



# Gut microbiota related to nutrition and physical activity: an integrative review

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## Abstract

**Introduction:** The gut microbiota (GM) is formed by millions of microorganisms present in the gastrointestinal tract, especially in the colon. This intestinal homeostasis can be triggered by the union of a good diet, and even recent studies have suggested that aerobic physical training can modify its composition. **Objective:** To analyze the influence of healthy eating added to the practice of physical exercise in changing the composition of the GM. **Methods:** The research was carried out with an exploratory, qualitative and bibliographic approach. A literature review that brings together important studies on the influence of physical exercise on GM. **Results:** Data collection for this literature review was carried out from March to September, using articles, in addition to trustworthy websites, with the following descriptors: gut microbiota, microbiota, intestinal flora, food, probiotics, and physical exercise. **Conclusion:** The training was efficient to change the GM composition in sedentary men, thus being able to minimize possible negative interferences of the sedentary pattern. Bacteria that reside in our body work with a commensalism strategy, where there are two different structures, the microorganism, and the individual's body, but both live together normally and thus work together to maintain the GM balance.

**Keywords:** Gut microbiota. Intestinal flora. Food. Probiotic. Physical exercise.

## Introduction

The Gut Microbiota (GM) is composed of microorganisms, in particular bacteria, that inhabit the gastrointestinal tract. The person responsible for this discovery was Antonie Van Leeuwenhoek, who was a great scientist and microscope builder. He studied the

diversity of the human microbiota, making comparisons between oral and fecal microbiota [1]. Several researchers are still trying to understand the role of GM in the development of some comorbidities, such as obesity. They observed that individuals with greater adiposity, high body mass index (BMI), insulin resistance, dyslipidemic profile, and greater inflammatory profile, had notably less bacterial diversification. These researchers suggest a greater diversity among bacterial species that make up GM and a greater abundance of commensal bacteria, respectively called diversity and species richness, which can positively contribute to the health of the host. Thus, the GM, or intestinal flora, plays an important role in preserving health, that is, it has physiological functions [2].

The composition, diversity, and richness of GM species are influenced throughout life, by environmental factors, such as eating habits. Aerobic physical training provokes physiological adaptations on the intestinal system and has been pointed out as one of the environmental factors capable of causing plausible changes in GM composition [3,4]. Among the physiological functions of GM is an aid in food digestion, aid in the production of vitamins, such as vitamin B and K; the influence on mood, by producing serotonin; protection of the integrity of the intestinal mucosa; the interrelationship with the immune system and several other beneficial functions. Furthermore, it also intervenes in the proliferation of pathological microorganisms [2].

In this context, GM dysbiosis can occur mainly in dependence on food and treatment with certain drugs [5]. There are indications that physical training can change the composition of GM. However, it has been questioned about the divergences reported in the

literature, regarding the type and time of physical training practiced. It is noteworthy that some studies with physical training interventions focused on aerobic training in overweight and obese people, protein supplementation, and aging. Furthermore, Allen et al (2017) [6] included men and women, while Estaki et al (2016) [7] suggest that gender can be an influencing factor. Some studies do not report on eating habits during the intervention and did not present a sedentary control group. These variables, when not properly controlled, can make it difficult to understand the relationship between the effect of physical training and GM [6].

Also, food contributes to balancing the body's adequate and necessary nutrition and providing intestinal bacterial balance, including prebiotics and probiotics [5]. For this, general knowledge about GM and how it is kept in balance is also important. It is important to emphasize that bacteria live in harmony in the intestinal flora and need to be in balance with the human body in a relationship of commensalism, in which both have health-promoting benefits.

Thus, this study aimed to carry out a literature review to analyze the influence that the practice of physical exercise and/or food has on the composition of the GM.

## Methods

The Bibliographic Research was carried out from the survey of theoretical references of articles from the databases and published by written and electronic means, such as books, scientific articles, and website pages. The theoretical references were analyzed to capture information or previous knowledge about the studied problem [8]. This methodology of bibliographical, qualitative, and descriptive-exploratory research was elaborated with the following steps: Choice of the theme, preliminary bibliographic survey, formulation of the problem, elaboration of the provisional subject plan, a search of sources, reading of the material, annotations, logical organization of the subject and wording of the text [9]. Reference databases were used: Medline, Scielo, academic google, books, using the keywords: gut microbiota, microbiota, intestinal flora, food, probiotics, and physical exercise. Using as inclusion criteria, articles were published between the years 2001 to 2019.

## Results

### Gut Microbiota

Microbial cells maintain a symbiotic relationship to maintain the balance of the intestinal flora, blocking

pathogenic bacteria that could cause imbalances or local and/or systemic diseases. Dietary behaviors are important factors that lead to the improvement and normalization of health and GM [10-12]. Until birth, the intestine is free of bacteria, but it has its first contact with the mother's microbiota, during normal delivery, and then it strengthens this system during breastfeeding, maintaining a diversified microbiota dependent on genetic and environmental factors. The latter include geography and environmental bacteria. The maturation of the GM to the adult type is reached at 3 years of age. This process seems to exert a great influence on the development of the immune system, promoting immunogenic tolerance against symbionts and immune activation against pathogens. Alterations in this process can induce inappropriate immune responses, favoring diseases. In adulthood, the composition of the human GM remains relatively stable over time, exhibiting resilience to disruptors such as stress, acute illness, or antibiotic administration. This means that after a brief exposure to disruptors, the microbiome faces substantial but transient disruption, followed by partial or full recovery [13,14].

The gut microbiome was recently designated as a virtual organ. With the advent of various genomic technologies, their significance has been correlated with health and disease conditions. The intestinal microbial ecosystem is composed of more than 10 species, of bacteria, viruses, fungi, and protozoa, which coexist with human cells [14]. The dominant phyla are Bacteroides and Firmicutes, followed by members of the phylum Actinobacteria, Proteobacteria and Verrucomicrobia. Fungi also coexist, including *Candida* and *Saccharomyces* species, viruses (mainly bacteriophages), as well as members of the archaeal domain. Although GM is stable in adults, certain factors can alter its structure, including diet, antibiotics, probiotics, and, in fact, exercise/physical conditioning. In some diseases, there is a reduction and alteration in GM, with consequent changes in metabolism, immune function, and oxidative stress. All these systems are essential for the performance of athletes [15].

The concentration of bacteria usually increases from the small intestine to the colon and different bacterial populations are housed in different areas of the gastrointestinal system. Although recent research has shown that the composition of the fecal microbiota does not completely match the microbiota associated with the intestinal mucosa, the composition of GM was determined from fecal samples in most studies. Dietary factors, particularly carbohydrate and protein intake, are generally considered to be the main determinants of GM composition. With aging, microbiome diversity

decreases and variability among individuals increases, and the resilience to disturbances is reduced [14].

### Gut Microbiota Dysbiosis

It is possible that short-chain fatty acids produced by healthy MI that are turned into energy for the host increase GLP-1 secretion (which improves insulin sensitivity), increase peptide YY secretion (which induces insulin) satiety and decrease the deposition of fat in the adipose tissue. Thus, individuals with wrong eating habits can suffer dysbiosis, causing the reduction of bacteria that produce short-chain free fatty acids. This cycle increases the pathogenic bacteria, which can generate a sick intestinal environment [16].

Obesity-associated GM may contribute to weight gain through energy gain and inflammation due to reduced integrity of the intestinal barrier. Obesity is an inflammatory disease mediated by oxidative stress and inflammatory agents that modify the intestinal structure, changing good bacteria and increasing obesogenic bacteria such as *Bacteroides* and *Firmicutes*, respectively. Being overweight also increases mortality and morbidity rates in adults and children, due to the association of other diseases such as Diabetes Mellitus, heart disease, and even some types of cancer [16].

Besides, adipose tissue can produce substances that act on the immune response. Toll-like membrane receptor proteins (TLR-4) are formed due to excess fat and free fatty acids that bind to subtype 4 of TLR. These proteins can respond to lipopolysaccharides and initiate immune responses due to its activation, increasing the inflammatory expression of the obese organism, which can lead to morbidities such as obesity or the development of diabetes due to insulin resistance [17].

Several other diseases, acute or chronic, not limited to the gastrointestinal system, are associated with changes in GM composition. These alterations are referred to as "dysbioses", including reduced diversity, loss of commensal relationship with beneficial metabolic activities, and growth of opportunistic pathogens. Dysbiosis involves the disruption of the mutual balance between intestinal bacteria and host physiology. As a consequence, intestinal permeability increases, allowing bacteria, toxins from these bacteria, and metabolites to enter the host's circulation and promote subclinical inflammation. Thus, dysbiosis also reduces the bioavailability of nutrients, affecting the microbial metabolism of several beneficial substances. Thus, GM can exert a great influence on the pathophysiology of several organs anatomically distant from the gastrointestinal tract. For example, GM may be involved in the pathophysiology of dementia, Parkinson's disease, chronic kidney disease, nephrolithiasis, asthma, and

even osteoporosis [14].

### Gut Microbiota And Physical Training

Despite the few data in the literature, these indicate that physical training can significantly modulate IM. Exercise is one of the environmental factors that most influence GM. Clarke et al. (2014) [18] demonstrated significant differences in the GM of professional rugby players compared to non-male athletes. These athletes possessed a high level of the *Akkermansia* genus. Physical training increases lean body mass, decreases fat percentage, increases bone mineral density, and improves (VO<sub>2</sub>max) both in lean and obese individuals. Physical training increased the fecal excretion of acetate, propionate, and butyrate, short-chain fatty acids, depending on the status of GM. These variations were concomitant with the relative increase in genes that regulate butyrate production. Functional groups of bacteria varied as a result of physical activity, to a greater extent in thin individuals than in obese individuals. Positive correlations were described with variations of butyrate and/or BCoAT gem (isolated bacterial DNA) for the genera *Roseburia spp*, *Lachnospira spp*, *Clostridiales spp*, *Faecalibacterium spp*, and classless *Lachnospiraceae* [18].

In another study, through metagenomic analysis of fecal samples, it was shown that athletes had a different GM, both from a functional point of view, and also had a greater representation of microbial genes involved in the metabolism of carbohydrates and amino acids and production of fatty acids from a short-chain. 30 out of 33 cyclists also showed an increase in *Akkermansia* abundance. It was also observed that the exercise regimen is proportional to the abundance of the *Prevotella* genus, which, in turn, was associated with an increase in amino acids important for muscle recovery. There has also been an increase in *Methanobrevibacter smithii* in professional cyclists compared to amateurs, a microbe that uses H<sub>2</sub> in the colon to form short-chain amino acids and adenosine triphosphate (ATP) [19].

Also, a subsequent study from the same cohort concluded that athletes had a greater abundance of short-chain fatty acid (SCFA) metabolic pathways. Short-chain fatty acids (two to six carbons) serve as a source of energy for various tissues, reducing inflammation, improving insulin sensitivity, and changing the morphology of the central nervous system [20]. Training intensity is also important: light exercise induces only small changes in GM composition in sedentary individuals. Therefore, the results of studies with athletes cannot be automatically transferred to all individuals who exercise [14].

In this sense, in humans, the maximum oxygen

consumption rate (VO<sub>2</sub>max), measured as maximum expiratory volume or vital capacity (maximum effort test) was positively correlated with bacterial diversity and butyrate-producing bacteria. The VO<sub>2</sub>max rate represents the integrity of the human cardiorespiratory system and the capacity for aerobic exercise [7]. Resende (2019) [21] reported that after ten weeks of aerobic physical training, at moderate intensity, young adults showed a significant increase in bacterial taxonomic groups. The main changes were an increase in the Lachnospiraceae family and *Bacteroides ovatus* and *Roseburia sp.* species, while there was a reduction in the abundance of the *Lachnospira sp* genus and bacteria belonging to the Proteobacteria phylum, such as the species *Biophilia sp.* In addition, the trained group had a greater abundance of commensal bacteria compared to the control group, after 10 weeks of physical training. These changes also correlated positively with VO<sub>2</sub>max measurements.

Finally, GM composition (or dysbiosis) can also influence other pathologies or metabolic alterations, involving protein synthesis, the release of pro-anabolic mediators, inflammation, and insulin sensitivity. All of these elements may also be related to the modulation of skeletal muscle physiology. Thus, dysbiosis of the GM can reduce the bioavailability of dietary proteins and particularly of some amino acids, such as tryptophan, involved in the modulation of inflammation and promotion of muscle protein synthesis.

In addition, intestinal bacteria are also involved in the synthesis of several vitamins, including folate, vitamin B12, and riboflavin, exerting various benefits and pro-anabolic effects on the body's cells as a whole, from amino acid biosynthesis to neutralization of acid. oxidative stress during exercise. Healthy GM can effectively transform some dietary nutrients into metabolic mediators that, once absorbed into the systemic circulation, can exert beneficial effects on inflammation, Pa insulin sensitivity, anabolism, and antioxidant capacity. However, an GM in dysbiosis can lose these functions, with some negative consequences on muscle health. Another mechanism involved in GM modulation is the bacterial production of metabolic mediators, including secondary bile acids. Short-chain fatty acids, as well as butyrate, are usually synthesized by a large number of bacteria, including *Faecalibacterium*, *Butyricimonas*, and *Succinivibrio*, found in healthy individuals [21].

## Conclusion

The gut microbiota composition, as well as its diversity and species richness, is influenced throughout life, mainly by environmental factors, such as eating

habits and physical exercise. It was observed that there are significant differences in the composition of gut microbiota present in feces, between trained and sedentary individuals. Physically active individuals and athletes have greater diversity and species richness compared to sedentary ones. Regular training of athletes is associated with increased biodiversity and the beneficial functions of gut microbiota. The microbiota can, therefore, represent a mediator of health benefits induced by exercise, although diet and body composition also play a relevant role in this association. The effects of exercise on the intestinal microbiome need to be better investigated, especially in humans, also in relation to exercise intensity. These studies may help to clarify this relationship.

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No additional data are available.

## Conflict of interest

The authors declare no conflict of interest.

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