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The role of Gut Microbiota and Probiotics in physical performance of athletes - Literature review

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ABSTRACT

INTRODUCTION: The human gut microbiota is an extremely diverse and complex ecosystem that inhibits the mucous membranes of the intestines. It is probable that the microbiota, with its capacity to influence the immune system and establish the conditions required for metabolic and structural functions essential for maintaining homeostasis, may significantly affect the health, well-being, and performance of athletes.

PURPOSE: The aim of the study is to present the current state of knowledge about the differences in athletes' gut microbiota, how these changes affect their physical performance and uncover the mechanisms behind gut microbiota and probiotics in physical performance among population of athletes.

MATERIAL AND METHODS: The following review was conducted using the articles from the Pubmed and Google Scholar databases, employing keywords related to gut microbiota, athletes, physical performance. We collected studies performed on populations of athletes, exploring different sport disciplines.

CONCLUSIONS:

Numerous studies have investigated the gut microbiota of athletes, emphasizing the impact of both training and diet. Athletes' unique dietary regimens, including higher protein or carbohydrates intake, influence their gut microbiome, leading to enhanced performance. These findings uncover that diet diversity correlates with gut diversity, which is linked to metabolic benefits and a lean phenotype. Studies on rugby players, cyclists, and marathoners reveal that certain microbial species, like Prevotella and Veillonella, are more abundant in athletes and play significant roles in nutrient metabolism and exercise recovery. These findings suggest that the interaction between athletic lifestyle and the gut microbiota affects positively the metabolism of the host, by enhancing microbiota diversity, and increasing the abundance of beneficial bacteria.

KEYWORDS: gut microbiota; athletes; physical performance; probiotics

1. INTRODUCTION

GUT MICROBIOTA- COMPOSITION

The human microbiome is the agglomeration of trillions of microbes such as bacteria, fungi, viruses with the vast majority living in the intestines and is categorized by groups called phyla [1]. Generally, the gut microbiota is composed of 6 major phyla: *Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, Fusobacteria, and Verrucomicrobia,* among which *Firmicutes* and *Bacteroidetes* are the major types [2].

Of course it is impossible to distinguish an exact composition of an ideal pattern of gut microbiota. Every healthy gut microbiota is unique and thanks to that characteristics there is still so much to discover in terms of species of microbes living in our intestines. Taking Western European population into consideration, including Polish there are 4 dominant species: *Bacteroidetes, Firmicutes, Actinobacteria, Verrucomicrobia.*

GUT MICROBIOTA AND HEALTH

The bidirectional interaction between microbiota and the host immune system starts at birth and develops throughout the host's lifetime. The intestinal immune system is in constant communication with gut microbiota, requiring it to distinguish between beneficial and harmful bacteria. This is achieved through pattern-recognition receptors, such as Toll-like receptors (TLRs), which detect microbial-associated molecular patterns (MAMPs) expressed by bacteria. Depending on the bacterial type, the immune system either establishes tolerance or triggers an immune response. The gut microbiota also immunostimulate the gut-associated lymphoid tissue (GALT) which is part of the mucosa-associated lymphoid tissue (MALT) immune system [3].

Another main role of gut microbiota is nutrient metabolism. These diversed microbes are responsible for active fermentation of carbohydrates, fat, protein but also exfoliated intestinal epithelial cells and mucous. Thus the immense amount of nutrients derived from the food can serve human body as source of energy and structural material [4]. The gut microbiota has been demonstrated to have a beneficial effect on lipid metabolism, by reducing the inhibition of lipoprotein lipase activity in adipocytes [5]. Gut microbes in the ileum and large bowel deconjugate bile salts to free bile acids by bile salt hydrolase [6]. The Human gut commensals such as *Bifidobacteria* can de novo synthesize and supply vitamins K and several components of vitamin B. Additionally, gut microbes form conjugated fatty acids (CFAs) that is known to be antidiabetic, antiatherogenic, antiobesogenic, hypolipidemic and have immunomodulatory properties [7]. Species like Clostridium spp. or Fusobacterium spp. are known for their capacity to ferment carbohydrates into short-chain fatty acids (SCFAs). Microbiota-derived short-chain fatty acids are crucial for protecting the intestinal barrier and regulating the immune response during infections [8]. One of the examples of such fermentation product is butyric acid, with its crucial impact on regulating transportation through the intestinal walls, oxidative stress and inflammation. Its biological effects have been widely studied, which includes therapeutic effect for gastrointestinal diseases (ulcerative colitis, inflammatory bowel disease).

It is proved that butyric acid have vital roles in the treatment of ulcerative colitis and inflammatory bowel disease by decreasing TNF-α and IL-13 [9].

Several studies have indicated that the gut microbiota may serve as a potential target in cancer therapy modulation, by enhancing the effectiveness of chemotherapy and immunotherapy [10].

Gut microbiota as creatures colonising the limited environment often compete with pathogens for nutrients. It is important to maintain a diverse microbiota, strong enough to win the interaction to protect our health from disease. Nevertheless, not all microbiota contribute to health benefits. Under specific circumstances certain microbiota can lead to inflammation of tissues.

FACTORS THAT INFLUENCE GUT MICROBIOTA

Numerous studies have shown that host factors such as age, genetics along with diet and antibiotic usage are crucial in determining the gut microbiota from early childhood through adulthood. Changes in the gut microbiota in older people include a general decrease in the diversity and abundance of beneficial gut bacteria, including the protective bacteria *Lactobacillu*s and *Bifidobacterium* potentially increasing the risk of obesity-related diseases [11],[12]. With regard to the mode of delivery, studies have shown that the composition of the intestinal microbiota in vaginally delivered infants appears to be similar to that of the maternal vaginal microbiota [13]. An increasing number of Cesarean sections performed, regardless recommendations, results in an infant gut microbiota imbalance and reduced diversity. Another important factor is stress. Having the evidence of a microbiota-oral-gut-brain axis, stress and depression can increase gut barrier permeability. This results in a "leaky gut" which allows bacteria to seep into circulation, producing an inflammatory response [14]. Similar studies indicate that more impact in research should be intent on modifiable factors such as diet and lifestyle that appear to be our next step in obtaining a healthy microbiota.

2. RESEARCH METHODS

Advances in technology, particularly in DNA sequencing and computational methods, have revolutionized the capacity to analyze gut microbiome community and comprehend their influence on human biology. In a mere ten years, a standard study has progressed from gathering a small number of sequences per sample to an impressing amount of hundreds of millions. These technological advancements such as Next-generation sequencing (NGS) contribute a better understanding of human gut microbiota by allowing for the discovery and characterization of unculturable microbes with prediction of their function [15]. One of the Key NGS method include 16S rRNA gene sequencing, which allow us to understand the impact of the microbiome on the human body by delivering information about classification of microbes and enables to investigate the history of its evolution. Thus currently, 16 rRNA gene surveys are the most commonly used as they are substantially economical and therefore scale to larger projects [16]. The complexity of samples is examined by sequencing genetic material obtained directly from the environment. This approach is called "metagenomics" [17]. Besides metagenomics, a major role in research plays also metatranscriptomics, since metagenomics itself does not deliver information about active gene expression in certain conditions [17].

3. CURRENT STATE OF KNOWLEDGE:

THE INTERPLAY BETWEEN ATHLETIC GUT MICROBIOTA AND PHYSICAL PERFORMANCE

Over the years numerous studies concerning the gut microbiota of athletes were performed. Along with a systematised training sessions that athletes need to follow on everyday basis, the other crucial factor forming the unique athletic gut microbiota is diet. Athletes frequently follow dietary regimens that differ significantly from overall population, affecting the composition of their gut microbiome, and thus contributing a better performance. Popular modifications include elevated protein consumption in resistance trained athletes or carbohydrate intake in endurance athletes and increased total energy and nutrient intake in general. In the following chapter several studies will be quote concerning the connection between the gut microbiota, professional trainings and diet.

First study by F. Clarke et al. [12] describes a group of 40 male professional international rugby players, who follow a diet featuring higher intakes of calories, protein, fat and carbohydrates. Diet diversity corresponded with the gut diversity representing 22 distinct phyla. It is worth mentioning that in this study microbiota diversity is positively correlated with protein intake and creatine kinase (CK) levels, indicating that both diet and exercise contribute to gut biodiversity.

Similar study by W. Barton et al. [1] performed on a group of 40 international rugby players compared to controls found that athletes exhibit relatively intensified pathways and higher amount of faecal metabolites such as SFAs associated with numerous metabolic benefits and a lean phenotype [18].

As observed in other studies [19], diversity is a leading change in the athletic gut microbiota, compared with control groups. Prolonged, intense exercise as for example high intensity trans-oceaning rowing have shown to have a positive impact on gut microbial diversity, increasing the relative abundance of butyrate producing species in 4 well-trained male athletes. These adaptations may contribute in managing the physiological stress associated with prolonged exertion as well as invalidating the negative consequences accompanying endurance exercise.

In a group of 33 both professional and amateur level cyclists [20], higher percentage of *Prevotella spp.* corresponded with greater weekly exercise duration. *Prevotella spp.* was positively correlated with a number of amino acid, carbohydrate (with branched chain amino acid- BCAA biosynthesis) and vitamin B6 metabolism pathways. BCAAs are shown to reduce exercise-induced muscle fatigue and attenuate muscle damage during prolonged endurance exercise [21]. Since BCAAs cannot be synthesized endogenously by the human organism and must be obtained through diet, possessing a gut microbial community that includes *Prevotella spp*., which can either produce BCAAs or stimulate other microbes to generate these amino acids, would be extremely advantageous for athletes who are in need of quick recovery from intense exercise. An increased abundance of another species- *Methanobrevibacter smithii* in a number of the professional cyclists in comparison to amateur cyclists was noted as well. It is worth mentioning that this archaeon exhibited upregulation of genes involved in fermentation of polysaccharides in the distal colon, resulting in the increased number of fermentation products such as SCFAs which then are absorbed by the organism of a host. Presumably, this enhancement could improve recovery from intense exercise and potentially augment race performance [20].

In an innovative study by Scheiman et al. [22], researchers recruited 15 top marathoners to run the Boston Marathon, along with a control group. The concept was to collect fecal samples from the athletes up to 7 days before and after Marathon. As a result, the genus *Veillonella* was found to be more abundant post-marathon and was the most significant differential feature between pre- and post-exercise conditions. *Veillonella spp.* are able to convert lactate into short-chain fatty acids (SCFAs) such as propionic acid and boost metabolism. These studies along with the secondary studies when the bacteria were fed to mice show that *V. atypica* enhances running performance. This discovery highlights a natural, microbiome-based enzymatic process that boosts athletic performance. Hence, while evidence supports an intimate relationship between the gut microbiota and exercise ability, the underlying mechanism of the relationship is not completely clear.

The aim of a study by Murtaza et al. [23] was to introduce a three week dietary intervention in elite race walkers who then undergone intensified training while following a ketogenic, low-carbohydrate, high-fat diet (LCHF). The results indicated an increased relative abundance of *Bacteroides spp.* and substantial increase in fat oxidation. Compared to groups following high or periodized carbohydrate diets, the LCHF diet had a more substantial impact on the gut microbiota, enhancing the relative abundance of bacterial taxa known for their lipid metabolism capabilities. It is also important introduce healthy fat in diet, because saturated fat intake is associated with decreased microbiota diversity and richness in humans and increased availability and transport of lipopolysaccharide, leading to proinflammatory Toll-like receptor (TLR) activation in preclinical models [24].

Collectively, these findings indicate that modulation of the microbiota by chronic exercise depends not only on the physiological state of the individual, but also on a diet.

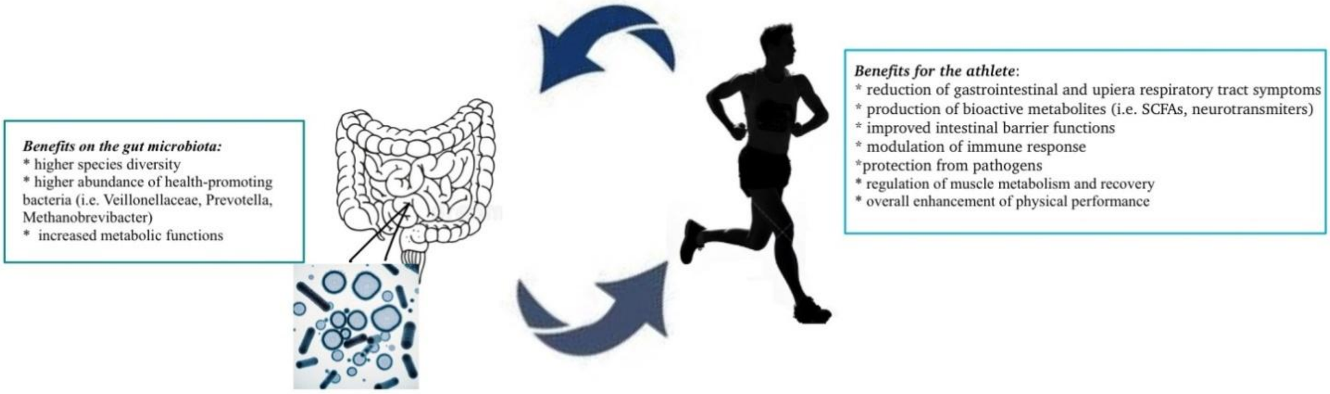

Figure 1. Interactions between gut microbiota and exercise [24].

THE USE OF PROBIOTICS IN ENHANCING PHYSICAL PERFORMANCE

A supplement carries an ergogenic value when it acutely enhances the ability of an athlete to perform an exercise task or enhances recovery from a single exercise bout [25]. Supplements with strong evidence in improving physical performance are identified by the International Olympic Comittee substances (caffeine, creatine, nitrate and sodium bicardbonate) [26]. However there is still little evidence that supports the efficacy of many supplements such as probiotics. Probiotics are "live microorganisms that, when administered in adequate amounts, confer a health benefit on the host" [27]. The aim of this chapter is to quote studies that show probiotics as safe and proven ergogenic dietary supplements which have much to offer in terms of competitive advantages for athletes. Probiotics are known for reducing inflammation [28] and muscle soreness [29], but also maintaining gastrointestinal barrier integrity [30] with the use of SCFAs produced by beneficial bacteria [31] and enhancing immunity [28]. Probiotics also improve mood–related outcomes and improve post-exercise recovery. One of the well-acknowledged and reviewed beneficial effects of probiotics are improvements on gastrointestinal (GI) health (by reducing the duration of gastrointestinal disturbances and alleviate GI symptoms in athletes) and upper respiratory tract (URT) (improvements in the incidence, duration and severity of upper respiratory tract infections, with indirectly improve athletic performance) [32]·[33]. An exercise study involving trained male runners found that a 4-week supplementation with a multi-strain probiotic significantly extended the time to fatigue during treadmill running in hot conditions compared to a placebo [34]. Despite the existence of shared, core mechanisms for probiotic function, health benefits of probiotics are strain- and dose-dependent [35]. *L. plantarum spp.* Supplementation, via modulation of microbiota, ameliorates oxidative stress and inflammation and improves performance under high-intensity exercise [36]. Probiotics significantly enhance protein absorption and utilization, leading to increased plasma levels of branched-chain amino acids (BCAAs) and improved exercise performance [37]. BCAAs reduce fatique during endurance exercise and are essential for the homeostasis of muscle energy metabolism and the adaptation to exercise training [9] . Probiotics have been shown to reduce inflammation and oxidative stress in liver cells, thus increased liver clearance of ammonia and other toxins [38]. In response to muscle-damaging resistance exercise, probiotic supplementation can accelerate recovery and decrease soreness and other indices of skeletal muscle damage [35]. To date, there have been relatively few human clinical studies examining the effects of probiotics on physical performance, and those that do exist have explored only a narrow range of exercise types and performance metrics. Such factors as individuals' baseline diet, immune status, and microbiota composition may contribute different findings, making it difficult to compare the effects between studies. More research is needed to fully understand the direct impact of probiotic supplementation on performance outcomes [39].

SUMMARY AND CONCLUSIONS

To summarize, considering the composition of the microbiota and its metabolic impact on human, there is a way to monitor and adjust athletes' well-being and performance**.** It has been proven that the athletic lifestyle (intense training sessions, diet) have been associated with compositional changes in the gut microbiota, including increased microbial diversity and increased abundance of beneficial microbial species, as well as enriched functional pathways, immune stimulation and improved barrier functions. Numerous studies have shown that certain species of bacteria that are present in the athletic gut microbiota are responsible for enhancing physical performance. Although evidence suggests a close connection between the gut microbiota and exercise performance, the precise underlying mechanism of this relationship remains somewhat unclear and warrant further research. Additionally, there is still limited number of clinical studies, focused on a population of professional athletes, therefore specific conclusions should be drawn carefully. The combination of athletic components such as type of exercise, distinct diet and host physiology confirmedly implicates a healthy gut microbiota. However, distinguishing between the effects of exercise and diet on gut microbiome is challenging, as they may work synergistically. Considering a unique dietary pattern that athletes usually need to follow, investigations should incorporate the impact of high-protein diet along with the variety of fiber and fat intake.

Probiotics can alter the gut microbiota and positively modulate athletic performance. However the variability in strains, doses, and individual factors complicate the identification of the performance-enhancing effects of these dietary strategies. Considering the growing popularity of supplements in sport, in order to determine the most effective bacterial strains and the optimal methods of administration, further studies are required. Future studies should also take into consideration other performance-enhancing procedures including prebiotics or transfer of the gut microbiota.

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REFERENCES:

[1] W. Barton *i in.*, „The microbiome of professional athletes differs from that of more sedentary subjects in composition and particularly at the functional metabolic level", *Gut*, t. 67, nr 4, s. 625–633, kwi. 2018, doi: 10.1136/gutjnl-2016-313627.

[2] K. Hou *i in.*, „Microbiota in health and diseases", *Sig Transduct Target Ther*, t. 7, nr 1, s. 1–28, kwi. 2022, doi: 10.1038/s41392-022-00974-4.

[3] C. Mazziotta, M. Tognon, F. Martini, E. Torreggiani, i J. C. Rotondo, „Probiotics Mechanism of Action on Immune Cells and Beneficial Effects on Human Health", *Cells*, t. 12, nr 1, s. 184, sty. 2023, doi: 10.3390/cells12010184.

[4] R. B. Sartor, „Microbial Influences in Inflammatory Bowel Diseases", *Gastroenterology*, t. 134, nr 2, s. 577–594, luty 2008, doi: 10.1053/j.gastro.2007.11.059.

[5] S. M. Jandhyala, R. Talukdar, C. Subramanyam, H. Vuyyuru, M. Sasikala, i D. N. Reddy, „Role of the normal gut microbiota", *World J Gastroenterol*, t. 21, nr 29, s. 8787–8803, sie. 2015, doi: 10.3748/wjg.v21.i29.8787.

[6] J. M. Ridlon, D. J. Kang, P. B. Hylemon, i J. S. Bajaj, „Bile Acids and the Gut Microbiome", *Curr Opin Gastroenterol*, t. 30, nr 3, s. 332–338, maj 2014, doi: 10.1097/MOG.0000000000000057.

[7] Y. Yu, F. Raka, i K. Adeli, „The Role of the Gut Microbiota in Lipid and Lipoprotein Metabolism", *J Clin Med*, t. 8, nr 12, s. 2227, grudz. 2019, doi: 10.3390/jcm8122227.

[8] „Microbiota-derived short chain fatty acids: Their role and mechanisms in viral infections - ScienceDirect". Dostęp: 28 maj 2024. [Online]. Dostępne na: https://www.sciencedirect.com/science/article/pii/S0753332223002020

[9] M. Xu *i in.*, „Endurance performance and energy metabolism during exercise in mice with a muscle-specific defect in the control of branched-chain amino acid catabolism", *PLOS ONE*, t. 12, nr 7, s. e0180989, lip. 2017, doi: 10.1371/journal.pone.0180989.

[10] Kunika, N. Frey, i A. Y. Rangrez, „Exploring the Involvement of Gut Microbiota in Cancer Therapy-Induced Cardiotoxicity", *Int J Mol Sci*, t. 24, nr 8, s. 7261, kwi. 2023, doi: 10.3390/ijms24087261.

[11] „Co się dzieje z mikrobiotą jelit wraz z wiekiem? - Instytut Mikroekologii". Dostęp: 17 maj 2024. [Online]. Dostępne na: https://instytut-mikroekologii.pl/co-sie-dzieje-z-mikrobiota-jelit-wraz-z-wiekiem/

[12] S. F. Clarke *i in.*, „Exercise and associated dietary extremes impact on gut microbial diversity”, *Gut*, t. 63, nr 12, s. 1913–1920, grudz. 2014, doi: 10.1136/gutjnl-2013-306541.

[13] A. Góralczyk-Bińkowska, D. Szmajda-Krygier, i E. Kozłowska, „The Microbiota–Gut–Brain Axis in Psychiatric Disorders”, *International Journal of Molecular Sciences*, t. 23, nr 19, Art. nr 19, sty. 2022, doi: 10.3390/ijms231911245.

[14] A. Madison i J. K. Kiecolt-Glaser, „Stress, depression, diet, and the gut microbiota: human–bacteria interactions at the core of psychoneuroimmunology and nutrition”, *Curr Opin Behav Sci*, t. 28, s. 105–110, sie. 2019, doi: 10.1016/j.cobeha.2019.01.011.

[15] C. R. Wensel, J. L. Pluznick, S. L. Salzberg, i C. L. Sears, „Next-generation sequencing: insights to advance clinical investigations of the microbiome”, *J Clin Invest*, t. 132, nr 7, s. e154944, doi: 10.1172/JCI154944.

[16] A. E. Mohr *i in.*, „The athletic gut microbiota”, *J Int Soc Sports Nutr*, t. 17, s. 24, maj 2020, doi: 10.1186/s12970-020-00353-w.

[17] A. Karney, „Mikrobiota a Otyłość”, *Dev Period Med*, t. 21, nr 3, s. 203–207, paź. 2017, doi: 10.34763/devperiodmed.20172103.203207.

[18] A. Koh, F. D. Vadder, P. Kovatcheva-Datchary, i F. Bäckhed, „From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites”, *Cell*, t. 165, nr 6, s. 1332–1345, cze. 2016, doi: 10.1016/j.cell.2016.05.041.

[19] D. M. Keohane *i in.*, „Four men in a boat: Ultra-endurance exercise alters the gut microbiome”, *Journal of Science and Medicine in Sport*, t. 22, nr 9, s. 1059–1064, wrz. 2019, doi: 10.1016/j.jsams.2019.04.004.

[20] L. M. Petersen *i in.*, „Community characteristics of the gut microbiomes of competitive cyclists”, *Microbiome*, t. 5, nr 1, s. 98, sie. 2017, doi: 10.1186/s40168-017-0320-4.

[21] B. K. Greer, J. L. Woodard, J. P. White, E. M. Arguello, i E. M. Haymes, „Branched-chain amino acid supplementation and indicators of muscle damage after endurance exercise”, *Int J Sport Nutr Exerc Metab*, t. 17, nr 6, s. 595–607, grudz. 2007, doi: 10.1123/ijsnem.17.6.595.

[22] J. Scheiman *i in.*, „Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism”, *Nat Med*, t. 25, nr 7, s. 1104–1109, lip. 2019, doi: 10.1038/s41591-019-0485-4.

[23] N. Murtaza *i in.*, „The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers”, *Nutrients*, t. 11, nr 2, Art. nr 2, luty 2019, doi: 10.3390/nu11020261.

[24] M. Wolters *i in.*, „Dietary fat, the gut microbiota, and metabolic health – A systematic review conducted within the MyNewGut project", *Clinical Nutrition*, t. 38, nr 6, s. 2504–2520, grudz. 2019, doi: 10.1016/j.clnu.2018.12.024.

[25] C. M. Kerksick *i in.*, „ISSN exercise & sports nutrition review update: research & recommendations", *J Int Soc Sports Nutr*, t. 15, nr 1, s. 38, sie. 2018, doi: 10.1186/s12970-018-0242-y.

[26] J. Ketterly, „Sports Medicine: Ergogenic Aids", *FP Essent*, t. 518, s. 23–28, lip. 2022.

[27] C. Hill *i in.*, „The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic", *Nat Rev Gastroenterol Hepatol*, t. 11, nr 8, s. 506–514, sie. 2014, doi: 10.1038/nrgastro.2014.66.

[28] P. C. B. Lollo *i in.*, „Probiotic cheese attenuates exercise-induced immune suppression in Wistar rats", *Journal of Dairy Science*, t. 95, nr 7, s. 3549–3558, lip. 2012, doi: 10.3168/jds.2011-5124.

[29] R. Jäger, M. Purpura, S. Farmer, H. A. Cash, i D. Keller, „Probiotic Bacillus coagulans GBI-30, 6086 Improves Protein Absorption and Utilization", *Probiotics & Antimicro. Prot.*, t. 10, nr 4, s. 611–615, grudz. 2018, doi: 10.1007/s12602-017-9354-y.

[30] H. A. G. Ducray *i in.*, „Prevention of excessive exercise-induced adverse effects in rats with Bacillus subtilis BSB3", *Journal of Applied Microbiology*, t. 128, nr 4, s. 1163–1178, kwi. 2020, doi: 10.1111/jam.14544.

[31] K. Hiippala *i in.*, „The Potential of Gut Commensals in Reinforcing Intestinal Barrier Function and Alleviating Inflammation", *Nutrients*, t. 10, nr 8, Art. nr 8, sie. 2018, doi: 10.3390/nu10080988.

[32] M. Rondanelli, M. A. Faliva, S. Perna, A. Giacosa, G. Peroni, i A. M. Castellazzi, „Using probiotics in clinical practice: Where are we now? A review of existing meta-analyses", *Gut Microbes*, t. 8, nr 6, s. 521–543, lis. 2017, doi: 10.1080/19490976.2017.1345414.

[33] Q. Hao, B. R. Dong, i T. Wu, „Probiotics for preventing acute upper respiratory tract infections", *Cochrane Database of Systematic Reviews*, nr 2, 2015, doi: 10.1002/14651858.CD006895.pub3.

[34] A. F. Carbuhn *i in.*, „Effects of Probiotic (Bifidobacterium longum 35624) Supplementation on Exercise Performance, Immune Modulation, and Cognitive Outlook in Division I Female Swimmers", *Sports*, t. 6, nr 4, Art. nr 4, grudz. 2018, doi: 10.3390/sports6040116.

[35] R. Jäger *i in.*, „International Society of Sports Nutrition Position Stand: Probiotics", *Journal of the International Society of Sports Nutrition*, t. 16, nr 1, s. 62, grudz. 2019, doi: 10.1186/s12970-019-0329-0.

[36] W.-C. Huang, C.-H. Pan, C.-C. Wei, i H.-Y. Huang, „Lactobacillus plantarum PS128 Improves Physiological Adaptation and Performance in Triathletes through Gut Microbiota Modulation", *Nutrients*, t. 12, nr 8, Art. nr 8, sie. 2020, doi: 10.3390/nu12082315.

[37] R. Jäger, A. E. Mohr, i J. N. Pugh, „Recent advances in clinical probiotic research for sport", *Current Opinion in Clinical Nutrition & Metabolic Care*, t. 23, nr 6, s. 428, lis. 2020, doi: 10.1097/MCO.0000000000000686.

[38] J. Liu, E. Lkhagva, H.-J. Chung, H.-J. Kim, i S.-T. Hong, „The Pharmabiotic Approach to Treat Hyperammonemia", *Nutrients*, t. 10, nr 2, Art. nr 2, luty 2018, doi: 10.3390/nu10020140.

[39] M. Marttinen, R. Ala-Jaakkola, A. Laitila, i M. J. Lehtinen, „Gut Microbiota, Probiotics and Physical Performance in Athletes and Physically Active Individuals", *Nutrients*, t. 12, nr 10, s. 2936, wrz. 2020, doi: 10.3390/nu12102936.