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REVIEW ARTICLE

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Major metabolic and metabolomic aspects of nutrition in the gut microbiota and sports performance: a systematic review

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Abstract

Introduction: In the context of sports performance, nutrition has been used to improve the health of the brain, bones, muscles, and cardiovascular system of athletes. However, recent research suggests that the gut microbiota (GM) may also play a role in athlete health and performance. **Objective:** It was to carry out a systematic review of the main clinical findings, involving the metabolic and metabolomic aspects, of the relationship between gut microbiota and sports performance under control and nutrological modulation. **Methods:** The systematic review rules of the PRISMA Platform were followed. The research was carried out from January to March 2023 in Scopus, PubMed, Science Direct, Scielo, and Google Scholar databases. The quality of the studies was based on the GRADE instrument and the risk of bias was analyzed according to the Cochrane instrument. **Results and Conclusion:** A total of 328 articles were found, and 132 articles were evaluated in full and 108 were included and developed in this systematic review study. Considering the Cochrane tool for risk of bias, the overall assessment resulted in 52 studies with a high risk of bias and 74 studies that did not meet GRADE. It was concluded that athletes must feed, train and utilize the entire supraorganism, including the GM, implementing gut-centered dietary strategies to achieve optimal performance. Current evidence suggests that the GM may contribute to sports performance through the production of dietary metabolites (short-chain fatty acids, secondary bile acids), influence on gastrointestinal physiology (e.g. nutrient absorption), and immune modulation (inhibition of pathogens). Dietary strategies common in athletes, such as a high intake of protein and simple carbohydrates and a low intake of nondigestible carbohydrates, may adversely affect the GM and predispose athletes to gastrointestinal problems and thus impair performance. However, adequate dietary fiber intake, a variety of protein sources, and an emphasis on unsaturated fats, especially ω-3 fatty acids, as well as supplementation with pre, pro, and synbiotics, have shown promising results in optimizing the health of the athletes and their GM with potential beneficial effects on performance.

Keywords: Nutrology. Gut microbiota. Metabolism. Sports performance. Athletes.

Introduction

In the context of sports performance, nutrition has been used to improve the health of the brain, bones, muscles, and cardiovascular system of athletes. However, recent research suggests that the gut

microbiota (GM) may also play a role in athlete health and performance. Therefore, athletes should consider dietary strategies in the context of their potential effects on GM, including the impact of sport-centered dietary strategies (e.g., protein supplements, carbohydrate loading) on the gut microbiota, as well as the effects of centered dieting. in the gut dietary strategies (eg, probiotics, prebiotics) on performance **[1,2]**.

In this regard, there is an interaction between diet, exercise, and GM, with a focus on dietary strategies that can affect both GM and athletic performance. Current evidence suggests that GM could contribute to the effects of dietary intake on athletic performance by influencing the production of microbial metabolites, gastrointestinal physiology, and immune modulation. Common dietary strategies such as high protein and simple carbohydrate intake, low fiber intake, and food avoidance can adversely affect gut microbiota and, in turn, performance **[1-3]**.

Furthermore, the intake of adequate dietary fiber, a variety of protein sources, and an emphasis on unsaturated fats, especially omega-3 fatty acids (ω-3), in addition to the consumption of prebiotics, probiotics, and symbiotics, have shown promising results in optimizing health and athlete performance. While this is an emerging and promising area of research, more studies are needed that incorporate, track, and manipulate all three of these elements (i.e., diet, exercise, and gut microbiome) to provide recommendations for athletes **[4]**.

In this regard, many of the established positive health benefits of exercise have been documented by historic discoveries in the field of exercise physiology. These investigations usually assess performance thresholds or exercise-induced health benefits **[5]**. Thus, several important findings were informed by studying athletes. Recent progress has been made regarding gut microbiota, regenerative nutrition, and skeletal muscle metabolism **[5-7]**.

Furthermore, regular physical training associated with nutritional health has broad benefits to the health of the gut microbiota, acting positively in almost all organic systems of the body **[8]**. The mysteries of human physiology and the adaptive response to acute and chronic physical training have been largely elucidated through exercise science. Thus, exercise physiologists have studied the physiological response to physical activity and sports **[9,10]**.

In the context of the triad physical exercise, nutrition, and gut microbiota for the muscle regeneration process, adult stem cells stand out as intestinal stem cells at the base (crypts) of the intestine and muscle stem cells outside the intestine. sarcolemma next to the basement membrane of the muscle **[11-13]**. The tissue niche is also able to influence adult stem cells metabolism. Tissue stem cell metabolism has focused on central carbon metabolism, ie the generation of metabolic building blocks via glycolysis, oxidative phosphorylation, or the pentose phosphate pathway **[13]**.

Furthermore, adult tissue stem cells mediate homeostasis and regeneration of tissues and organs by making decisions about whether to remain quiescent, proliferate, or differentiate into mature cell types. These decisions are directly integrated with the body's energy balance and nutritional status. Metabolic by-products and substrates that regulate epigenetic and signaling pathways are considered to play an instructive rather than an observer role in regulating cell fate decisions **[13]**.

In this sense, it is suspected that the quiescent state of stem cells is characterized by an inherently glycolytic metabolism, followed by a transition to favor mitochondrial oxidative phosphorylation during differentiation **[14-17]**. However, increasing evidence suggests that metabolism during quiescence, activation, and differentiation may vary between tissues, integrating signaling cues and metabolic inputs from both the niche and the organism as a whole, primarily by signaling from nutrients and the gut microbiota **[15,16]**.

In this scenario, metabolomics provides information on cellular pathways, observing substrates and metabolic products through different pathways **[18,19]**. Along with transcriptomics and proteomics analysis, it is observed that metabolism can affect cell fate (and vice versa) **[20]**.

Based on this context, the present study carried out a systematic review of the main clinical findings, involving metabolic and metabolomic aspects, the relationship between gut microbiota and sports performance under the control and modulation of nutrition.

Methods

Study Design

The systematic review rules of the PRISMA Platform were followed. Available at: www.prisma-statement.org/. Accessed: 03/12/2023.

Data Sources and Quality of Studies / Risk of Bias

The search strategies for this systematic review were based on the keywords (MeSH Terms): *"Nutrology. Gut microbiota. Metabolism. Sports performance. Athletes"*. The research was carried out from January to March 2023 in Scopus, PubMed, Science Direct, Scielo,

and Google Scholar databases. In addition, a combination of keywords with the Booleans "OR", "AND" and the operator "NOT" were used to target scientific articles of interest. The quality of the studies was based on the GRADE instrument and the risk of bias was analyzed according to the Cochrane instrument.

Results and Discussion

Summary of Findings

A total of 328 articles were found. Initially, duplication of articles was excluded. After this process, the abstracts were evaluated and a new exclusion was performed, removing the articles that did not include the theme of this article, resulting in 184 articles. A total of 132 articles were evaluated in full and 108 were included and developed in this systematic review study (Figure 1). Considering the Cochrane tool for risk of bias, the overall assessment resulted in 52 studies with a high risk of bias and 74 studies that did not meet GRADE.

Figure 1. Flowchart showing the article selection process.

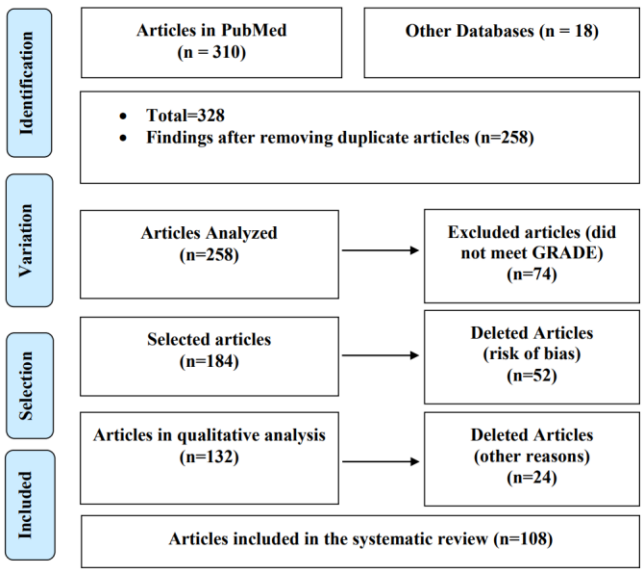
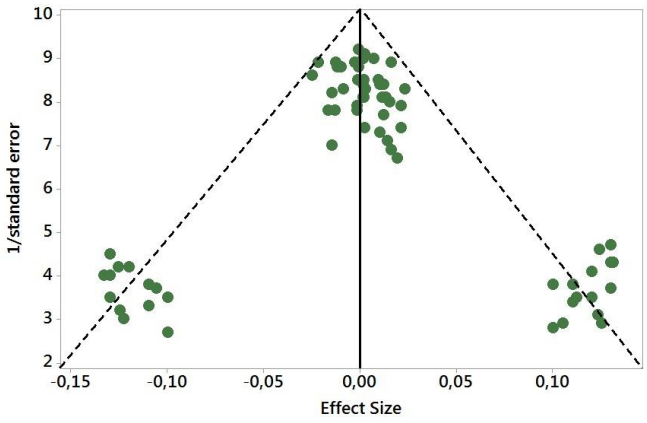


Figure 2 presents the results of the risk of bias of the studies through the Funnel Plot, showing the calculation of the Effect Size - Cohen Test (d). The sample size was indirectly determined by the inverse of the standard error. This graph showed symmetrical behavior, not suggesting a significant risk of bias, both between studies with small sample sizes (lower precision) that are shown at the bottom of the graph and in studies with large sample sizes that are displayed in the upper region.

Figure 2. The symmetrical funnel plot does not suggest a risk of bias among the small sample size studies that are shown at the bottom of the plot. High confidence and high recommendation studies are shown above the graph (NTotal=108 studies evaluated in full in the systematic review).



Source: Own authorship.

Nutrients, Gut Microbiota, and Sports Performance

Biochemical processes manifest various aspects of the human body's metabolic phenotype. In this sense, the athlete seeks to optimize this complex system to improve performance. Nutrition has long been used as a tool by athletes to promote peak performance. Nutrition can also influence athletic performance through the gut microbiota (GM). As a result, GM can modulate many of the effects of diet, nutrition, and health, such as the risk of chronic diseases including obesity, type 2 diabetes, and cardiovascular disease **[4]**.

In this regard, GM can influence athletic performance and its responsiveness to diet. Sport-centric and gut-centric dietary strategies modulate GM composition and function. Human digestive processes produce amino acids and fatty acids from ingested proteins and fats, respectively, while non-digestible carbohydrates reach the large intestine intact. These components, as well as ingested supplements such as probiotics, interact with GM, which produces metabolites that influence local barrier function, as well as systemic functions such as glycogen storage, fuel utilization, and muscle function that have the potential to affect athletic performance **[4]**.

Furthermore, nitrate supplementation is an effective, evidence-based dietary strategy for improving sports performance. The effects of dietary nitrate appear to be mediated by the ability of oral bacteria to reduce nitrate to nitrite, thereby increasing levels of circulating nitrite that can be further reduced to nitric oxide in the body. GM can improve muscle function by providing certain metabolites. Skeletal muscle can also serve as a nitrate reservoir. The bacteria in the oral cavity involved in the reduction of nitrate to nitrite and

the possible changes induced by nitrite and its effect on gastrointestinal balance and GM homeostasis are gradually being evidenced by researchers. The potential role of gut bacteria in reducing nitrate to nitrite and in providing the signaling molecule nitric oxide to the bloodstream and muscles has not been explored in great detail **[21]**.

In this context, nutritional supplements are popular among athletes to improve performance and physical recovery. Protein supplements fulfill this function by improving performance and increasing muscle mass. Dietary changes can induce GM imbalance, with beneficial or deleterious consequences for the host. In light of this, a randomized trial analyzed diets that were supplemented with a protein supplement (whey isolate and beef hydrolyzate) (n=12) or maltodextrin (control) (n=12) for 10 weeks. GM, water content, pH, ammonia, and short-chain fatty acids (SCFA) were analyzed in fecal samples, while malondialdehyde levels (markers of oxidative stress) were determined in plasma and urine. Fecal pH, water content, ammonia, and SCFA concentrations did not change, indicating that protein supplementation did not increase the presence of these fermentation-derived metabolites. Likewise, it had no impact on plasma or urine malondialdehyde levels; however, it increased the abundance of the phylum Bacteroidetes and decreased the presence of health-related taxa, including Roseburia, Blautia, and *Bifidobacterium longum*. Thus, long-term protein supplementation may harm GM **[22]**.

Added to this, it is highlighted that metabolism encompasses the interactions between the diet, the microbiome, and the cellular enzymatic processes that generate the chemical pathways necessary to maintain life. The small intestine, comprising the duodenum, jejunum, and ileum, is the most rapidly self-renewing organ in men. The small intestine exhibits specific metabolites with the highest levels of fatty acid oxidation occurring in the upper part of the small intestine and decreasing distally towards the ileum **[23]**. High rates of intestinal self-renewal are enabled by intestinal stem cells (LGR5+) at the base of intestinal crypts **[24]**. Cells in the gut can communicate via metabolic signals, with differentiated Paneth cells secreting lactate to support the LGR5+ function **[14]**.

In this sense, the balance between LGR5+ and differentiated cell fate may also be affected by cell-intrinsic changes in central carbon metabolism. The mitochondrial pyruvate carrier (MPC), comprising the MPC1 and MPC2 subunits, is required for crossspecies pyruvate oxidation, allowing entry of pyruvate into mitochondria **[24,25]**. Genetic deletion of the MPC1 subunit or MPC inhibition distorts cellular metabolism towards glycolysis and increases LGR5+ proliferation. On the other hand, overexpression of MPC1/MPC2 reduces the activity of LGR5+ **[26]**.

One study demonstrated that the expression of the enzyme 3-hydroxy-3methylglutaryl-CoA synthase (Hmgcs2), which regulates the ratio-limiting step in ketone body synthesis, is enriched in LGR5+. Loss of Hmgcs2 impairs regeneration and promotes promiscuous differentiation for the Paneth cell line **[27]**. The ketone body βhydroxybutyrate inhibits class I histone deacetylases to increase transcriptional activation of Notch signaling and maintain stem cell self-renewal **[28]**.

Furthermore, the intestine is constantly encountering dietary-derived nutrients and therefore is responsive to nutrient types **[28]**. For example, studies performed on patientderived normal and tumor-derived intestinal organoids have demonstrated that vitamin D levels can change the balance between stem cell fates as well as their differentiation **[29]**. Therefore, LGR5+ activity, including proliferation and differentiation rates, is affected by large shifts in nutrient availability, as occurs on a high-fat diet or fasting **[30-32]**.

Nutrients and Regenerative Processes

The practice of physical activity, endogenous metabolites, and dietary nutrients can directly influence epigenetic enzymes. Epigenetic modifications to DNA and histone proteins alter cell fate by controlling chromatin accessibility and downstream gene expression patterns **[20]**.

Thus, many substrates and cofactors for chromatin-modifying enzymes are derived from metabolic pathways involving the tricarboxylic acid cycle, the methionine cycle, the folate cycle, glycolysis, β-oxidation, and the hexosamine pathway. These metabolites can serve as activators or inhibitors of epigenetic writers, such as Jumonji C domain-containing proteins (JmjC), DNA methyltransferases (DNMTs), histone acetyltransferases (HATs), ten-eleven DNA translocase demethylases (TETs), and histone deacetylases (HDACs). In this sense, metabolites can influence nutrient-sensing signaling pathways **[20]**.

Thus, the mechanistic target of rapamycin complex 1 (mTORC1) can be activated by growth factor-induced signaling only when the amino acids arginine and leucine, as well as the cofactor S-adenosyl methionine (SAM), are detected within the cell. In addition, energy balance communicated via the cellular AMP/ADP-ATP ratio can be detected by AMP-activated protein kinase (AMPK). Furthermore, transcription factors can be directly regulated by metabolites, for example, the kynurenine metabolite of tryptophan is an endogenous

aryl hydrocarbon receptor agonist, and alpha-ketoglutarate (α-KG) binds to and activates IKKβ and initiates IKKβ signaling. NF-κβ **[16,20]**.

In this scenario, dietary manipulations and metabolites may affect tissue stem cell fate decisions, as highlighted in the small intestine (intestinal stem cells (LGR5+)), hematopoietic system (hematopoietic stem cells (HSCs), liver, muscle (muscle stem cells/satellite cells) and hair follicles (hair follicle stem cells (HFSC). For example, in HFSCs, mitochondrial pyruvate carrier 1 (MPC1) and lactate dehydrogenase (LDHA) regulate the balance between telogen and anagen during the hair cycle. In LGR5+, 3hydroxy-3-methylglutaryl-CoA synthase (Hmgcs2) is highly expressed while MPC1/2 is expressed at low levels. The ketogenic or high-glucose diet regulates the balance of autorenewal of LGR5+ HSC self-renewal and differentiation can be regulated by manipulation of vitamin C, A, or D levels and valine restriction **[20]**.

Regarding muscle regeneration, the nicotinamide riboside-rich diet may increase muscle stem cell numbers and function in a histone deacetylase (SIRT1) dependent manner. Muscle stem cells, called satellite cells, are responsible for the maintenance of adult muscle mass and repair after injury. Several studies have demonstrated how changes in innate metabolism interfere with the differentiation of satellite stem cells into mature myocytes **[33]**. For example, mapping a single cell with histone acetylation has shown that acetylation levels tend to be low in quiescent cells.

In this context, one study found that isolated quiescent muscle stem cells express fatty acid oxidation enzymes/transporters, however, as they exit quiescence and enter the cell cycle for proliferation, a metabolic transition occurs to favor glycolysis **[34]**. In this sense, SIRT1 is a target of increased glycolysis. SIRT1 represses the mature expression of skeletal muscle-specific genes, as well as genes involved in mitochondrial biogenesis. Advanced glycolysis depletes NAD+, an essential metabolic cofactor of SIRT1, reducing SIRT1 activity and promoting downstream activation of these mature muscle-specific genes and differentiation **[35]**.

Thus, metabolic pathways and chromatin modifications are closely linked and therefore many changes in metabolism influence epigenetic changes and alter gene expression. For example, signaling pathways including mTORC, AMPK, MAPK, and others are all sensitive to changes in nutrient levels. Furthermore, transcription factors are directly regulated by metabolites **[36,37]**. Furthermore, it is possible that the transcriptional machinery itself also responds to nutrients, for example, RNA polymerase II is modified by O-GlcNAc, a metabolite derived from the hexosamine biosynthesis pathway **[38]**.

Thus, epigenetic signaling pathways and transcription are affected by changing nutrient levels. Furthermore, the focus of the literature on stem cell metabolism is centered on central carbon metabolism and the balance between glycolysis and oxidative phosphorylation in the regulation of cell fate **[38]**. Therefore, future research that defines dietary and metabolic control of decisions about the fate of cells in muscle tissues will be of great importance in the fields of metabolism and regenerative medicine.

Nutritional Genomics and Gut Microbiota

The gut microbiota is composed of about 100 trillion bacteria, viruses, fungi, and protozoa that live in perfect symbiosis with our body **[39]**. About 90% of the bacteria living in the human gastrointestinal tract belong to 5 main phyla Bacteroidetes characterized by some well-known genera such as Prevotella and Bacteroides **[40]**, Firmicutes to which the genera Ruminococcus, Lactobacillus and Streptococcus belong **[40]**. Actinobacteria belong to the genus Bifidobacterium **[41]**. Proteobacteria (Gramnegative) and possibly pathogenic, and Verrucomicrobia, known mainly by the genus Akkermansia **[42-44]**.

The individual response to nutrients and non-nutritive molecules can be largely affected by three important biological layers. The gut microbiome can alter the bioavailability of nutrients and other substances, the genome can influence the kinetics and dynamics of molecules, while the epigenome can modulate or amplify the properties of the genome. The use of omics and bioinformatics techniques allows the construction of individual multilayer networks and, thus, the identification of personalized strategies that have recently been considered in all medical areas, including sports medicine **[45]**. In this sense, the composition of each athlete's microbiome influences sports performance both directly by acting on energy metabolism and indirectly by modulating the availability of nutrients or non-nutritive molecules, which ultimately affects the individual epigenome and genome. Among non-nutritive molecules, polyphenols can enhance physical performance through different epigenetic mechanisms. In this way, polyphenols interact with the gut microbiota, undergoing extensive metabolism to produce bioactive molecules, which act on transcription factors involved in mitochondrial biogenesis, antioxidant systems, glucose and lipid homeostasis, and DNA repair **[45]**.

Thus, omics disciplines, including epigenomics (the study of the complete set of epigenetic modifications in

the genetic material of a cell, known as the epigenome), aim at the complete characterization and quantification of pools of biological molecules that affect the structure, function, and dynamics of an organism. body. In nutrition, omics technologies are useful to customize dietary strategies for each individual, providing personalized dietary approaches **[46,47]**.

In this regard, the standardized nutritional approach, preferably related to guidelines for healthy nutrition, such as those established by the World Health Organization (WHO), should be reviewed and updated, considering the influence that genetic, environmental, and microbiota factors have on each one. individual, to optimize nutritional and nutraceutical choices and promote the health of individuals according to their characteristics **[48]**.

At the genetic level, two nutritional fields look at the intricate relationships between nutrients, genes, and biological systems nutrigenetics and nutrigenomics. Nutrigenetics aims to understand how our genetic background can modulate the absorption, distribution, metabolism, and elimination of nutrients, affecting the response to diet. Nutrigenomics focuses on individual sensitivity to nutrients in terms of their influence on gene and protein expression and subsequently metabolite production, thereby providing actionable information on the effects of diets and allowing for effective personalization of dietary intervention strategies to prevent disease-related diseases. diet **[49,50]**.

One of the most useful applications of nutritional genomics is certainly in sports performance. Genetic factors account for about 50% to 80% of the interindividual variation in body mass, and this has a critical impact on the muscle growth response **[51]**. Furthermore, endocrine functions, muscle fiber composition, psychological aspects, and nutrition may have differences associated with genotype and influence athletic performance **[52]**.

Polyphenols and Athletic Performance

Polyphenols represent a considerable heterogeneous class of compounds with common phenolic structural units present in nature in a wide variety of foods, such as fruits, vegetables, cereals, tea, and chocolate, among others **[53]**.

The various polyphenol groups are distributed according to the number of phenolic rings in flavonoids (> 10,000 natural compounds) which can be further subclassified into many flavones, flavonols (Capparis spinosa), flavones or flavan-3-oils or catechins (*Theobroma cacao, Camellia sinensis*), anthocyanins or anthocyanidins (*Vaccinium myrtillus*), isoflavones and chalcones (Glycine max); and non-flavonoid polyphenols such as tannins, diferuloylmethane (*Turmeric Longa*), coumarins, benzophenones, secoiridoids, stilbenes (*Polygonum cuspidatum*), phenolic acids, etc. **[54,55]**.

In general, several health properties have been attributed to polyphenols, including antioxidant, anti-inflammatory, antibacterial, antiviral, antipruritic, antiparasitic, and cytotoxic **[56-59]**. In athletic performance, several studies have investigated the antioxidant and anti-inflammatory potential of various polyphenols **[60,61]**. Accordingly, individuals who carry specific genetic mutations (e.g., N-acetyltransferase (NAT) 1/2, SOD1/2, glutathione peroxidase (GPX) 1, paraoxonase (PON) 1, X-ray repair crosscomplementation family (XRCC) 1) may be less efficient at modulating oxidative stress and inflammation during exercise and therefore require a significant increase in antioxidants with epigenetic mechanisms such as polyphenols **[62-66]**. One of the most innovative areas for understanding the health-related mechanisms of polyphenols in sports performance is the study of bidirectional interactions with gut microbiota **[53]**.

In plants, polyphenols are generally found in their glycosylated form, although esterified or polymerized forms may also be present **[67]**. Once ingested, polyphenols are recognized by the human body as xenobiotics, therefore their absorption rate is notably lower than that of nutrients introduced through the diet and varies greatly depending on the degree of polymerization or the complexity of their chemical structure. Only 5-10% of polyphenols are absorbed in the small intestine, while the remaining 90-95% reach the colon, where they undergo fermentation processes by the gut microbiota and subsequently generate metabolites with different physiological implications. After oral ingestion of 10 to 500 mg of polyphenols, the maximum plasma concentration generally does not exceed 1 μM, mainly due to poor absorption and metabolism by tissues and gastrogut microbiota.

Also, polyphenols are also substrates for ATP-binding transporters, which are primarily efflux transporters and which eliminate their substrates outside the cell. These proteins may influence the oral availability and tissue distribution of polyphenols, limiting their beneficial effects **[68,69]**. Genetic mutations that affect these transporters, such as those that affect hepatic and intestinal cytochromes, must be taken into account when determining polyphenol dosage based on the subject's genotypic characteristics (poor, intermediate, or extensive metabolizers) **[70-72]**.

Once in the large intestine, polyphenols can modulate the proliferation of specific bacteria and act as prebiotics for some other microorganisms **[73,74]**. A meta-analysis showed that polyphenol supplementation increases the abundance of Lactobacillus and Bifidobacterium and reduces the abundance of some pathogenic Clostridium in the human gut microbiota **[75,76]**.

In practice, polyphenol supplementation should be provided before or after physical exercise and not immediately after, mainly because post-exercise inflammatory processes are essential for muscular hypertrophy and learning of muscular actions. With the advent of omics technologies, it has become possible to analyze the individual genome, epigenome, and other classes of biologically relevant molecules, as well as the genetic makeup of the gut microbiota (microbiome). The biological data contained in the genetic/epigenetic fingerprint and the composition of the individual microbiota together provide valuable information for understanding a subject's sensitivity and response to external/internal stimuli and dietary xenobiotics. This, in turn, may allow for personalized interventions across all medical fields, including sports medicine, where personalized nutritional and nutraceutical regimens can be undertaken to maximize athletic performance **[77-83]**.

In recent years, the consumption of chocolate and, in particular, dark chocolate has been "rehabilitated" due to its high content of antioxidant cocoa polyphenols. While it is recognized that regular exercise improves energy metabolism and muscle performance, excessive or unusual exercise can induce cellular damage and impair muscle function, triggering oxidative stress and tissue inflammation **[84-92]**. The interpretation of the available results on the antioxidant and anti-inflammatory activities of cocoa polyphenols remains questionable, probably due to the variety of physiological networks involved **[93-97]**. More experimental studies are mandatory to clarify the role of cocoa polyphenol supplementation in exercise-mediated inflammation **[98]**.

One study investigated the effects of polyphenol supplementation on gut microbiota composition in humans. The study followed a randomized, double-blind, placebo-controlled (PLA) design, 37 overweight and obese men and women (18 men / 19 women, 37.8 ± 1.6 years, body mass index: 29.6 ± 0.5 kg/m2) received epigallocatechin3-gallate and resveratrol (EGCG + RES, 282 and 80 mg/day, respectively) or PLA for 12 weeks. A fecal abundance of Bacteroidetes was higher in men than in women, while other bacterial rates assessed were comparable. EGCG+RES supplementation significantly decreased Bacteroidetes and tended to reduce *Faecalibacterium prausnitzii* in men (p=0.05 and p=0.10, respectively), but not in women (p=0.15 and p=0.77, respectively). Other bacterial genera and species were not affected by EGCG + RES supplementation **[99]**.

It is increasingly recognized that an athlete's GM responses to diet are personalized depending on characteristics such as the presence or abundance of key species such as *Ruminococcus bromii* or *Prevotella copri* **[100,101]** or metabotypes **[102]**. Interindividual variability in microbial responses contributes to variability in metabolic responses (glycemic response) and health outcomes (weight loss) **[103,104]**. Therefore, dietary strategies require a differentiated approach to optimizing health through GM.

Therefore, future research should also integrate other "omics" data to determine potential metabolites, genes, and epigenetic modifications that may cause, contribute to, mediate, or modulate the effects of diet and exercise on the gut microbiota **[105-107]**. The use of "omics" data together with machine learning methods has the potential to discover new associations between the gut microbiota and its metabolites, diet, and athletic performance, as well as to predict personalized responses to dietary strategies **[108]**. The impacts of these findings include the potential to enhance performance in athletes and improve health, particularly gastrointestinal and respiratory health.

Conclusion

It was concluded that athletes must feed, train and utilize the entire supraorganism, including the gut microbiota, implementing gut-centered dietary strategies to achieve optimal performance. Current evidence suggests that the gut microbiota may contribute to sports performance through the production of dietary metabolites (short-chain fatty acids, secondary bile acids), influence on gastrointestinal physiology (e.g. nutrient absorption), and immune modulation (inhibition of pathogens). Dietary strategies common in athletes, such as a high intake of protein and simple carbohydrates and a low intake of non-digestible carbohydrates, may adversely affect the gut microbiota and predispose athletes to gastrointestinal problems and thus impair performance. However, adequate dietary fiber intake, a variety of protein sources, and an emphasis on unsaturated fats, especially ω-3 fatty acids, as well as supplementation with pre, pro, and synbiotics, have shown promising results in optimizing the health of the athlete and his or her gut microbiota with potential beneficial effects on performance.

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Similarity check
It was applied by Ithenticate@.

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