

The Impact Of Fruit Consumption Patterns On Gut Microbiome Composition And Exercise Performance In Athletes

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Abstract

Summary

The gut microbiota is a diverse and intricate microbial population that is influenced by both internal and external stimuli. Nutrition and physical exercise are external factors that might potentially influence microbial diversity, both in terms of taxonomy and function. These factors may also have an impact on the endocrine system and can even operate as an endocrine organ itself. Currently, there is a dearth of definitive evidence identifying the specific microbial populations that are altered and the methods via which these alterations occur. Furthermore, the connection between the changes in microorganisms and the functional capacity of the gut microbiota remains uncertain. Additional research using longitudinal and well-designed studies is necessary to examine whether manipulating the microbiome could be a viable method for enhancing human health and athletic performance. Furthermore, it is important to determine if these effects can be extended to promoting overall health in the general population. This study aims to assess and condense the existing understanding of the interplay and communication between hormonal alterations, physical performance, and the composition and functioning of the microbiota.

Keywords: gut microbiota; microbial composition; health; exercise; athletes; physical performance; hormones.

1. Introduction

Extensive evidence has shown that an improper diet and lack of physical activity are strongly associated with a significant occurrence of chronic metabolic disorders, including cardiovascular disease (CVD), type 2 diabetes mellitus (T2DM), cancer, and osteoporosis [1]. Conversely, exercise plays a crucial role in both preventing and managing these conditions [2]. The health benefits of exercise are facilitated by metabolic and immune effects that operate through various mechanisms. These mechanisms include promoting an anti-inflammatory state, activating the hypothalamic-pituitary-adrenal (HPA) axis, enhancing synaptic plasticity, and strengthening neuromuscular function [3,4]. In addition, skeletal muscle functions as an endocrine organ by secreting several hormones and cytokines in response to muscular contraction. These substances have various effects on multiple organs and tissues [5].

Scientific research has recently focused on the gut microbiota as a potential target for the impact of physical activity on health. The gut microbiome profile, including its qualitative and quantitative features such as microbial richness, presence or absence of certain taxa, and their numbers, is not a fixed trait but instead responds to environmental and lifestyle factors. [6] Changes in the composition and function of the gut microbiota

have been associated with several illnesses, including obesity [7], metabolic disorders [8], and brain-related dysfunctions [9,10]. Several studies have shown that manipulating the gut microbiota and its by-products by exercise prescription might be a potential new method for preventing and treating metabolic pathological disorders [11,12,13,14]. Furthermore, several studies indicate that altering the gut microbiome (namely, increasing the presence of beneficial bacterial species and enhancing microbial diversity) via exercise might provide valuable information for enhancing athletic performance and reducing recovery time after training [15,16,17,18]. This review will assess recent research on changes in the gut microbiota caused by exercise, in both animals and people. The study will specifically examine the impact of exercise on physical performance and athletes.

2. Gut Microbiota: Structure, Identification, and Role

The human gut microbiota is an intricate network of mutually beneficial bacteria that inhabit the whole gastrointestinal tract (GI tract), progressively growing in quantity and variety from the stomach to the colon. The human body contains almost 39 trillion germs, with a microbial to eukaryotic cell ratio of 1:1. There are more than 1000 distinct bacterial species and over 3 million unique genes present [19,20]. In addition to bacteria, the gut microbiota also contains additional prokaryotes (namely Archaea), fungi, and viruses (10). The dominant bacterial phyla in healthy adults are Gram-positive Firmicutes (comprising 60% to 80%) and Gram-negative Bacteroidetes (comprising 15% to 30%) [21,22]. The Firmicutes phylum comprises more than 250 bacterial genera, such as *Lactobacillus* and *Clostridium*. On the other hand, the Bacteroidetes phylum consists of approximately 20 genera, with *Bacteroides* being the most prevalent [23]. The remaining bacteria belong to the Proteobacteria, Actinobacteria, Fusobacteria, and Verrucomicrobia phyla [24].

Next-generation DNA sequencing has replaced culture-based methodologies for studying gut microbes with culture-independent genomic analysis of microbiota. The most commonly used method is amplicon sequencing of the 16S ribosomal ribonucleic acid (rRNA) gene in archaea and bacteria [18,25]. This method enables the categorization of bacteria into specific genera or species, providing an overall understanding of the taxonomic makeup of a microbial ecosystem. This technique differs from amplicon sequencing because it generates sequences from random fragments of the entire microbiota DNA. Through advancements in combining complete metagenome-assembled genomes with shotgun analyses, it enables the detection of bacterial taxa, even at the strain level [26-28]. The strain level refers to the lowest level of taxonomic classification that describes genetic variants or subtypes of a species. The microbiota plays a crucial role in maintaining and balancing human health by performing diverse protective, metabolic, and structural tasks. These functions are carried out via the synthesis and release of different compounds, including amino acids, short-chain fatty acids (SCFAs), and regulatory enzymes [29].

3. The gut microbiota generates molecules that have endocrine activity

In addition to its local effects on the gastrointestinal functions, the gut microbiota also influences distant organs and systems by releasing molecules into the bloodstream that function as hormones [30]. This interaction is two-way, as certain members of the overall microbial community can be influenced by hormones secreted by the host, such as stress and catabolic hormones. This emerging field of study, known as Microbial Endocrinology, has shed light on this phenomenon [31-33]. Due to this, microbiota is currently recognized as a complex endocrine organ that has a virtual impact on host metabolism and energy balance. It achieves this by controlling various functions such as insulin sensitivity, fat storage, adiposity, and body weight, ultimately impacting the health and disease of the host. Furthermore, the microbiota is regulated by the endocrine secretions of the host.

4. Internal and external factors impact on the composition of gut microbiota

The composition of gut microbial communities exhibits significant interindividual heterogeneity, particularly at taxonomic levels below the phylum [34]. Host-specificity is determined by various factors, both internal and external. These factors include host genetics, gender, geographic origin, pregnancy, type of birth (natural or caesarian), method of infant feeding (breastfeeding or infant formula), stress, drugs, and diet [35-40].

Undoubtedly, the makeup of gut microbiota is significantly influenced by dietary patterns. Western diets, which are heavy in sweets and fats and poor in fiber, have been associated with a reduction in community variety, irreversible loss of bacteria, and dysbiosis [41]. In contrast, consuming diets rich in fiber, such as those that include fruits, vegetables, legumes, and whole-wheat grain products, might enhance the variety of microorganisms present in the body [42]. Changes in the microbial community due to various factors disrupt the mutually beneficial relationship between harmful and harmless bacteria, leading to the development of an inflammatory state and an imbalance in the gut, which can have negative effects on health. These effects include autoimmune and allergic conditions, colorectal cancer, and metabolic diseases. While it is known that changes in gut microbiota can contribute to various diseases, it is still unclear whether there are specific microbial profiles associated with good health. Some bacterial species have been proposed as important for maintaining a healthy microbiota [20].

Enhanced variety and/or abundance of gut microbial species are seen as characteristics of persons in good health [43], and are positively correlated with total gut microbial richness. Roager et al. [44] have found that there is a strong correlation between slower colonic transit time in humans, as measured by radiopaque markers, and a shift in colonic metabolism from carbohydrate fermentation to protein catabolism. On the other hand, shorter colonic transit time seems to be associated with metabolites that may indicate increased renewal of the colonic mucosa. These findings suggest that gut microbial diversity alone may not be the only factor influencing healthy gut ecology. Other parameters, such as colonic transit time, should also be taken into account [44]. Furthermore, it appears that the presence and variety of genes in the intestinal tract could serve as a more accurate indicator of physiological conditions. Consequently, the functional and metabolic activity of the gut microbiota may have a more significant influence than the composition of microbes themselves on the initiation and/or progression of human health or disease.

5. The Influence of Exercise on Gut Microbiota

The prescription of physical exercise is essential in preventing several illnesses, including cardiovascular disease (CVD), colon and breast cancer, type 2 diabetes mellitus (T2DM), osteoporosis, sarcopenia, cognitive impairment, and depression [45]. In recent years, there have been several reports indicating that exercise may have positive effects on the gastrointestinal tract, metabolic illnesses, mood, and other brain-related problems via changes in the gut microbial population and its metabolites [11,13,14,43]. Multiple research have shown that engaging in physical activity enhances the variety of microbiota and influences its distribution and functional ability [15,16,17]. However, there is still inconsistency in the findings.

Moreover, the available information about the connection between physical activity, the permeability of the gut, and the inflammation caused by lipopolysaccharide (LPS) is inconclusive. The variations seen in studies may be attributed to the specific characteristics of the exercise, including its kind, intensity, duration, and adaptability [46]. Currently, it is unclear whether a sudden increase in LPS (lipopolysaccharide) levels in the body, known as "mild endotoxemia," during prolonged or intense exercise is a temporary physiological effect or if it could have negative long-term health consequences, especially for recreational athletes who engage in regular physical activity. In addition, the specific ways in which

exercise can lead to changes in the microbiota are not yet completely comprehended. These mechanisms likely involve a series of interconnected pathways, as summarized in Figure 1.

These pathways include modifications in bile acid profiles, increased production of short-chain fatty acids (SCFAs), activation of toll-like receptors (TLRs) in the muscle by lipopolysaccharides (LPS), release of myokines from muscle fibers, maintenance of glucose homeostasis, weight loss resulting from energy expenditure, exercise-induced heat stress, activation of the hypothalamic-pituitary-adrenal (HPA) axis, and other contributing factors that have not been fully recognized (Figure 1) [47,48].

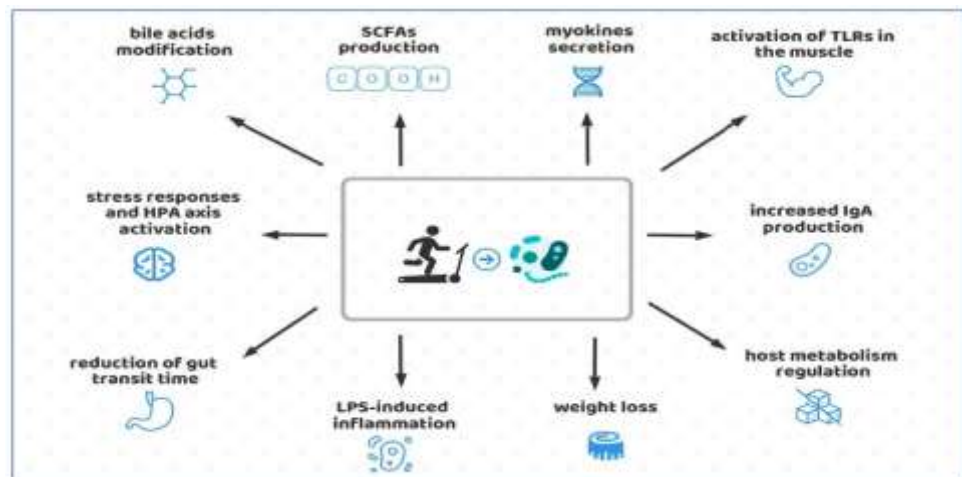


Figure 1. A diagrammatic description of how physical exercise impacts the gut flora.

6. Summary

Engaging in physical activity at the levels suggested by the World Health Organization (WHO) enhances fitness and quality of life via several processes, perhaps including alterations to the gut flora. Existing data suggests that engaging in regular exercise boosts the variety of microorganisms in the gut and fosters the formation of mutually beneficial bacteria populations and functional pathways. This ultimately results in improved health and maybe enhanced physical performance among athletes. The impact of exercise on the gut microbiome appears to be influenced by various factors, including the individual's physiological condition, as indicated by a more diverse microbiota in physically active individuals, exercise-related variables such as intensity and timing, which may have both positive and negative effects, and long-term dietary habits, especially protein and carbohydrate (fiber) consumption.

An arduous endeavor is to disentangle the influence of many external and internal factors on the microbial population. The relationship between physical activity and gut microbiota needs to be more thoroughly examined by considering confounding variables, implementing standardized methods in study design (such as fecal sampling protocols, sequencing and analytical techniques, and statistical analysis), controlling calorie intake as well as the quality and composition of nutrients, and establishing exercise parameters (such as acute or chronic exercise, cardio and/or resistance training, duration, and frequency). Moreover, it is necessary to clarify the fundamental processes by which exercise influences the composition and activity of the gut microbiota by combining research on taxonomy with metagenomics, metatranscriptomics, metaproteomics, and metabolomics.

The major factor that determines a well-functioning microbial habitat and, as a result, the health of the host, is functional diversity [49]. Another aspect that requires further

investigation is the gut microbial sampling methodology. It has been suggested that the composition of the fecal compartment may not accurately reflect the true complexity of the gut microbiota. This is because it may either underestimate or overestimate the presence of certain bacteria genera and species. Additionally, there is a need to differentiate between the microbial populations and metabolites residing in the mucus layer and those in the lumen [35,36,37]. Existing data on athletes indicate that this group exhibits unique microbial characteristics compared to sedentary individuals. These characteristics include increased microbial diversity and a greater abundance of beneficial bacteria that are associated with improved fitness and overall health [15,16,17].

The interaction between exercise and dietary habits leads to changes in the gut microbial community, which can potentially enhance athletic performance and decrease recovery time during training. However, additional research is needed to fully understand the relationship between the microbiota and exercise, and to explore new possibilities such as predicting responses to interventions and improving athletic performance. Meta-omics data, when combined with interpretable machine learning (ML) approaches, can be instrumental in uncovering the interactions between microorganisms and their host. This can help identify various scenarios of healthy microbiota that are relevant for human health and performance enhancement.

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