

# Impact of the exercise on the Gut microbiota and short-chain fatty acids (SCFAs) production

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**Abstract.** The gut microbiome has an integral role in regulating metabolism, endocrine, and immune functions. The involvement of gut microbiota in the modulation of various biochemical pathways which are connected to the gut-brain axis is documented by different researchers. Short-chain fatty acids (SCFAs), which can resist starch, are energetic metabolites produced in the colon by the fermentation of dietary fiber through bacteria. One of the most persuasively debated processes of how gut bacteria affect the host physiological environment is the digestion of dietary fibers and the subsequent fermentation of monosaccharides to SCFAs. These SCFAs play a significant role in gut microbes. The fiber decreases the energy density of the diet, and SCFAs stimulate intestinal gluconeogenesis, incretin synthesis, and subsequent satiety. Similarly, SCFAs also provide energy to the host and facilitate gluconeogenesis. We analyzed the SCFAs in this review as metabolic regulators and their potential to enhance endurance performance in athletes. If further research supports their effectiveness, SCFAs can assist athletes in improving their performance in various contests in the future

**Key words:** SCFAs, gut microbiota, exercise, athlete health.

## Introduction

The important class of bioproducts of the gut microbiome produced by the fermentation of indigestible carbohydrates, like dietary fiber, which is accessible to the intestinal microbiota are termed Short-chain fatty acids, abbreviated as SCFAs (1). Fiber fermentation is critical in the improvement of gut ecology and structure, SCFAs affect the health of the host at the cellular, tissue, and organ levels via intestinal barrier function, glucose metabolism, immune regulation, and obesity (2). Researchers have discovered a broad range of neuroactive substances and metabolites as well as processes linking the gut microbiome to brain activity (3). The gut microbiome is fundamental for normal homeostasis and fitness throughout the organism's entire existence. In contrast, the imbalance and dysregulation in the biological diversity of the microbiota is termed as 'dysbiosis' that causes a number of diseases, including metabolic disorders that affect glucose homeostasis. It is observed that microbial production of SCFAs in the body is among

the mechanisms through which prebiotics promote human health, which include the major end products like acetate, butyrate, and propionate (4,5). These positive health results are primarily caused by increased microbial SCFA synthesis, which involves higher gut barrier function and decreased intestine inflammation. Additionally, colonocytes' primary source of fuel is the SCFA butyrate, and a disruption in that supply may contribute to diminished gastrointestinal function. Additionally, gastrointestinal transit and mobility may be impacted by SCFA. Additionally, due to its effects on gastrointestinal health, SCFA can have a significant impact on how the body regulates its weight in terms of energy intake, energy use, and insulin sensitivity, which can have a negative impact on the pathophysiology of obesity and related abnormalities like type 2 diabetes mellitus [T2DM] (6-8). Among various microbial metabolites SCFAs plays a key role like acetate, propionate and butyrate, they are developed and absorbed primarily in proximal colon, where intestinal bacteria live like *Lactobacillus*, *Clostridium*, and *Prevotella* ferment undigested

food (9,10). Therefore, the gut microbiome offers a protracted range of molecules and metabolites that affect the host's health. Among them, (SCFAs) produced by the bacteria-dependent hydrolysis of fibers have drawn a significant amount of attention due to their importance to host health (Fig. 1). This systematic review enlightens critical information about bacterial SCFAs and their physiological significance in the gut, with more focus on the athlete's microbiota.

### The role of probiotic bacteria's SCFAs on the host's energy intake

Complex dietary carbohydrates are broken down and metabolized by the gut microbiota using a wide range of enzymes, many of which are not present in mammals that belong to the extensive family of carbohydrate-active enzymes [CAZyme]. These enzymes have been shown to have a variety of beneficial influ-

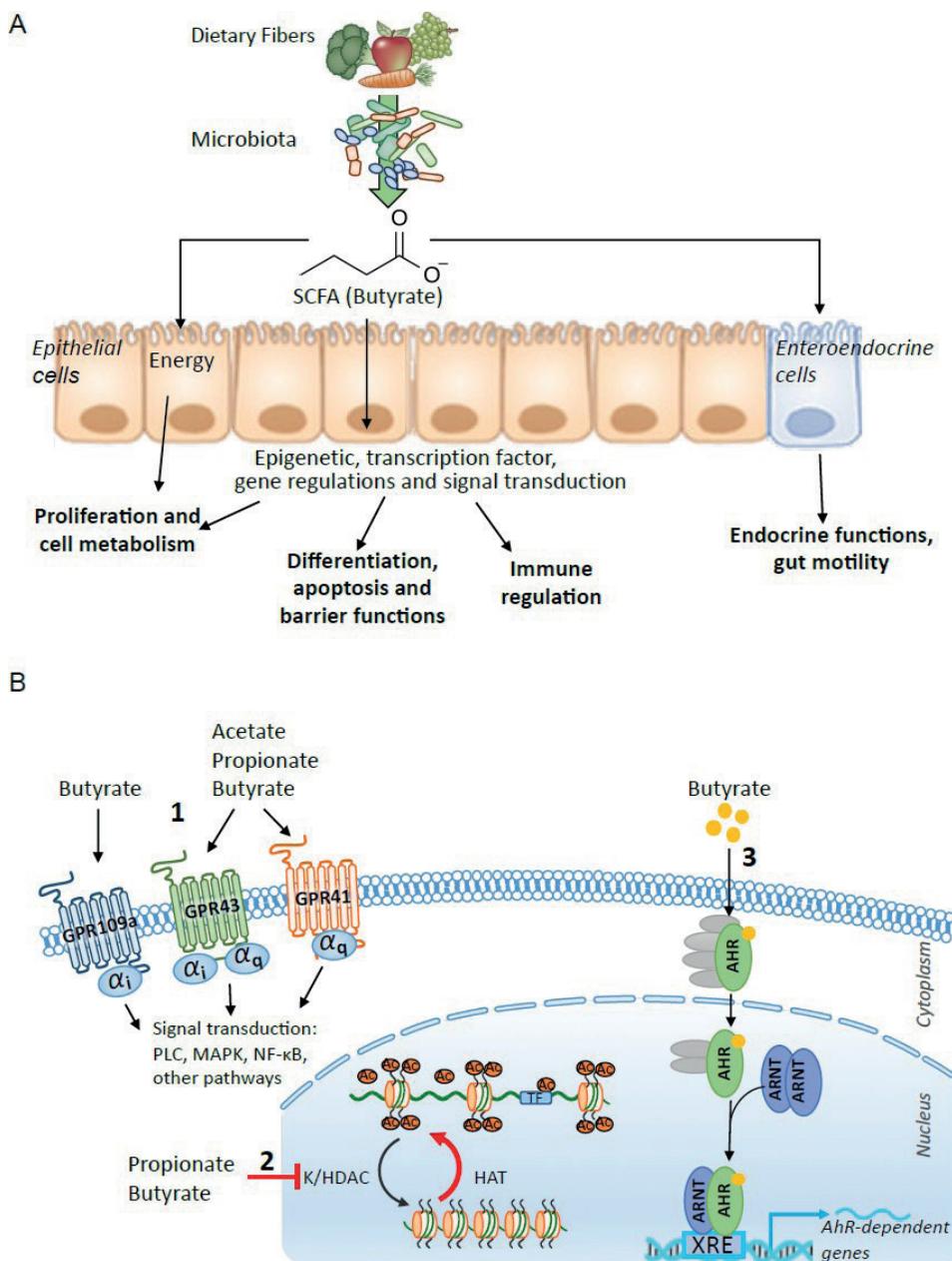


Figure 1. SCFAs produced by bacteria-dependent fiber hydrolysis

ences on the energy metabolism of mammals. These SCFAs, often referred to as volatile fatty acids, are used by mammals as a provider of metabolic energy in addition to glucose (11,12). Besides the availability of carbohydrates (like dietary fibers and prebiotics) is important for sustaining the metabolic functions that lead to the fermentation of carbohydrates (12). In contrast, anaerobic bacteria in the colon metabolize non-digestible carbs such as xylans, resistant starch, and inulin to produce SCFAs as end products and energy for microbial development (13). Dietary fibers are metabolized by the gut microbiome to release organic acids, gases, and a sizable amount of SCFAs. When present in sufficient amounts, major SCFAs like acetate, butyrate, and propionate (14) are formed in the human colon in a ratio of 60:20:20 mmol/kg. In the colon, SCFAs can reach a cumulative mass of 50–150 mM where there is a high level of microbial biomass (15–18). SCFAs have been suggested as a linkage between host energy metabolism, nutrition, and gut microbiota (19). Similarly, the majority of SCFAs are used as source of energy and, when consumed, can deliver up to 10% of our daily caloric needs (20).

The intestinal epithelial cells (IEC) consume 70% of their energy from butyrate released by commensal bacteria, especially Clostridia species, of the Firmicutes family (21) (Table 1).

Currently, studies performed with categorized SCFAs pervaded in mice models, 62% propionate was utilized as a source of gluconeogenic in the body's normal process of glucose synthesis. It has been reported

that 69% of the glucose is derived from propionate glucose synthesis and liver palmitate, and while propionate was either not present or produced in small amounts, cecal butyrate and acetate served as the substrate for cholesterol production (22). Based on the findings, SCFAs (acetate, propionate, and butyrate) generated by the human gut micro biota play a crucial role as a substrate for the metabolism of cholesterol, glucose, and lipids. The intestinal epithelium uses butyrate as an energy substrate, whereas peripheral tissues use acetate and propionate (22–23).

### Exercise and Gut Microbiome

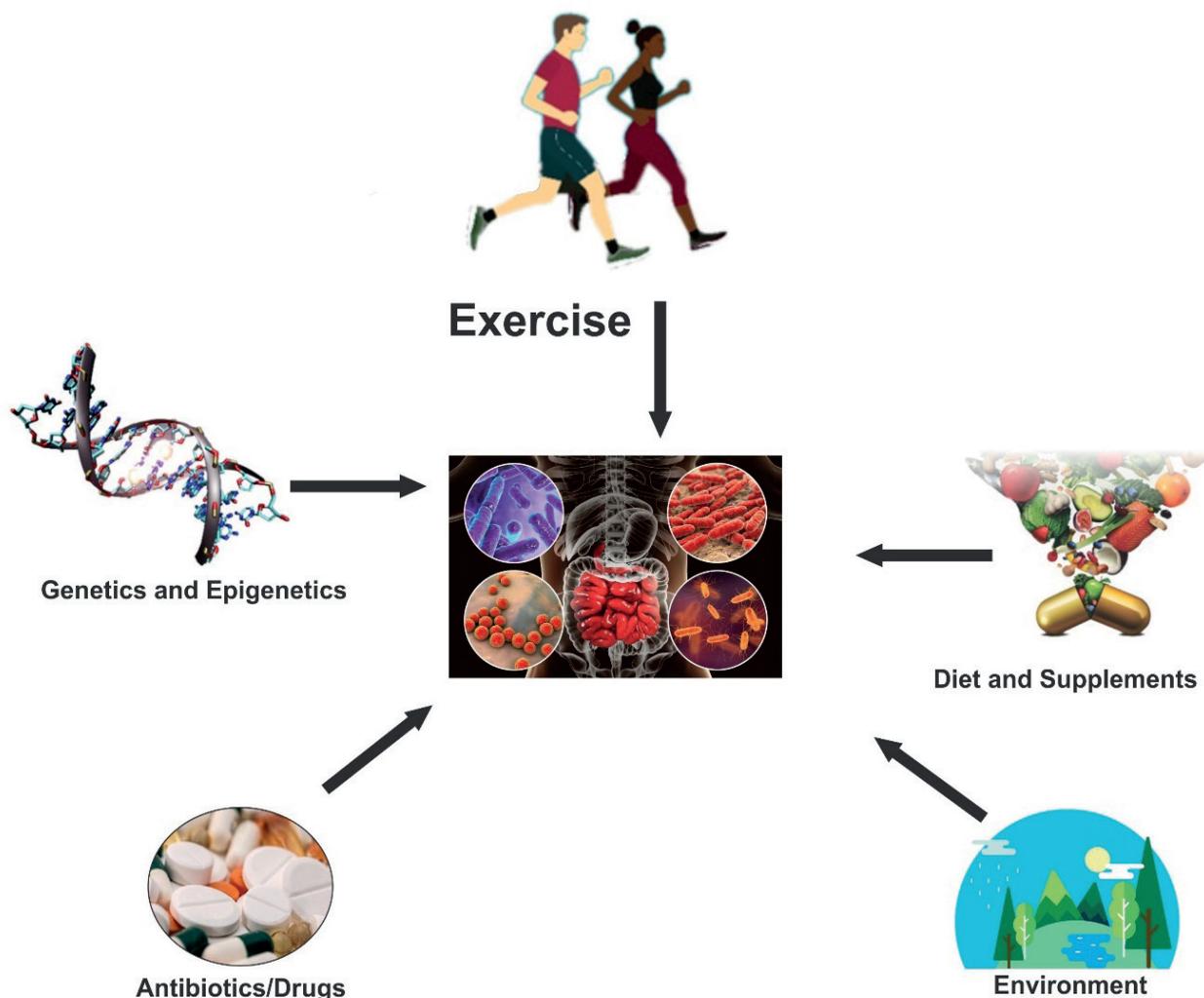
The human body is made up of a diversified range of microbes that includes bacteria, viruses, and fungi (24). These microorganisms are termed as the micro biota, and they can be found throughout the body on all epithelial surfaces, including the skin, oral cavity, gastrointestinal, and reproductive tracts with most microbiota present in the colon (25–29). The gastrointestinal tract (GIT) is the main site for the microbiome, especially the large intestine, which contain up to 100 trillion ( $1 \times 10^{14}$ ) microbes (30), such data shoes approximately 25 times as many genes as the individual human genome. This microbiota, in turn, encodes thousands of genes with different roles that are absent from the human genome and are often linked to beneficial physiological effects on their hosts (31–33). The crucial significance of microbiota is progressively rec-

**Table 1.** Bacterial strains with short chain fatty acids (SCFAs) production capability.

Microorganisms	Type	Compounds	Reference
<i>Rumminococcus Faecalibacterium</i>	Commensal	Butyrate	Serpa et al., 2009
<i>Bifidobacteria</i>	Probiotic	Acetate/lactate	Pessione., 2012
<i>L. salivarius spp salicinius</i> JCM 1230, <i>L. agilis</i> JCM 1048	Probiotic	Propionate /butyrate	Meimandipour et al., 2010
<i>L. acidophilus</i> CRL 1014	Probiotic	Acetate Propionate butyrate	Sivieri k et al., 2013, Salazar et al., 2011, Amaretti et al., 2007, Abdin et al., 2008
LGG	Probiotic	Propionate	Leblanc et al., 2017
<i>B. longum</i> SP 07/3	Probiotic	Propionate/ Acetate	Leblanc et al., 2017
<i>B. bifidum</i> MF 20/5	Probiotic	Propionate/ Acetate	Leblanc et al., 2017
<i>L. gasseri</i> PA/16/8	Probiotic	Propionate	Leblanc et al., 2017

ognized in human physiology and in the metabolism of nutrients and vitamins, regulation of inflammation, immunological functions, hypersensitivity, and in the mental and overall health of the body (34-36). Two-thirds of a person's gut microbiome is unique and is highly influenced by their food and exercise habits including disease, ethnicity, genetics, age, and gender (Fig 2). Specifically, it might contribute to enhancing athletic performance and reducing recovery time (37). Gut health, a condition of the gastrointestinal defenses and, more significantly, the structure and composition of the luminal microbiota can have a major impact on athletes, reducing chronic injuries while improving performance (38).

The gut micro biota is crucial in the sustenance of human health and regulation of metabolism (39-40). It has been linked to several chronic nutritional disorders like obesity and diabetes (41-45) and demonstrated to stimulate systemic functions such as immunity [46-47] and brain functioning (48-49). The gut micro biome may have an impact on health through various mechanisms like production of metabolites (40,50) [e.g., SCFAs which have the potential to affect numerous host systems and metabolic processes (51-53)]. Recent research studies have emphasized on the influence of nutritional factors like diet (54-56) and exercise (57-58) on the gut micro biota. The inconsistent composition and function of the gut microbiome (59-61)

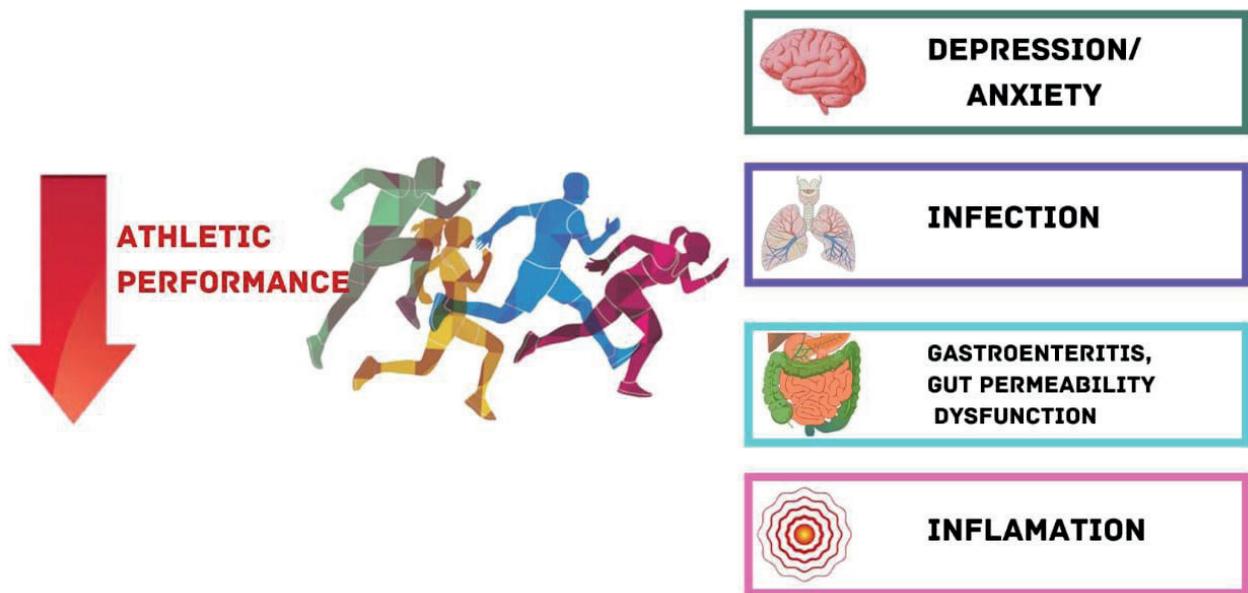


**Figure 2.** lifestyle factors like nutrition, genetics, antibiotics, exercise, and the environment (e.g., pollution, urban vs. rural, etc.) Impact on gut micro biota.

has also contributed to research exploring the associations between features of the gut microbiota, such as diversity or the presence, absence, or number of certain taxa, and host health. Personalized nutrition research is currently looking into how to estimate variations in the glycemic responses among people, triglyceride levels, cholesterol, and other health measures. This is for the purpose of personalized nutritional counselling and the prevention of nutrition-related chronic diseases like obesity and type 2 diabetes. Previous Studies have (62–63) examined how the gut microbiota affects inter-individual variation with respect to diet and how this may subsidize to metabolic health. It indicates that the microbiome has an impact on various aspects of human health. In addition to a role for specific microbes, or groups of microbes, the significance of microbial variety has been demonstrated in numerous studies, with a lower diversity related with GIT Conditions such Crohn's disease (64), some malignancies (65), and type 1 diabetes (66). A numerous physiological processes are affected by altered microbiome like oxidative stress, immunological response, and energy metabolism, all of which are essential for the health and performance of athletes (67).

As mentioned earlier, various factors, such as individual's lifestyle and diet can change the micro biota

structure. Numerous research has found out athletes' gut microbiota diverseness is higher than that of sedentary controls (68–70). Clark *et al* (69) found significant variations among male and professional rugby players and a cohort of non-athlete male controls. The athletes had greater gut microbial diverseness, with higher levels of the genus *Akkermansia*. Further studies of the same cohort (68) found that athletes have a high rate of SCFAs metabolic pathways. Similarly, Peterson *et al* (70) studied the gut microbiota of cyclists and found 30 out of 33 having higher level of *Akkermansia*. The exercise plan was found to be proportional to the prevalence of *Prevotella*, which is related with greater branched-chain amino acid (BCCA) pathways that are required for muscle recovery. Furthermore, *Methanobrevibacter smithii* [(a microbe in the colon that uses H<sub>2</sub> to produce SCFAs and ATP] (69) was found to be more prevalent among professional cyclists than amateur cyclists. Jang *et al.* (70) evaluated the gut microbiomes of bodybuilders, long runners, and controls (n=45) by feeding each group by a personalized specific sports diet. Research findings shows that bodybuilders consumed high protein and high fat diets increased *Facelibacterium*, *Sutterella*, *Clostridium*, *Heamophilus* and *Eisenbergiella* numbers, while *Bifidobacterium*, *Parasutterella* and *Eubacterium*



**Figure 3.** Effect of overtraining on the health of an athlete.

numbers decreased. According to the study, individuals who practice anaerobic sports display similar intestinal microbiome patterns to bodybuilders (70).

Similarly, Scheiman *et al* (71) found that marathon runners' gut microbiomes were richer in the genus *Veillonella* than those of non-runners. Moreover, a mouse model has been used to show increase endurance, reduce inflammatory cytokines, and convert lactate to acetate / propionate (72). The recent findings support that exercise may have a beneficial effect on the microbiome, where changes in the microbiome's composition can be connected to improved health indicators and consequently have a positive impact on athletic performance. At the same time, exercise exerts a variety of physical effects on the body, including the regulation of mood (72), improvement of cardiovascular symptoms (73), fatigue reduction (74) and inflammatory effects, which is important to maintain a healthy balance between training load and recovery to avoid overtraining (75). In earlier research, the consequences of excessive exercise on the microbiome have been demonstrated.

## Conclusion

This review provides a comprehensive theoretical perspective on SCFA influence on gut microbiota with specific emphasis on athlete's health. It is very challenging to measure the impact of intestinal microbes and gut barrier defense on athlete health and performance. There are several aspects of training and contests that put the athlete at risk for injury. Moreover, self-medication, supplement use, and food choices can negatively impact the gut microbiota, leading to a state of low-grade systemic inflammation, increased immune response, and a distortion of healing. In addition, extensive research investigations is required in numerous athletic cohorts exploring the effect of nutrition on the composition, function, and structure of gut microbiome. This method is critical because certain athletes may adhere to dietary rules, such as during pre-competition physical training and offseason times. The exercise related interactions that underpin adaptation and performance should be examined through

research studies confirming the kinetics and clinical effects of microbial by-products as the dietary status and metabolic requirements during exercise. Finally, the variation of the microbiota and its yeast potential can be evaluated in athlete dietary prescriptions, which could include specific dietary advice on how to increase performance by fixing particular metabolites during exercise. Exercising, improving, and limiting the consumption of harmful metabolites that may reduce the importance of exercise stress.

**Conflicts of interest:** Each author declares that she has no commercial associations (e.g., consultancies, stock ownership, equity interest, patent/licensing arrangement etc.) that might pose a conflict of interest in connection with this article

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