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REVISÃO

Effect of Dietary Patterns on Human Gut Microbiota: a narrative review

Efeito de Padrões Dietéticos na Microbiota Intestinal Humana: uma revisão narrativa

Mateus Pontes Silva[1], Thais Alves Cunha[2], Karla Mônica Dantas Coutinho[2], Lucia Leite Lais[3]

[1]*Department of Nutrition, Federal University of Rio Grande do Norte (UFRN), Natal, RN, Brazil*

[2]*Postgraduate Program in Health Sciences, Federal University of Rio Grande do Norte (UFRN), Natal, RN, Brazil*

[3]*Federal University of Rio Grande do Norte, Natal (UFRN), RN, Brazil*

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Correspondência: Lucia Leite Lais, lucia.leite@ufrn.br

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Abstract

Introduction: Diet plays a crucial role in shaping the human gut microbiota (GM), but studies investigating the effects of dietary patterns on the GM are still limited. *Objective:* This study aimed to review the effects of different dietary patterns on the human GM. *Methods:* This review included observational and clinical studies published in PubMed/MEDLINE between 2019 and 2023. *Results:* Initially, 1,148 articles were identified and 12 articles were included. Studies were conducted in various countries, predominantly in the USA (n=3), and most evaluated the effects of the Mediterranean diet (n=3) and vegetarian/vegan diet (n=3). No included study evaluated the DASH (Dietary Approaches to Stop Hypertension) diet. The Western diet showed negative effects on the GM, characterized by an increase in Firmicutes bacteria and a reduction in bacterial diversity and richness. These effects are associated with cardiovascular and inflammatory diseases. The low carb diet showed conflicting results among studies. The ketogenic diet appears to be associated with a decrease in the Firmicutes/Bacteroidetes ratio, especially when whey protein or plant proteins are the main protein sources in the diet. Mediterranean and vegetarian/vegan diets had beneficial effects on the GM, mainly associated with high fiber intake from fruits, vegetables, and legumes, leading to a reduction in the Firmicutes/Bacteroidetes ratio, an increase in Akkermansia bacteria, and higher production of short-chain fatty acids (SCFAs). *Conclusion:* Dietary pattern exerts distinct effects on the GM, influencing bacterial richness and diversity differently. Further studies are recommended in this area, including investigation of the DASH diet's impact on the GM.

Keywords: Gastrointestinal microbiome; dietary patterns.

Resumo

Introdução: A dieta desempenha um papel crucial no perfil microbiota intestinal (MI) humana, mas os estudos que investigam os efeitos dos padrões dietéticos na MI ainda são escassos. *Objetivo:* Este estudo teve como objetivo revisar os efeitos de diferentes padrões dietéticos na MI humana. *Métodos:* Esta revisão incluiu estudos observacionais e clínicos publicados no PubMed/MEDLINE entre 2019 e 2023. *Resultados:* Inicialmente, foram identificados 1.148 artigos e 12 artigos foram incluídos. Os estudos foram realizados em diversos países, predominantemente nos EUA (n=3), e a maioria deles avaliou os efeitos da dieta mediterrânea (n=3) e dieta vegetariana/vegana (n=3). Nenhum estudo incluído avaliou a dieta DASH. A dieta ocidental mostrou efeitos negativos na MI, caracterizados por um aumento de bactérias do gênero Firmicutes e uma redução na diversidade e riqueza bacteriana, associados a doenças cardiovasculares e inflamatórias. A dieta low carb apresentou resultados conflitantes entre os estudos. A dieta cetogênica parece estar associada a uma diminuição na razão Firmicutes/Bacteroidetes, especialmente quando proteínas de soro de leite ou proteínas vegetais são as principais fontes proteicas na dieta. As dietas mediterrânea e vegetariana/vegana tiveram efeitos benéficos na MI, principalmente associados ao alto consumo de fibras de frutas, vegetais e leguminosas, resultando em uma redução na razão Firmicutes/Bacteroidetes, um aumento na bactéria Akkermansia e uma maior produção de ácidos graxos de cadeia curta (AGCC). *Conclusão:* Padrões dietéticos exercem diferentes na MI, influenciando a riqueza e a diversidade bacteriana. Recomenda-se realizar mais estudos nessa área, incluindo a investigação do impacto da dieta DASH na MI.

Palavras-chave: Microbioma gastrointestinal; padrões alimentares.

Introduction

The gut microbiota (GM) is one common topic studied in health sciences due to its significance for the health of both the host and the microorganisms. The GM is responsible for functions that ensure the homeostasis of the human body, including the production of short-chain fatty acids (SCFAs), synthesis of vitamins, reabsorption of bile salts, protection of the intestinal barrier, and resistance to bacterial translocation [1,2,3]. Gut microorganism colonization begins at birth, and its composition can be influenced by factors such as delivery mode, gestational age, and whether breastfeeding is exclusive or artificial [4,5,6].

The GM is comprised of various microorganisms, primarily bacteria, which play a beneficial role in regulating numerous physiological processes. The dominant bacterial phyla are Firmicutes and Bacteroidetes, with other microorganisms present in smaller proportions. Maintaining an appropriate balance of these phyla fosters a favorable environment and interaction for host health. In children, adults, and the elderly, the Firmcutes/Bacteroidetes ratio found were 0.4, 10.9, and 0.6, respectively [7]. These bacteria are distributed throughout the gastrointestinal tract, with smaller quantities found in the stomach and small intestine, and larger quantities in the large intestine due to reduced intestinal secretions, peristalsis, and the presence of fermentable material [3,7].

Bacteria colonizing the GM may undergo alterations due to habits practiced in the host's daily life, such as a poor diet, alcohol and drug consumption, and lack of physical exercise. These changes can lead to an imbalance in the bacterial population, consequently affecting homeostasis. Therefore, various modulations can be implemented to restore the microbiota balance at the intestinal level. These modulations primarily involve dietary adjustments, lifestyle changes, the utilization of prebiotics, probiotics, synbiotics, and postbiotics, as well as fecal microbiota transplantation [8].

Although many factors can influence the composition of the GM, diet stands out as the primary one, as it provides nutrients directly utilized as substrates for the maintenance and growth of intestinal microorganisms [9]. We hypothesize that dietary patterns can induce different effects on gut microbiota. Despite this topic being addressed in the literature, there is a scarcity of comprehensive studies examining the effect of dietary patterns on the GM in humans. Therefore, this study aims to provide a narrative review of this subject. We believe it will foster reflection and knowledge, thereby advancing individual or collective nutrition care.

Methods

This study is characterized as a narrative review, constructed from articles published in the last 5 years (2019-2023) and indexed in the PubMed/MEDLINE database, without language restrictions. Observational studies and clinical trials were included, while literature reviews, guidelines, animal studies, and case reports were excluded.

The following Medical Subject Headings (MeSH) terms were used: “gastrointestinal microbiome,” “gut microbiota,” “feeding patterns,” “Mediterranean diet,” “Western diet,” “DASH diet,” “low carbohydrate diet,” “ketogenic diet,” “vegetarian diet,” and “vegan diet.” Boolean operators “and” and “or” were employed to construct search equations, aiming to broaden the identified articles. The PRISMA flowchart model [10] was utilized to describe the structure of the article selection process.

Upon application of the inclusion criteria, the articles underwent an initial screening process involving a review of their titles and abstracts. Subsequently, the selected articles were read in their entirety, resulting in only those meeting the review's criteria being retained.

The selected articles were then entered into a Microsoft Excel® spreadsheet to establish a concise database, which included the following categories: authors and year of publication, study country, title, study type, investigated dietary pattern, study population, and the dietary pattern's effect on the GM. The findings were summarized narratively, with each dietary pattern's effect addressed as a separate topic.

Results

The search strategy identified 1,148 records in the PubMed/MEDLINE database. Following the application of inclusion and exclusion criteria, 63 articles were retained. Subsequently, after reviewing the titles and abstracts, 31 articles were chosen for full-text reading. Of these, 12 articles met the eligibility criteria and were included in this review (Figure 1).

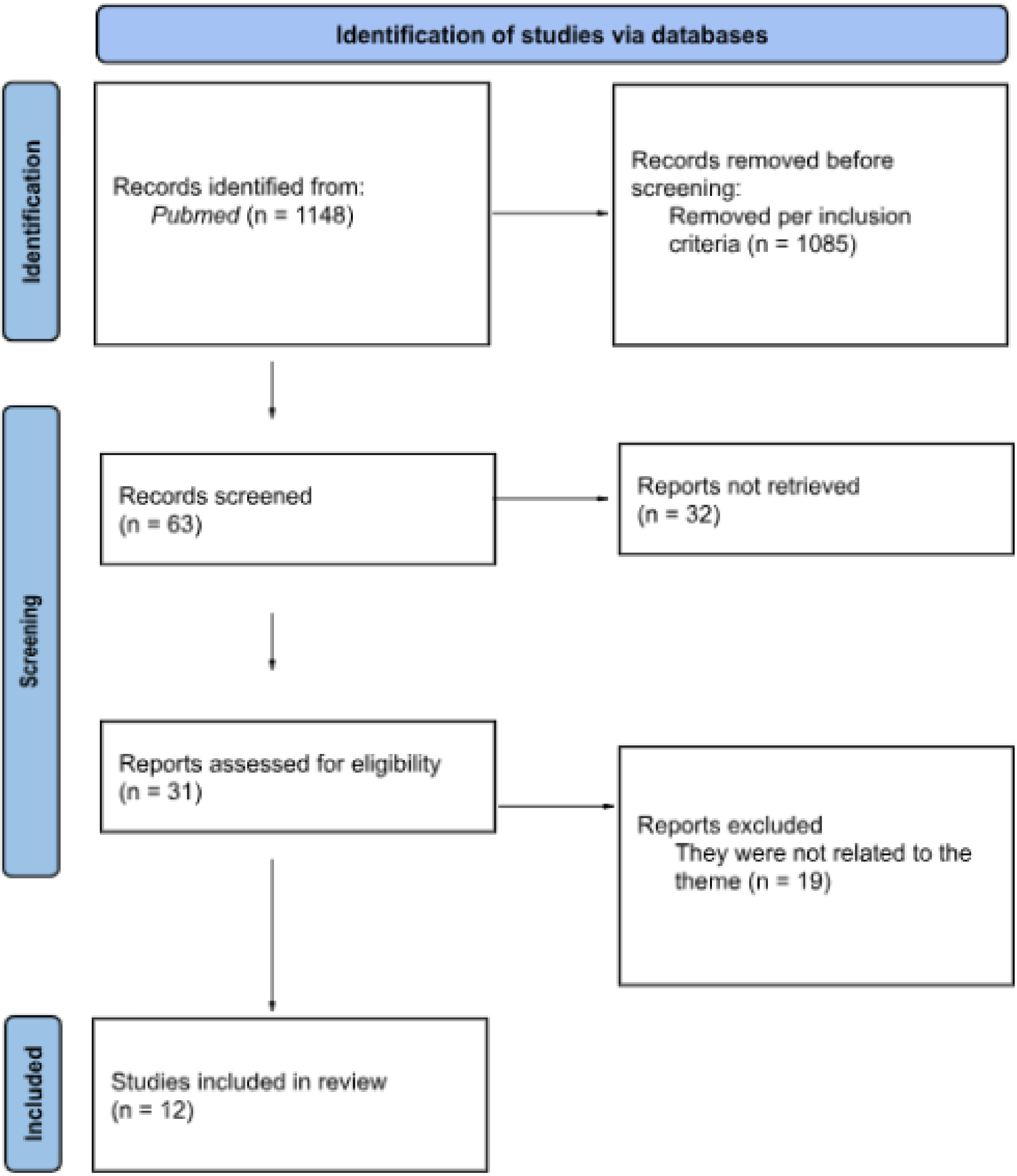


Figure 1 - *PRISMA flow diagram of literature search and selection process.*

The selected articles encompass studies conducted in various countries, with a predominance from the USA (n=3), and most of them assessed the effects of Mediterranean (n=3) and vegetarian/vegan diets (n=3) on the human GM. No study addressed the DASH diet. Clinical trials predominated among the study types (n=9). The population consisted of adults and elderly individuals, healthy or with comorbidities. The characteristics of the studies included are describe in Table 1 and the main effect of dietary patterns on human gut microbiota are summarized on Figure 2.

Table 1 - *Characteristics of the studies included*

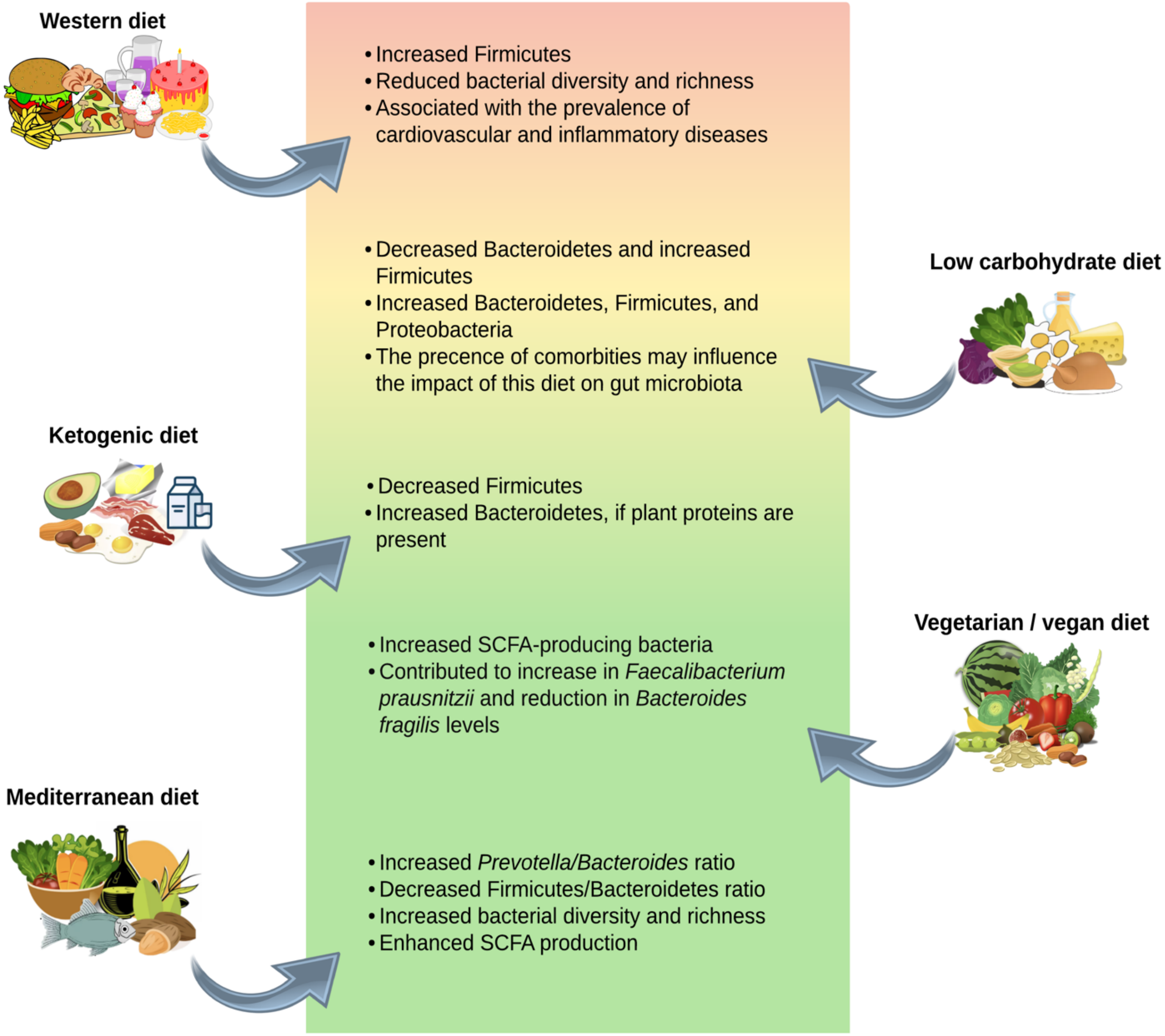
Author (Year) Country [Reference]	Study Design	Aim of the Study	Dietary Pattern	Study Participants	Effect of the dietary pattern on gut microbiota
Ismael et al. (2021) Portugal [11]	Clinical Trial (pilot study)	To evaluate the effectiveness of Mediterranean diet intervention on the gut microbiota of type 2 diabetes individuals		Men and women (n=9) with the mean age of 66 ± 9 years, nonsmokers, diagnosed with type 2 diabetes	Adherence to the Mediterranean diet increased bacterial richness and resulted in a better glycemic control. Increase in Prevotella/Bacteroides ratio. Decrease in Firmicutes/Bacteroidetes ratio
Choo et al. (2023) Australia [13]		To evaluate the effects of a Mediterranean diet supplemented with dairy foods on the gut microbiome of Australians at risk of cardiovascular disease		Men and women (n=34) with the mean age of 61.1 ± 6.9 years, with high systolic blood pressure, cardiovascular risk factors, and not on hypertensive medication	The diet intervention was associated with changes in the relative abundance of several bacterial taxa, including an increase in Butyricicoccus and a decrease in Colinsella and Veillonella. These changes were associated with clinical parameters such as systolic blood pressure and fasting glucose levels

Barber et al. (2021) Spain [17]		To determine the effect of Western diet and fiber-enriched Mediterranean diet on gut microbiota, digestive function, and other parameters		Healthy men (n=20), aged between18-38 years	The abundance of butyrate producers such as *A. butyriciproducens* and *A. hadrus* was significantly higher after fibre-enriched Mediterranean diet compared to Western diet. Despite this little difference observed in gut microbiota composition, microbial metabolism differed substantially as demonstrated by urinary metabolite profiles and microbial metabolic pathways
Tindall et al. (2020) United States [20]		To examined between-diet differences in gut bacterial composition in individuals at risk for cardiovascular disease. The diets used were standard Western diet (SWD), walnut diet (WD), walnut fatty acid-matched diet (WFMD), and oleic acid replaces α-linolenic acid diet (ORAD)	Western diet vs. diet with different amounts of walnuts or oils	Men and women (n=42), aged between 30-60 years, with overweight or obesity, high blood pressure and/or high LDL-cholesterol	Both the WFMD and WD led to significant enrichment in Roseburia, Eubacteria eligens, and Butyricicoccus compared to the SWD. These bacteria are butyrate producers and contribute to health benefits
Malinowska et al. (2022) Poland [18]	Cross-sectional	To evaluate differences in gut microbiota composition after intervention with healthy (HDP) or western (WDP) dietary pattern	Western diet vs. healthy diet	Healthy adults (n=200), aged between 31 and 50 years of age	The α-diversity did not differ between people with WDP and HDP. People with HDP had higher relative abundance of Firmicutes and Faecalibacterium and lower relative abundance of Bacteroidota and Escherichia-Shigella than participants with WDP

Ren et al. (2020) China [23]		To determine the effect of an almond-based low carbohydrate diet (a-LCD) on depression and glycometabolism, as well as gut microbiota and fasting glucagon-like peptide 1 (GLP-1) in patients with type 2 diabetes (T2DM)	Low	Men and women with T2DM (n=45), aged 71.98 ± 5.63 years, without any change to oral anti-diabetic drugs or insulin in the half-month before the intervention	The a-LCD diet significantly increased the populations of SCFA-producing bacteria such as Roseburia, Ruminococcus, and Eubacterium. Additionally, a-LCD could have a beneficial effect on depression and glycometabolism in these patients
Fragiadakis et al. (2020) United States [25]		To investigate the association between baseline microbiota composition or diversity and weight-loss success. Also, to track the longitudinal associations of changes to lower-carbohydrate or lower-fat diets, weight loss, and the composition and diversity of the gut microbiota	Low	Healthy adults (n=609), nondiabetic, with BMI ranging from 28 to 40 kg/m^2.	The low carbohydrate diet increased the relative abundance of taxa within the Proteobacteria, Bacteroidetes, and Firmicutes phyla after 3 months. Conversely, the low-fat diet showed decreases in Actinobacteria and Firmicutes after 3 months
Basciani et al. (2020) Italy [28]		To compare the efficacy and safety of very-low-calorie ketogenic diets (VLCKDs) incorporating either whey, plant, or animal protein on metabolic and body composition parameters and on the composition of the gut microbiota in a population of patients with obesity and insulin resistance	Ketogenic diet	Men and women with obesity (n=48), aged 56.2 ± 6.1 years, BMI 35.9 ± 4.1 kg/m^2, and homeostatic model assessment (HOMA) index ≥ 2.5	An observed decrease in the relative abundance of Firmicutes and an increase in Bacteroidetes were noted. Whey and vegetable proteins demonstrated a safer profile and shifted the intestinal microbiota towards a healthier composition compared to animal protein
Nakamura et al. (2022) Japan [30]		To investigate the effects of ketogenic formulas (KF) and ketogenic diets (KD) on blood ketone bodies, gut microbiota composition, and safety	Ketogenic diet	Healthy male adults (n=20), aged 20 to 40, and BMI 18.5-25.0 kg/m^2	ketogenic diets lead to changes in gut microbiota. KF showed a decrease in phylum *Firmicutes*

Djekic *et al.* (2020) Sweden [32]		To investigate the effects of a vegetarian diet (VD) on cardiovascular disease risk factors in subjects with a history of ischemic heart disease treated by percutaneous coronary intervention, compared with an isocaloric meat diet (MD)		Elderly individuals (n=31) with a mean age of 67 years and a median BMI of 27.5 kg/m²	Differences were observed between the VD and MD in the relative abundance of several microbial genera within the families *Ruminococcaceae*, *Lachnospiraceae*, and *Akkermansiaceae*. A trend of increased fecal (short chain fatty acids) SCFAs was found with the VD, which is consistent with the slightly higher increase in fiber intake compared to the MD
Hegelmaier *et al.* (2020) Germany [35]	Case-control Study	To investigate the influence of a vegetarian diet including a high proportion of SCFAs acting as anti-inflammatory compounds on the microbiome and the clinical course in patients with Parkinson's disease (PD)		Patients with idiopathic PD (n=54), aged 61 (±9.2) years, and healthy controls (n=32), aged 52.8 (±12.6) years	A tendency towards a reduction in *Prevotellaceae*, *Bacteroidetes*, the genus *Butyricimonas* and *Odoribacter* was observed in patients with PD. Furthermore, *Negativicutes* and the phylum Proteobacteria showed a tendency to increase. Also, there was a significant association between gut microbiome diversity and the Unified Parkinson disease Rating Scale (UPDRS) III and the abundance of *Ruminococcaceae*
Kahleova *et al.* (2020) United States [38]		To test the effect of a low-fat vegan diet on gut microbiota and its association with weight, body composition, and insulin resistance in overweight men and women	Low-fat vegan diet	Adult men and women with overweight or obesity (n=168), body mass index (BMI) 28-40 kg/m^2	The low-fat vegan diet resulted in an increased relative abundance of *Faecalibacterium prausnitzii* and a smaller decrease in the relative abundance of *Bacteroides fragilis*, compared to control group. Both changes correlated negatively with alterations in body weight, fat mass, and visceral fat volume

Abbreviations: a-LCD, almond-based low carbohydrate diet; GLP-1, glucagon-like peptide 1; HDP, healthy dietary pattern; KD, ketogenic diets; KF, ketogenic formulas; MD, meat diet; ORAD, oleic acid replaces α-linolenic acid diet; PD, Parkinson's disease; SCFAs, short chain fatty acids; SWD, were standard Western diet; T2DM, type 2 diabetes; UPDRS, unified Parkinson disease rating scale; VD, vegetarian diet; VLCKDs, very-low-calorie ketogenic diets; WD, walnut diet; WFMD, walnut fatty acid-matched diet; WDP, Western dietary pattern.



- Increased Firmicutes
- Reduced bacterial diversity and richness
- Associated with the prevalence of cardiovascular and inflammatory diseases

- Decreased Bacteroidetes and increased Firmicutes
- Increased Bacteroidetes, Firmicutes, and Proteobacteria
- The precence of comorbities may influence the impact of this diet on gut microbiota

- Decreased Firmicutes
- Increased Bacteroidetes, if plant proteins are present

- Increased SCFA-producing bacteria
- Contributed to increase in *Faecalibacterium prausnitzii* and reduction in *Bacteroides fragilis* levels

- Increased *Prevotella/Bacteroides* ratio
- Decreased Firmicutes/Bacteroidetes ratio
- Increased bacterial diversity and richness
- Enhanced SCFA production

Figure 2 - *Main effect of dietary patterns on human gut microbiota*

Discussion

Mediterranean diet and gut microbiota

Current literature demonstrates that incorporating the Mediterranean diet into a healthy lifestyle is associated with beneficial effects on the human GM. Ismael et al. (2021) [11] demonstrated that adopting the Mediterranean dietary pattern by individuals with type 2 diabetes mellitus for four weeks resulted in an increased Prevotella/Bacteroides ratio, as well as increased bacterial diversity and richness. Additionally, it led to a decrease in the Firmicutes/Bacteroidetes ratio. The increase in the Prevotella/Bacteroides ratio is associated with a high intake of fiber-rich foods. Therefore, the high prevalence of Prevotella in the GM is linked to an increased capacity for fermenting complex carbohydrates, thereby producing more SCFAs than the Bacteroides-dominated GM [12]. On the other hand, the decrease in the Firmicutes/Bacteroidetes ratio associated with the Mediterranean diet demonstrates a beneficial effect of this dietary pattern, as this ratio is increased in individuals with type 2 diabetes [3].

Choo et al. (2023) [13] found that after eight weeks of intervention with a Mediterranean diet enriched with dairy products, study participants showed an increase in Butyricicoccus and a decrease in Collinsella and Veillonella. Butyricicoccus is a butyrate-producing genus that preserves tight junction and intestinal barrier integrity, thus acting therapeutically on gastrointestinal inflammation, such as ulcerative colitis [14]. Increased dietary fiber intake tends to contribute to reducing the number of Collinsella bacteria [15]. Additionally, the Mediterranean diet helps reduce the high prevalence of this genus in metabolic diseases, including cardiovascular diseases [16], leading to beneficial health outcomes.

In the study of Barber et al. (2021) [17] the consumption of foods from a Mediterranean diet resulted in increased butyrate production, one of the main SCFAs. The findings of this study suggest that dietary substrates reaching the colon have a fundamental impact on microbial metabolic functions. Metabolic potential can be rapidly adapted to changes in substrate availability. However, this may not be the case in individuals with long-term dietary restrictions.

In this regard, the Mediterranean diet promoted beneficial effects by increasing the Prevotella/Bacteroides ratio, as well as bacterial diversity and richness, while decreasing the Firmicutes/Bacteroidetes ratio. Additionally, it enhanced SCFA production due to the high quantity of fiber-rich foods, such as fruits, vegetables, legumes, and whole grains.

Western diet and gut microbiota

Studies have demonstrated detrimental effects of the Western diet on human GM and host health. Malinowska et al. (2022) [18] compared the effects of the Western dietary pattern with a healthy dietary pattern and observed a higher prevalence of bacteria from the phylum Firmicutes, particularly from the genus *Ruminococcus*. The Western diet adopted by the study participants included foods high in simple sugars, salt, ultra-processed products, and low intake of fiber-rich foods, indicative of a high-calorie intake pattern. This characteristic contributes to the proliferation of Firmicutes bacteria, leading to reduced microbial diversity and alterations in the richness and composition of the GM [19]. Consequently, this dietary pattern is associated with cardiovascular diseases, type 2 diabetes, chronic kidney disease, peripheral neuropathy, among other conditions [12].

Similarly, Tindall et al. (2020) [20] demonstrated that, compared to other dietary patterns, the Western diet promoted an increase and predominance of bacteria from the phylum Firmicutes. The presence of bacteria from this phylum was associated with cardiovascular disease risk factors. Furthermore, there was a positive association between this bacterial profile and increased permeability of the intestinal barrier, leading to a dysbiosis state and altered metabolites, promoting local inflammation with the presence of lipopolysaccharide (LPS) in the bloodstream, contributing to systemic endotoxemia and chronic inflammation [21]. The literature indicates that transitioning from a Western diet to a Mediterranean diet result in anti-inflammatory and antioxidant actions, crucial for GM homeostasis. [22].

The Western diet was responsible for increasing the population of Firmicutes bacteria and reducing the diversity and richness of the GM. This increase occurred due to high consumption of calorie-dense and ultra-processed foods, favoring the association of this dietary pattern with the prevalence of cardiovascular and inflammatory diseases, thus resulting in negative outcomes for the GM.

Low carbohydrate diet and gut microbiota

The selected articles for this review that discuss the low carbohydrate diet had different results. According to Ren et al. (2020) [23], a low carbohydrate diet based on almonds decreased the population of the Bacteroidetes phylum and increased bacteria from the genera *Roseburia* and *Ruminococcus*, both belonging to the phylum Firmicutes. The reduction in Bacteroidetes bacteria observed with this dietary pattern was consistent with the findings of Dhillon et al. (2019) [24], in which a primary decrease in the *Bacteroides fragilis* species was observed. The increase in the genera *Roseburia* and *Ruminococcus* contributed to the enhanced formation of SCFAs.

The findings reported by Fragiadakis et al. (2020) [25] revealed that administering a low-carbohydrate diet to healthy individuals resulted in elevated levels of bacteria belonging to the phyla Bacteroidetes, Firmicutes, and Proteobacteria. The augmentation of Firmicutes bacteria is concomitant with dietary fat abundance, as commonly encountered in low-carbohydrate diets [26]. Nonetheless, sustained adherence to a low-carbohydrate diet may present challenges, as patients frequently discontinue adherence to this dietary regimen due to issues related to tolerance or restricted array of food choices available within the diet [27].

The effects on the GM induced by the low-carbohydrate diet varied slightly in their outcomes. While one study showed a decrease in Bacteroidetes and an increase in Firmicutes levels, the other study showed increased levels of three bacterial phyla: Bacteroidetes, Firmicutes, and Proteobacteria. This discrepancy may be explained by differences in study populations among the articles, as participants in one study were healthy individuals while those in the other study had type 2 diabetes, thus reflecting a different composition of the IM.

Ketogenic diet and gut microbiota

Both studies included in this review addressing ketogenic diet yielded similar results. Basciani et al. (2020) [28] conducted an intervention in obese patients, using a ketogenic diet containing whey protein, animal protein, or plant protein. The final effect was a decrease in the Firmicutes phylum and an increase in the Bacteroidetes phylum after 45 days of dietary intervention. The conclusion of this study further indicated that the various protein sources influenced the ratio between these phyla differently. The ketogenic diet containing whey protein and plant protein had a greater impact on reducing the percentage of Firmicutes than the ketogenic diet containing only animal protein. Regarding the increase in Bacteroidetes, whey protein and plant protein had a greater influence compared to animal protein. Another study, conducted with children affected by refractory epilepsy and consuming a ketogenic diet, also demonstrated an increase in Bacteroidetes and a decrease in Firmicutes [29].

Nakamura et al. (2022) [30] demonstrated that a dietary intervention in healthy adult men, combining a ketogenic diet with a ketogenic formula containing medium-chain triglycerides and using a 3:1 ketogenic ratio decreased the

Firmicutes phylum. Ketone bodies can selectively inhibited bifidobacterial growth and ketogenic diet may decrease the levels of pro-inflammatory Th17 cells in the intestine [30]. Additionally, individuals diagnosed with epilepsy and affected by dysbiosis also benefit from these effects of this dietary pattern [31].

The studies showed a decrease in Firmicutes, and in one of them, there was also an increase in Bacteroidetes, influenced by the combination of the ketogenic diet with whey and plant proteins. These proteins may be beneficial to manage gut dysbiosis in individuals with epilepsy.

Vegetarian/vegan diet and gut microbiota

The effect of the vegetarian diet on the GM was similar among studies. A dietary intervention conducted over four weeks by Djekic et al. (2020) [32] revealed that a vegetarian diet, specifically ovolactovegetarian, resulted in an increase in bacteria of the genus *Akkermansia*, primarily due to the high consumption of polyphenols and fibers. Because of this effect on the GM, the production of SCFAs was also increased due to the dietary fibers obtained. Another similar study demonstrated that adopting a vegetarian diet also led to an increase in SCFA-producing bacteria, thus contributing to beneficial health effects [33]. Lastly, *Akkermansia* is also associated with positive outcomes in individuals with obesity, improving body fat distribution and reducing fasting triglyceride levels [34].

Hegelmaier et al. (2020) [35] demonstrated the beneficial effects of an ovolactovegetarian diet in patients with Parkinson's disease. Through the consumption of foods rich in fiber, the gut bacteria increased the production of SCFAs, thereby contributing to an improvement in the function of the GM in these patients. Studies indicate that patients with Parkinson's disease have a higher population of bacteria belonging to the Firmicutes phylum and a reduced presence of Bacteroidetes, favoring a state of intestinal dysbiosis [36]. Therefore, the vegetarian dietary pattern helps managing gut dysbiosis by increasing the production of SCFAs which have anti-inflammatory effects [37].

Kahleova et al. (2020) [38] demonstrated that a low-fat vegan diet led to an increase in the abundance of the bacterial species *Faecalibacterium prausnitzii* and a smaller decrease in *Bacteroides fragilis* in the vegan group compared to the control group. Participants assigned to a vegan diet had greater body weight loss, fat mass reduction, visceral fat reduction, and increased insulin sensitivity. Current studies confirm that the consumption of resistant starch is linked to an increase in species producing SCFAs such as *Faecalibacterium prausnitzii*, which degrades starch and other plant polysaccharides, primarily for butyrate production [39, 40].

Like the Mediterranean diet, the vegetarian and vegan diets have shown beneficial effects on the GM, mainly attributed to the increase in species producing SCFAs due to high fiber intake. Additionally, the vegetarian dietary pattern serves as a favorable intervention for individuals experiencing dysbiosis, such as those with Parkinson's disease. Conversely, the vegan diet facilitated an increase in *Faecalibacterium prausnitzii* bacteria species, alongside a reduction in *Bacteroides fragilis* levels, yielding positive results on GM.

The limitations of this study include the absence of a systematic approach in the methodology used and the reliance on a single database. PubMed was selected because it is the leading resource in the biomedical field and encompasses MEDLINE (the National Library of Medicine's journal citation database).

Conclusion

The literature has demonstrated that each dietary pattern exerts distinct effects on the GM, influencing bacterial richness and diversity differently. Notably, only the Western dietary pattern demonstrated adverse effects on GM, attributed to the high consumption of processed foods. Among the studies reviewed, findings regarding the low carbohydrate diet yielded conflicting outcomes. All other dietary patterns exhibited beneficial effects on GM, particularly concerning the management of individuals with gut dysbiosis. The search performed did not identify studies examining the effect of the DASH diet on GM. We suggest that more studies be carried out on this topic, including investigations into the impact of the DASH diet on the GM.

Conflicts of interest

The authors declare no conflicts of interest of any nature.

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Authors' contributions

Project conception and supervision: Lais LL; Data collection and interpretation: Silva MP, Cunha TA; Draft writing: Silva MP; Review and editing, Cunha TA, Coutinho KMD; Critical final revision: Silva MP, Lais LL.

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