurance athletes show that extreme exertion is associated with GI symptoms, transient increases in potentially pathogenic taxa, and shifts in microbial metabolic pathways related to oxidative stress and tissue damage. [6,13,14,15]

The idea of a bidirectional “gut–exercise axis” has therefore emerged: exercise can remodel the microbiome, and the microbiome, in turn, can shape exercise capacity, training adaptation, and health outcomes. [1,6,16] This axis operates through multiple mechanisms, including microbial production of SCFAs and other metabolites that influence muscle energetics and mitochondrial function, modulation of gut barrier integrity and systemic inflammation, and signaling along the gut–brain and gut–muscle axes via immune, endocrine, and neural routes. [2,5,6,17] Preclinical models demonstrate causal links: germ-free or antibiotic-treated rodents exhibit impaired endurance and muscle function that can be rescued by fecal microbiota transplantation (FMT) or SCFA supplementation, and transplantation of “athletic” microbiota can improve insulin sensitivity and increase muscle glycogen stores in recipient mice. [6,9]

Despite rapidly growing interest, the human evidence base remains heterogeneous, spanning small randomized controlled trials, longitudinal interventions, narrative and systematic reviews, and case studies in athletes and sedentary adults. [1,7,18] Methodological differences in exercise prescription, dietary control, microbiome analytics, and outcome measures complicate synthesis. Recognizing these gaps, several recent reviews have called for integrated, multi-omics, sport-specific, and mechanistic research agendas. [2, 6, 7, 16]

The present systematic narrative review synthesizes current evidence on the role of the gut microbiome in exercise physiology and athletic performance, focusing on: (1) exercise-induced modifications of microbial diversity and composition across training paradigms and populations; (2) sport-specific microbiome signatures and their associations with performance; (3) mechanistic pathways linking microbial metabolites and host physiology; and (4) microbiome-targeted interventions, including diet, probiotics, and prebiotics, aimed at optimizing performance, recovery, and health in athletes and physically active individuals. Building on prior reviews and recent empirical studies, we highlight consistent patterns, unresolved controversies, and priorities for future research.

2. Research materials and methods:

2.1. Data collection and analysis

A comprehensive literature review was conducted by utilising Google Scholar, Scopus and PubMed databases. The following keywords were used for the search: “gut microbiota”, “gut microbiome”, “exercise”, “physical activity”, “endurance”, “resistance training”, “high-intensity interval training”, “athlete”, “sports performance”, “cardiorespiratory fitness”, “short-chain fatty acids”, “probiotics”, “prebiotics”, and “microbiome interventions”. The search included human and animal studies that examined exercise-induced microbial changes, associations between microbiome features and performance, mechanistic links involving microbial metabolites, and the effects of microbiome-targeted nutritional or probiotic strategies in active populations.

The author reviewed articles referring to direct physiological effects, performance outcomes, immune and gastrointestinal health, and microbiome-targeted interventions in athletes and physically active individuals. The author took note of the journals of publication to identify reliable sources, and appropriate measures were taken to check the reliability of citations that provided the relevant information.

Only articles available in the uploaded library were included in this review. Where multiple reports addressed similar questions, recent systematic reviews or higher-quality randomized and longitudinal studies were prioritised, with primary studies drawn upon to illustrate key findings or provide mechanistic detail. No formal meta-analysis was performed due to heterogeneity in study designs, exercise protocols, microbiome methods, and outcome measures.

3. Results:

3.1. Exercise-induced modifications of gut microbial diversity and composition

3.1.1. Cross-sectional comparisons: athletes versus sedentary individuals

Early evidence for an “athletic” microbiome came from cross-sectional comparisons between elite athletes and non-athletic controls. In a landmark study of professional rugby players, Clarke et al. reported that athletes exhibited significantly higher alpha diversity (with representation from 22 distinct phyla) and higher proportions of health-associated taxa, including *Akkermansia*, compared with matched controls, alongside greater energy and protein intake. [19] Similarly, Barton et al. observed that professional athletes differed markedly from sedentary subjects in both compositional and functional microbiome profiles, with enrichment of pathways related to amino-acid biosynthesis, carbohydrate metabolism, and SCFA production. [20]

Other cross-sectional work in athletes has reinforced these findings. Competitive cyclists and endurance athletes show distinct microbial community structures and metabolomes compared with recreationally active or sedentary individuals, with higher abundance of SCFA-producing taxa (e.g., *Faecalibacterium*, *Ruminococcaceae*, *Roseburia*) and, in some cohorts, increased *Prevotella*. [4,7,21,22] Studies of women with active lifestyles versus sedentary controls report higher alpha diversity and enrichment of butyrate producers (e.g., *Faecalibacterium prausnitzii*, *Roseburia hominis*) in active individuals. [1,6,23] Endurance athletes also display altered *Firmicutes*:*Bacteroidetes* ratios and a greater representation of mucin-degrading *Akkermansia muciniphila*, though results across studies are not completely consistent and are confounded by dietary differences. [1,5,6]

3.1.2. Cardiorespiratory fitness and habitual physical activity

Beyond categorical athlete–non-athlete comparisons, several studies have explored continuous associations between cardiorespiratory fitness (CRF) and gut microbiota. Estaki et al. showed that VO_2max was a strong predictor of microbial diversity and metagenomic functions, independent of age, BMI, and dietary intake, with fitter individuals harboring a microbiome enriched in butyrate-producing *Clostridiales*, *Roseburia*, and *Lachnospiraceae*. [1,24] Bressa et al. and Yang et al. similarly found that CRF correlated positively with alpha diversity and the abundance of SCFA producers in adults and premenopausal women. [25,26] These findings support a graded relationship whereby higher habitual fitness is associated with richer, functionally more versatile microbiomes.

Large population-based analyses also identify physical activity as a significant, though modest, contributor to microbiome variation relative to diet, BMI, and other lifestyle factors. [4] Deng et al.'s bibliometric analysis of 327 publications confirms that “exercise” and “gut microbiota” have become major research hotspots since 2014, with cardiorespiratory fitness, inflammation, obesity, and athletes among the most frequently co-occurring topics. [21]

3.1.3. Longitudinal training interventions in non-athletic adults

Randomized and controlled training interventions provide more direct evidence for causal effects of exercise on the human microbiome. In a six-week endurance training study, Allen et al. demonstrated that previously sedentary lean and obese adults exhibited exercise-induced shifts in microbiota composition and SCFA production, with greater increases in SCFA-producing taxa in lean participants; changes largely regressed after a six-week detraining period, indicating that continued exercise is required to maintain microbiome adaptations. [6,7,27]

Munukka et al. reported that a six-week supervised endurance program in overweight women altered gut metagenomic profiles without markedly changing systemic metabolomics, suggesting subtle but functionally meaningful shifts in microbial gene content. [23] Kern et al. showed that six months of structured exercise (active commuting or leisure-time moderate/vigorous training) in individuals with overweight or obesity modestly increased Shannon alpha diversity in the vigorous-intensity group and enhanced inferred microbial functional potential, particularly in carbohydrate and SCFA pathways. [18]

Shorter interventions show mixed findings. Taniguchi et al. observed that five weeks of endurance exercise in elderly men did not significantly alter overall diversity beyond inter-individual variability, but changes in alpha diversity correlated inversely with changes in systolic and diastolic blood pressure, and there were specific shifts in taxa such as decreased *Clostridium difficile* and increased *Oscillospira*. [28] Other trials of 8–10 weeks of aerobic training in inactive adults and older women report modest compositional changes, including increases in *Bacteroides* and potentially beneficial taxa, but no large, consistent restructuring of the microbiome. [29,30,31]

Exercise modality appears to matter. Bycura et al. conducted parallel eight-week interventions comparing cardiorespiratory exercise and hypertrophy-oriented resistance training. They found that aerobic training produced early, transient microbiome changes that partially reverted toward baseline over time, whereas resistance training had limited impact on overall community structure, although individual-level patterns were heterogeneous. [32] Rapid-review evidence focused on resistance training alone suggests minimal effects on bacterial diversity or composition, with some indication of decreased zonulin and increased mucin expression, consistent with improved barrier function. [33]

High-intensity interval training (HIIT) has been less consistent. A short-term HIIT intervention in lean and overweight men did not alter diversity or broad taxonomic profiles, despite improvements in VO_2max. [34] Conversely, in competitive swimmers undergoing a seven-week high-intensity program, both probiotic and control groups exhibited increased alpha diversity, suggesting that training load itself contributed to microbiome enrichment. [35]

3.1.4. Effects of extreme and prolonged exercise

At the other end of the intensity spectrum, extreme endurance appears to exert strong, bidirectional effects, with beneficial adaptations intermingled with signs of stress and dysbiosis. Keohane et al. longitudinally tracked four ultra-endurance rowers during a 33-day, 5,000-km ocean crossing and observed increased alpha diversity and up-regulation of microbial metabolic pathways (e.g., amino-acid, SCFA, and antioxidant metabolism), despite substantial metabolic stress and energy deficit. [15] However, dietary changes and small sample size limit generalizability.

Case reports in ultra-marathon and mountain trail runners describe marked shifts in *Firmicutes:Bacteroidetes* ratios, increases in *Veillonella* and *Streptococcus*, and reductions in certain commensal taxa, suggesting that acute, extreme exertion may select for lactate-utilizing and stress-tolerant microbes. [2,36] Morishima et al. found that female endurance runners with high training volumes exhibited gut dysbiosis, characterized by increased potentially deleterious metabolites and altered SCFA profiles, compared with non-athletic controls. [14]

Systematic reviews emphasize a “J-curve” response: regular, moderate exercise tends to enhance microbial diversity and SCFA production, whereas chronic, high-volume or high-intensity training - particularly without adequate recovery - may predispose to dysbiosis, increased intestinal permeability, and gut-derived inflammation. [3,6,13] Dziewiecka et al.’s review of 38 human studies concluded that athletes generally harbor more diverse microbiota but may exhibit reduced abundance of SCFA and lactic acid producers under intense, long-term exercise, potentially reflecting adverse effects of chronic training stress. [13]

3.2. Sport-specific gut microbiome signatures and links to performance

3.2.1. Enterotypes and multidimensional stratification in elite athletes

Han et al. conducted an in-depth stratification of gut microbiota in elite and non-elite female rowers, collecting 306 fecal samples from adult elite, youth elite, and youth non-elite athletes. They identified three distinct athlete enterotypes, with the majority of elite athletes clustering into enterotype 3, characterized by higher diversity, enrichment of SCFA-producing *Clostridiales*, *Ruminococcaceae*, and *Faecalibacterium*, and increased representation of ATP metabolism and carbohydrate transport pathways. [22] Using random forest classifiers trained on taxonomic and functional features, the authors could distinguish elite from non-elite athletes with high accuracy, underscoring that microbiome composition reflects performance level and training status.

Kulecka et al. showed that top Polish endurance athletes differed from sedentary controls in both composition and richness, with enriched SCFA producers and metabolic pathways related to oxidative energy production and branched-chain amino-acid metabolism. [37] Humińska-Lisowska and colleagues combined microbiome and blood biomarkers to demonstrate that endurance and strength-trained collegiate men exhibit differential microbial signatures correlating with aerobic capacity, anaerobic power, and muscle remodeling markers: endurance athletes showed higher *Prevotella* and lactate-utilizing *Veillonella,* whereas strength athletes exhibited greater abundance of butyrate-producing *Eubacterium rectale* and *Blautia wexlera*e associated with power output. [38]

O'Donovan et al. examined elite Irish athletes across 16 disciplines and reported sport-specific microbiome and metabolome patterns. High-dynamic sports (e.g., race walking, field hockey) showed distinct species-level profiles compared with high static/dynamic disciplines (e.g., triathlon, rowing), with differences in metabolites such as lactate, succinic acid, and creatinine independent of diet. [39] This supports the notion that the microbiome adapts not only to overall training volume, but also to the specific physiological demands and energy systems predominant in each sport.

3.2.2. Lactate-utilizing taxa and endurance performance

A particularly compelling example of performance-linked taxa is *Veillonella*. Scheiman et al. identified higher *Veillonella* abundance in marathon runners post-race and showed in mice that colonization with *Veillonella atypica* improved treadmill time to exhaustion by converting exercise-derived lactate into propionate, which in turn enhanced energy yield and reduced fatigue. [40] Similarly, endurance athletes often display enriched *Prevotella*, a genus adept at degrading complex carbohydrates and generating SCFAs, especially propionate and acetate. [2,9,21]

In ultra-endurance contexts, Keohane et al. and Grosicki et al. found increased *Veillonella* and changes in SCFA-related pathways after prolonged events, alongside elevated markers of metabolic stress. [15,41] These findings suggest a feed-forward loop in which intense exercise generates lactate that fuels specific microbes, whose metabolites support endurance performance.

3.2.3. Strength, power, and mixed-mode athletes

Strength and power athletes appear to harbor different microbial assemblages compared with endurance athletes. Jang et al. observed that bodybuilders consuming high-protein, low-carbohydrate diets displayed reduced SCFA-producing taxa and lower diversity relative to distance runners and non-athletic controls, despite higher protein intake. [42] Similarly, some studies report greater abundance of *Bacteroides* and protein-fermenting taxa in power athletes, with corresponding increases in proteolytic metabolites, although the implications for performance and health remain unclear. [12,43]

Team-sport athletes (e.g., soccer, rugby, volleyball) exhibit mixed microbiota profiles reflecting the combined demands of intermittent high-intensity efforts and strength elements. [2,6] In professional footballers, intensive training appears to reduce oral microbial diversity and, in some cases, decrease gut diversity, while off-season periods are associated with partial recovery of diversity and shifts toward more "sedentary-like" communities. [44] These dynamics highlight the need to consider seasonality, periodization, and training load when interpreting athlete microbiome data.

Recent evidence suggests that gut microbiome composition may differ not only between athletes and non-athletes, but also across levels of athletic performance. Cross-sectional analyses within endurance-trained populations indicate that higher competitive status is associated with distinct taxonomic profiles, supporting the notion that microbiome variation may reflect cumulative training load, performance capacity, and long-term adaptation to endurance exercise. [45]

3.2.4. Microbiome as a marker and modulator of training adaptation

Emerging work suggests that microbiome stability and specific taxa may predict responsiveness to training. In elite race walkers undergoing dietary periodization, Furber et al. found that athletes with more stable microbiota during intensified training maintained better endurance performance and experienced fewer GI symptoms, whereas those with larger microbial perturbations performed worse and showed signs of gut stress. [46]

Liu et al. demonstrated that in prediabetic men, baseline microbiome fermentation capacity influenced the effectiveness of exercise for diabetes prevention; individuals with SCFA-rich microbiota derived greater improvements in glycemic control, and FMT from responders transferred enhanced insulin sensitivity to recipient mice. [47] Evidence suggests the presence of distinct “responder” and “non-responder” phenotypes in exercise–microbiome interactions, indicating that baseline microbial composition may partially determine the extent to which individuals benefit from training interventions. [1,48]

3.3. Mechanistic pathways: SCFAs, gut–muscle and gut–brain axes, inflammation, and barrier function

3.3.1. SCFAs and skeletal muscle metabolism

SCFAs - primarily acetate, propionate, and butyrate - are key microbial metabolites that link diet, microbiota, and host energy metabolism. They serve as energy substrates for colonocytes, regulate gene expression via G-protein–coupled receptors and histone deacetylase inhibition, and influence glucose and lipid metabolism, insulin sensitivity, and appetite. [3,5,17] In the context of exercise, SCFAs can be oxidized in skeletal muscle, contribute to gluconeogenesis, and activate AMP-activated protein kinase (AMPK) and mitochondrial biogenesis pathways, thereby enhancing fatty-acid oxidation and endurance capacity. [2,48]

Human studies consistently associate higher fecal SCFA levels and SCFA-producing taxa with better fitness and athletic status. [1,7] Estaki et al. linked VO_2max to a microbiome enriched in butyrate producers; [24] Mohr et al. and O’Brien et al. report elevated SCFA pathways and fecal SCFA concentrations in professional athletes compared with controls. [7,49] Martin et al. found that elite athletes with very high exercise capacity had reduced bacterial diversity but higher fecal SCFA levels, particularly propionate, and that FMT from these donors improved insulin sensitivity and muscle glycogen storage in mice. [9]

Animal experiments provide causal support. Germ-free or antibiotic-treated mice exhibit reduced endurance and muscle contractility, which can be restored by FMT from exercise-trained donors or by acetate supplementation. [6] Furthermore, rodent studies show that voluntary wheel running and treadmill training increase cecal butyrate concentrations and up-regulate SCFA-producing taxa, with concomitant improvements in metabolic health. [4,50]

3.3.2. Gut barrier integrity, endotoxemia, and inflammation

Intense and prolonged exercise, especially in heat or under hypohydration, redistributes blood flow away from the splanchnic bed, causing intestinal ischemia-reperfusion, increased permeability (“leaky gut”), and translocation of lipopolysaccharide (LPS) and other microbial products into circulation. This can trigger systemic low-grade inflammation, oxidative stress, and immune perturbations, contributing to GI symptoms, fatigue, and increased illness risk in athletes. [3,6,12]

The microbiome modulates this process via its effects on epithelial tight junctions, mucous layer integrity, and immune signaling. [3,12] SCFAs, particularly butyrate, enhance barrier function by fueling colonocytes, up-regulating tight-junction proteins, and inhibiting pro-inflammatory cytokines. [5,51] Exercise interventions in obese children and adults show that training can reduce *Proteobacteria* and *Gammaproteobacteria*, taxa often associated with endotoxemia, and inhibit activation of inflammasome pathways like NLRP3. Quiroga et al. demonstrated that a 12-week combined strength and endurance program in obese children decreased *Proteobacteria,* shifted metabolite profiles, and reduced NLRP3 signaling in mononuclear cells, suggesting that exercise-induced microbiome changes contribute to anti-inflammatory effects. [52]

In overweight women, endurance training altered gut metagenomes and modestly reduced markers of metabolic endotoxemia without large changes in systemic metabolites; structured exercise in adults with obesity similarly improved endotoxemia and insulin sensitivity alongside modest microbiome shifts. [23,53,54] These findings align with reviews concluding that the gut microbiome is an important mediator of exercise-induced improvements in inflammatory tone and metabolic health. [1,6,43]

3.3.3. Immunity, infection risk, and the "open window"

Athletes often experience a transient period of immune suppression ("open window") after prolonged, high-intensity exercise, during which they are more susceptible to upper respiratory tract infections (URTIs) and GI illness. [12 ,43] The gut microbiota plays a central role in shaping mucosal and systemic immunity, influencing T-cell differentiation, antibody production, and innate responses. [3,4]

Athletes with diverse, SCFA-rich microbiota tend to exhibit more robust immune responses and fewer illness episodes, whereas dysbiosis and reduced diversity have been linked to increased infection risk and delayed recovery. [7,12] Probiotic trials in athletes show that specific strains (e.g., *Lactobacillus*, *Bifidobacterium*, multi-strain formulations) can reduce URTI incidence and duration, mitigate GI symptoms during heavy training, and modulate inflammatory and oxidative markers, although effects vary by strain, dose, and context. [5,55,56] Daily multi-strain probiotics at $\geq 10^{10}$ CFU for ≥4 weeks can provide meaningful ergogenic and immunological benefits in endurance and team-sport athletes, particularly under high training loads. [55,57]

3.3.4. Gut–brain axis, stress, and cognitive function

The gut–brain axis, comprising bidirectional communication between the microbiota, enteric nervous system, and central nervous system, is increasingly recognized as relevant to exercise-induced stress, mood, cognition, and sleep in athletes. [2,21,51] Microbial metabolites (SCFAs, tryptophan metabolites, neurotransmitter analogues) influence serotonergic and dopaminergic signaling, HPA-axis activity, and neuroinflammation. [17,51,58]

Exercise-induced stress behavior and mood disturbances are linked to microbiome alterations, including reductions in SCFA producers and changes in taxa such as *Turicibacter*, *Ruminococcus gnavus*, and *Oscillospira* that are implicated in mucus degradation and immune function. [51] Animal models show that stress and forced exercise can exacerbate intestinal inflammation and dysbiosis, whereas voluntary exercise and probiotic or prebiotic supplementation can ameliorate behavioral and neurochemical disturbances. [4,59,60 ,61]

In humans, microbiota-targeted probiotics have been associated with improved sleep quality, reduced perceived stress, and enhanced cognitive function in athletes and active individuals, although data remain limited. [2,17] Jarrett et al. highlight preliminary evidence that probiotic-driven improvements in sleep and mood may translate into better training quality and performance, mediated by gut–brain signaling. [55,57].

3.4. Microbiome-targeted interventions: diet, probiotics, prebiotics, synbiotics, and personalized strategies

3.4.1. Diet quality, macronutrients, and periodization

Diet is the primary modulator of gut microbiota and interacts intimately with exercise. Athletes often consume diets high in total energy, protein, and simple carbohydrates, with variable fiber and fat intakes depending on sport and training phase. [5,7] Hughes and Holscher outline that high-protein, low-fiber diets commonly adopted by strength athletes can increase proteolytic fermentation and potentially detrimental metabolites (e.g., p-cresol, ammonia), whereas high-carbohydrate, fiber-rich diets in endurance athletes synergize with exercise to enhance SCFA production and microbial diversity. [5]

Periodized nutrition strategies - such as high-carbohydrate (HCHO), low-carbohydrate high-fat (LCHF), and periodised carbohydrate (PCHO) approaches - can produce distinct microbiome outcomes. In elite race walkers, Murtaza et al. found that HCHO and PCHO maintained microbiome diversity and improved race performance, while LCHF reduced exercise economy, slowed race times, and induced unfavorable shifts including reduced *Dorea* and increased *Faecalibacterium* and *Bacteroides*. [62] It was also observed that HCD strategies improved endurance performance and maintained microbiota stability, whereas high-protein diets had the opposite effect. [46]

Jang et al. showed that bodybuilders consuming chronically high-protein, low-fiber diets had lower microbial diversity and decreased SCFA-producing commensals compared with distance runners and non-athletes, highlighting potential long-term gut health risks of extreme sport-specific diets. [42] There is a call for athlete-specific dietary guidelines that explicitly consider microbiome health, emphasizing adequate intake of fermentable fibers, plant polyphenols, and omega-3 fats alongside sport-specific macronutrient targets. [5,17]

3.4.2. Probiotics and performance

A growing body of human trials has assessed probiotic supplementation in athletes and active individuals. Systematic reviews and expert consensus documents conclude that probiotic supplementation can: (1) reduce the incidence and duration of upper respiratory tract infections; (2) decrease gastrointestinal symptoms during periods of heavy training and competition; (3) modulate inflammatory and oxidative stress markers; and, in some cases, (4) improve endurance performance and recovery. [7,17,48] Evidence is strongest for multi-strain formulations at doses $\geq 10^{10}$ CFU/day over at least four weeks in endurance and team-sport athletes. [55]

Specific strains, such as *Lactobacillus plantarum* TWK10 and *Bifidobacterium longum* OLP-01, have been shown in animal and human studies to increase muscle mass, extend time to exhaustion, and reduce fatigue. [17] In a randomized trial of competitive swimmers, daily consumption of Bryndza cheese (a natural probiotic source) during seven weeks of high-intensity training increased *Lactococcus* abundance and alpha diversity, although training alone also raised diversity in both probiotic and control groups. [35] What is more probiotics can attenuate exercise-induced increases in intestinal permeability, LPS, and inflammatory cytokines, particularly in heat and ultra-endurance contexts. [5]

However, results are heterogeneous. Some trials find no ergogenic effects on VO_2max or time-to-exhaustion, and benefits appear strain-, dose-, and context-specific. [43] Varghese et al. caution that differences in probiotic formulations, outcome measures, and participant characteristics complicate comparisons and that individualized, “microbiome-informed” probiotic prescriptions may ultimately be required. [16]

3.4.3. Prebiotics, synbiotics, and dietary fibers

Prebiotics - non-digestible fibers that selectively stimulate beneficial microbes - offer another avenue for modulating the athletic microbiome. Increased fiber and prebiotic intake can enhance SCFA production, support barrier function, and potentially improve bone density, immune function, and recovery in athletes, although dedicated sport-specific trials remain sparse. [4,5,17,58] Synbiotic combinations (probiotic + prebiotic) may provide additive benefits, with some studies showing improved lean mass maintenance, reduced markers of muscle damage, and enhanced immune responses in athletes. [2,48]

Periodized fiber intake may be necessary to balance GI comfort and microbial needs: restricting fermentable fibers immediately before and during competition can reduce GI distress, whereas higher fiber intake during training and recovery phases may support microbiome diversity and long-term gut health. [7,51]

3.4.4. Fecal microbiota transplantation and “athletic donors”

Preclinical work suggests that transferring microbiota from highly fit or training-adapted donors can confer metabolic and performance benefits. Martin et al. transplanted microbiota from athletes with very high VO_2max into mice and observed improved insulin sensitivity and increased muscle glycogen stores, although endurance capacity did not increase in the absence of concurrent training. [9] Liu et al. showed that FMT from human exercise responders improved glycemic control and insulin sensitivity in mice, whereas FMT from non-responders did not, implicating gut fermentation capacity as a determinant of exercise benefits. [47]

These data have prompted speculation about “athletic donor” FMT as a therapeutic strategy for metabolic disease or even performance enhancement; however, ethical, safety, and regulatory considerations are substantial, and human data are lacking. [6,9] Recent findings indicate that, in the near term, microbiome monitoring could be integrated into athlete support systems to assess gut health, detect dysbiosis, and inform personalized nutritional and probiotic strategies. [7,48]

4. Discussion:

The evidence reviewed here supports a bidirectional, context-dependent relationship between exercise and the gut microbiome with important implications for exercise physiology and athletic performance. Cross-sectional studies in athletes and high-fitness individuals consistently show that habitual physical activity is associated with increased microbial diversity, enrichment of SCFA-producing and mucin-degrading taxa, and expanded functional capacity for carbohydrate and amino-acid metabolism. [1,2,7] Longitudinal interventions demonstrate that endurance training can modestly but reproducibly alter microbiome composition and function, particularly when sustained over at least six weeks, and that these changes may regress upon detraining. [18,23,27]

Sport-specific patterns emerge: endurance and ultra-endurance athletes often harbor microbiomes enriched in lactate-utilizing *Veillonella* and carbohydrate-fermenting *Prevotella*, whereas strength athletes display higher abundance of protein-fermenting taxa and, in some cases, reduced SCFA producers due to high-protein, low-fiber diets. [55,42] Elite athletes across disciplines exhibit distinct enterotypes and metabolomic profiles linked to performance markers such as VO_2max, lactate thresholds, and power outputs. [2,22] However, extreme training loads and environmental stressors can push the system toward dysbiosis, with increased intestinal permeability, endotoxemia, and perturbations in microbial communities. [2,14,44]

Mechanistically, SCFAs emerge as central mediators, bridging diet, microbiota, and host metabolism. [3,5,17] They support colonocyte and muscle energetics, enhance mitochondrial function, modulate inflammatory pathways, and influence appetite and insulin sensitivity. [6,48] Exercise can enhance SCFA production by increasing the relative abundance of SCFA producers and potentially by increasing colonic delivery of fermentable substrates through altered transit time and diet. [1,6,7] Conversely, inadequate fiber intake or chronic high-protein, low-carbohydrate diets may reduce SCFA generation and increase proteolytic metabolites, undermining some benefits of exercise. [5,42]

The microbiome also plays a crucial role in modulating immune function and gut barrier integrity, thereby influencing illness risk, recovery, and potentially training adaptations. [3,43,48] Exercise-induced microbiome changes can reduce pro-inflammatory *Proteobacteria*, down-regulate inflammasome pathways (e.g., NLRP3), and lower endotoxemia in obesity and metabolic syndrome, while probiotics and prebiotics can further reinforce barrier function and mucosal immunity. [52,53] However, under extreme or poorly recovered training, these protective mechanisms may be overwhelmed, leading to increased GI symptoms, systemic inflammation, and susceptibility to infection. [6,12,14]

The gut–brain axis represents an additional layer, where microbial metabolites influence mood, stress resilience, cognition, and sleep - factors integral to performance yet under-studied in athlete microbiome research. [2,17,51] Preliminary data suggest that probiotic interventions can improve sleep quality and perceived stress, but more rigorous, sport-specific trials are needed. [2,55,48]

From a practical standpoint, microbiome-targeted strategies offer promising adjuncts to training and nutrition, but translation is still in its infancy. High-quality diets that emphasize diverse plant fibers, polyphenol-rich foods, and balanced macronutrients appear to synergize with training to support a “health-associated” microbiome. [5,17,58] Probiotics - particularly multi-strain, high-dose formulations - can reduce illness burden and GI distress, and may in some contexts improve endurance and recovery, but strain-specific evidence and personalization remain key challenges. [48] Synbiotics and prebiotics hold potential to enhance SCFA production and gut integrity, while FMT from athletic donors remains experimental. [2,9,47]

Taken together, the available evidence suggests that:

Regular, moderate-to-vigorous exercise is generally beneficial for gut microbiome diversity and function, whereas extreme or poorly recovered training can be detrimental.

The microbiome may contribute meaningfully to inter-individual variability in training responses, metabolic health, and performance, through SCFAs, immune modulation, and gut–brain signaling.

Diet and microbiome are tightly intertwined; ignoring microbiome health in sport nutrition planning risks undermining long-term health and possibly performance.

However, substantial uncertainties remain, particularly regarding causality, optimal intervention strategies, and the magnitude of microbiome contributions relative to other determinants of performance such as genetics, training history, and psychology.

Limitations of the study include small sample sizes, relatively short intervention durations, and imperfect control of diet and other lifestyle factors in many of the human trials reviewed, which collectively reduce statistical power and constrain the ability to disentangle the independent effects of exercise from confounders such as habitual dietary intake, medications, sleep, and environmental exposures. These issues are further compounded by pronounced methodological heterogeneity in microbiome assessment - ranging from the use of 16S rRNA versus shotgun metagenomic sequencing, differences in targeted variable regions, sequencing depth, and bioinformatic pipelines, to variability in how microbial diversity, composition, and functional capacity are reported - making direct cross-study comparisons difficult and precluding a robust quantitative meta-analysis. The available evidence base is also demographically skewed: most athlete cohorts comprise young, healthy, predominantly male participants from Western countries, with limited inclusion of female athletes, older adults, para-athletes, and individuals from non-Western or low- and middle-income settings, thereby restricting the generalizability and ecological validity of the conclusions. Moreover, a substantial proportion of mechanistic insight into gut - exercise interactions is derived from animal models, which differ from humans in gut anatomy, diet, microbiota composition, and exercise paradigms; although these models are invaluable for hypothesis generation, extrapolation of their findings to human athletic populations must be undertaken cautiously. In addition, the body of literature is dominated by observational and short-term interventional studies, raising the possibility of residual confounding and reverse causality, and publication bias toward positive or novel findings cannot be excluded. Finally, this review employs a narrative synthesis rather than a formal systematic review with predefined risk-of-bias assessment and grading of evidence strength, which may influence how individual studies are weighted and interpreted and limits the ability to provide definitive, quantitative estimates of effect sizes.

Future research should prioritize well-designed, adequately powered, longitudinal human studies that integrate standardized exercise prescriptions with rigorous dietary control and detailed microbiome and metabolome profiling. Specific priorities include:

Sport- and sex-specific cohorts: Systematic characterization of microbiome trajectories across training cycles, competition seasons, and career stages in diverse sports and in both male and female athletes, including older and para-athletes.

Dose–response and modality studies: Randomized trials comparing different exercise intensities, volumes, and modalities (endurance, resistance, HIIT, mixed) with fixed diets, to determine thresholds and patterns of beneficial versus detrimental microbiome changes.

Mechanistic multi-omics: Integration of metagenomics, metatranscriptomics, metabolomics (including SCFAs, bile acids, neurotransmitters), and host omics (transcriptomics, proteomics, epigenetics) to map causal pathways linking specific microbes and metabolites to muscle energetics, immune function, and brain health.

Responder phenotypes and personalization: Identification of microbiome-based predictors of training responses and probiotic/prebiotic efficacy, including exploration of “responder” and “non-responder” microbial signatures, to enable personalized exercise and nutrition prescriptions.

Intervention trials: Rigorous, double-blind, placebo-controlled trials of strain-specific probiotics, prebiotics, synbiotics, and dietary strategies in athletes, with performance, health, and microbiome outcomes, and long-term follow-up to assess sustainability and safety.

Non-bacterial components: Expansion beyond bacteria to include fungal (mycobiome), viral (virome), and archaeal communities, which may also be shaped by exercise and contribute to metabolic and immune responses. [63]

Clinical and translational applications: Evaluation of microbiome-informed exercise interventions and athletic FMT in populations with metabolic disease, sarcopenia, or chronic inflammation, to determine whether “exercise-trained” microbiomes can be leveraged therapeutically.

5. Conclusions

The gut microbiome is emerging as a critical, modifiable determinant of exercise physiology and athletic performance. Regular physical activity, particularly sustained endurance training, generally enhances microbial diversity, enriches SCFA-producing taxa, and strengthens gut barrier function, creating a positive feedback loop that supports metabolic efficiency, immune resilience, and possibly cognitive and psychological robustness in athletes. Elite athletes display distinct, sport-specific microbial signatures reflective of their chronic training adaptations and dietary practices, with taxa such as Veillonella and Prevotella exemplifying potential microbial contributors to endurance performance.

Conversely, extreme training loads, inadequate recovery, and suboptimal diets can tip the gut ecosystem toward dysbiosis, with increased permeability, inflammation, and GI and respiratory illness risk, underscoring the importance of balance in training and nutrition. Microbiome-targeted strategies - including high-quality, fiber-rich diets, prudent use of strain-specific probiotics and prebiotics, and, in the future, perhaps microbiome-informed personalized interventions - hold promise as adjuncts to conventional training and sports nutrition.

Nevertheless, the field remains in an early phase. Many questions regarding causality, effect sizes, and optimal intervention strategies are unresolved, and current evidence is limited by methodological heterogeneity and small samples. To fully realize the potential of the gut–exercise axis for enhancing performance and protecting athlete health, future research must adopt rigorous, integrative, and personalized approaches that place the microbiome alongside training load, diet, recovery, and psychological factors in a truly systems-level understanding of the athletic organism.

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Supplementary materials

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Wiktoria Michnowska - investigation, resources, formal analysısı
Patryk Hebda - investigation, formal analysis, project administration
Mieszko Czapliński - formal analysis, resources
Natalia Bruska - formal analysis, resources
Bartłomiej Błaszkowski - investigation, data curation
Andrii Bilyk - resources, writing - rough preparation
Adam Wolski - resources, data curation
Mateusz Kubicki - data curation, writing - rough preparation
Katarzyna Więckowska - data curation, visualization

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Not applicable.

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Not applicable.

Conflict of interest

The author declares no conflict of interest in relation to this study.

Declaration of Generative AI and AI-Assisted Technologies

During the preparation of this work, the author used ChatGPT (OpenAI) to improve grammar and language clarity. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication

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