

The impact of intestinal microbiota imbalance on the development of obesity

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ABSTRACT

Objective: review current databases to identify the impacts of intestinal dysbiosis on obesity, as well as serve as a pillar for carrying out preventive, diagnostic and therapeutic measures. **Methodology:** this is an integrative review carried out from the collection of data obtained from the SciELO, PubMed, VHL, and LILACS platforms using the descriptors “dysbiosis”, “obesity” and “gastrointestinal microbiome”; Inclusion criteria were: articles published in the last five years (from 2017 to 2022), original articles, meta-analyses, and observational studies (clinical trials and cohort study) and written in Portuguese, English, or Spanish. **Results:** Western diet and use of sweeteners cause anthropometric changes, blood pressure, glucose intolerance, among others, in addition to leading to the prevalence of deleterious bacteria in the body, culminating in obesity and diabetes mellitus; on the other hand, a diet rich in fiber and administration of probiotics can generate beneficial changes in the diversity of the intestinal flora, in addition to combating the inflammatory state generated by obesity.

Keywords: Dysbiosis, Obesity, Gastrointestinal microbiota.

INTRODUCTION

According to the Brazilian Society of Endocrinology and Metabology (SBEM), obesity is a chronic, non-transmissible disease (CND), multifactorial and of complex pathogenesis.¹ It is defined by the accumulation of fat in adipose tissue cells, since the Energy balance has a positive balance, that is, there is a greater acquisition of energy from food to the detriment of its expenditure.² This disturbance in the regulation of energy balance is characterized by excess adiposity and sufficient weight to harm health.

According to data released by the Brazilian Institute of Geography and Statistics (IBGE), in a sample of 108,000 households in the country, the proportion of obese people in the population aged 20 or over reached alarming levels between 2003 and 2019, leaving the mark of 12.2% to 26.8%.³ In this time interval, obesity among men increased from 9.6% to 22.8% and, among women, increased from 14.5% to 30.2%.

It is known that obesity is a predisposing factor for the development of Type 2 Diabetes

Mellitus (DMT2) since the excessive accumulation of body fat is responsible for increased insulin production by the pancreas, leading to the pathogenesis of diabetes.⁴ An Official guideline of the Brazilian Society of Diabetes characterizes DMT2 as a disease of insidious onset and that presents peripheral resistance to insulin, as well as inefficiency of pancreatic beta cells.⁴

Data from the Brazilian Society of Diabetes (BSD) show that 60% to 90% of patients with DMT2 are obese, with a body mass index greater than 30 kg/m², and the incidence is higher after 40 years of age, corroborating the predisposition from obesity to DMT2.⁴ Moreover, in Brazil, every 2 minutes a new case of diabetes is diagnosed, making the country occupy the 4th place among the 10 countries with the highest number of individuals with diabetes.⁴

Studies such as “Microbial dysbiosis-induced obesity: role of gut microbiota in homeostasis of energy metabolism”, demonstrated in animal models that a high-fat diet associated with a dysbiotic intestinal microbiota can influence the development of metabolic diseases such

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as obesity and DMT2 since they act by inducing increased adiposity and poor glycemic control.⁵

The intestinal microbiota refers to the population of microorganisms that inhabit the entire gastrointestinal tract, consisting of trillions of bacteria that the individual acquires throughout its existence, which develop and adapt according to the nutritional and metabolic status of the human organism at each stage of life.⁶ It has a metabolic and protective function, acting in the maintenance of energy homeostasis and host immunity and, therefore, it is considered an endocrine organ.⁶ Thus, it is presumed that quantitative and qualitative changes in their constitution, called dysbiosis, possibly act as an influential factor in the development of metabolic diseases such as diabetes mellitus and obesity, which is characterized by the WHO as a multifactorial global epidemic.⁶

Given this scenario, it is suggested that in addition to the behavioral, genetic, socioeconomic, psychic, and environmental aspects, biological factors related to the disturbance of the intestinal microbiota are linked to the development of obesity and type 2 diabetes mellitus. Thereby, it is important to highlight the need of studies that deepen the knowledge about the intimate relationship between these variables.

Thus, the present work aims to integratively review the available literature on the possible impact of dysbiosis on the development of obesity, in addition to serving as a pillar for optimizing preventive, diagnostic, and therapeutic measures, aiming at improving the quality of life of the population.

METHODOLOGY

The present work, carried out from April 2021 to February 2022, consists of an exploratory study, based on the literature review method with synthesis of evidence structured in six steps: elaboration of the research guiding question; definition of databases and criteria for inclusion and exclusion of studies; assessment of studies included in the review; definition of the information to be extracted from the selected studies; interpretation of results; presentation of the knowledge review/synthesis. In this way, the

guiding question of the research was configured in: What is the evidence identified in scientific studies about the impact of the intestinal microbiota imbalance in the development of obesity?

The identification of scientific evidence was carried out through virtual access to the databases: PubMed® portal, Latin American and Caribbean Literature in Health Sciences (LILACS), Virtual Health Library (VHL), and Scientific Electronic Library Online (SciELO), using the descriptors "dysbiosis", "obesity" and "gastrointestinal microbiome". Several searches were conducted on PubMed at different times; the first took place in August 2021 and the last in February 2023.

Initially, articles published in the last 6 years (from 2017 to 2023) were used as inclusion criteria so that the present work covered up-to-date studies that had the following designs: original articles, meta-analyses, and observational studies (clinical trials and cohort study) related to the focus of the work; and those written in Portuguese, English or Spanish.

Due to the peculiarities of each data platform, the search strategies for the articles were adapted for each one based on the problem in question and the previously established inclusion criteria using the descriptors "dysbiosis", "obesity" and "gastrointestinal microbiome".

RESULTS

During the search, 6 articles were found in the LILACS database, all of which were excluded for not responding to the guiding question. No article was found in the SCIELO database. In the VHL, 819 studies were noted, of which 23 were selected for title and abstract analysis; of these, 17 were excluded for not answering the guiding question, with 6 being included. In 2021, 708 articles were found, of which 295 were pre-selected; of these, 284 were not included because they did not answer the guiding question, because they were review articles or were in Turkish, 11 were selected. In 2022, 887 studies were found, of which 16 articles were pre-selected; of these, 11 were excluded for not meeting the guiding question and 5 studies were chosen. Finally, a new search was carried out in the LILACS, SciELO,

VHL and PubMed databases, covering only studies published in 2023 with the same designs and languages described above, however, no results were obtained that fit the criteria and, consequently, none study was included in this work.

At the end of the search, 22 studies were included in this research; 4 additional references

identified through other sources were also used to make this work. After selecting and analyzing the studies, the information collected from them was defined. Subsequently, the results obtained were interpreted and compared to prepare this knowledge review. Identification, screening, eligibility, and inclusion of articles are shown in Figure 1.

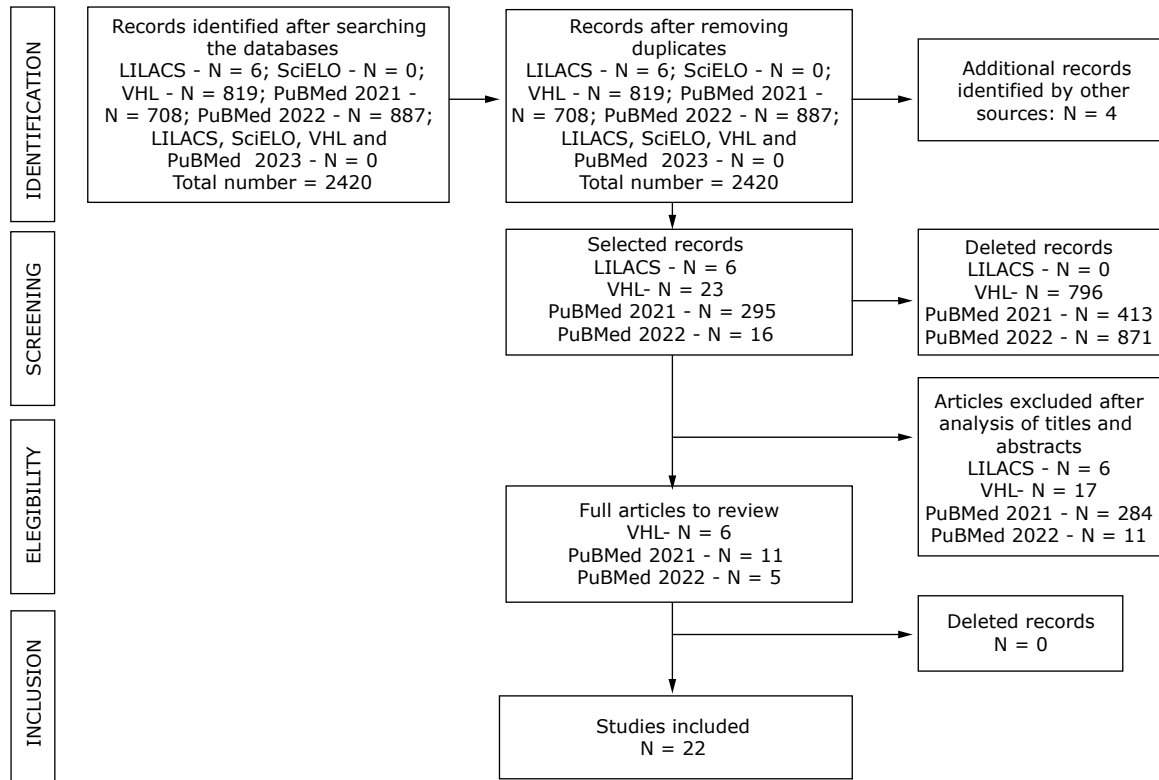


Figure 1: Flowchart representing the identification, screening, eligibility, and inclusion of articles for this review. The impact of intestinal microbiota imbalance on the development of obesity.

The selected studies seek to relate the impact of different types of diet, use of probiotics and chronic diseases to the diversity of the intestinal microbiota. Thus, it was observed that non-Western diets, rich in fiber and natural foods, increase the production of gasses favorable to the organism and lead to a greater diversity of the microbiota, with an increased prevalence of bacteria beneficial to humans, such as *Bacteroides*, *Prevotella* and *Ruminococcus*, *Bifidobacterium*. On the other hand, Western diets, fat stripes, milk formulas, and sweeteners cause a decrease in the

diversity of the microbiota, with a decrease in beneficial bacteria and an increase in pathogenic ones, such as those of the Proteobacteria phylum and the Lachnospiraceae family, leading to the risk of developing obesity and Diabetes Mellitus. Chronic diseases and the use of antibiotics also lead to loss of diversity. Administration of probiotics such as 1-kestose, galacto-oligosaccharides, and Lactobacilli, in turn, restored the variety of the microbiota.

All the 22 studies selected for the preparation of this work, according to the inclusion and exclusion criteria, are presented in Table 1.

Table 1

Authors and general characteristics of the articles targeted by this study.

Author	Kind of study	Main result
Ojo, O., Feng, QQ, Ojo, OO, & Wang, XH 2020	Systematic review and meta-analyses	Fiber diet can follow significantly increase the abundance of <i>Bifidobacterium</i> , total SCFA and glycated hemoglobin.
Wilkins, LJ, Monga, M., & Miller, AW 2019	Cross section	People with chronic diseases show, compared to healthy people, loss of microbiota diversity.
Joseph N., Clayton JB, Hoops SL, Linhardt CA, Mohd Hashim A., Mohd Yusof BN, Kumar S., & Amin Nordin S. 2020	Original article	Gut microbiota can be successfully altered by the use of probiotics, but these changes are distinct between overweight and normal-weight children.
Nardelli C., Granata I., D'Argenio V., Tramontano S., Compare D., Guarracino MR, Nardone G., Pilone V., & Sacchetti L. 2020	Case-control	A significant increase in Proteobacteria and a decrease in Lachnospiraceae (Firmicutes) characterize the microbiota of obese individuals.
Barczyńska R., Litwin M., Sliżewska K., Szalecki M., Berdowska A., Bandurska K., Libudzisz Z., & Kapuśniak J. 2018	Clinical study	The intestinal microbiota of obese and overweight children is significantly different from lean children with respect to short-chain fatty acids and branched-chain fatty acids.
de la Cuesta-Zuluaga, J., Corrales-Agudelo, V., Velásquez-Mejía, EP, Carmona, JA, Abad, JM, & Escobar, JS 2018	Cross section	The Lachnospiraceae family, present in the microbiota of the western population, is associated with an increased risk of cardiometabolic disease and obesity.
Farup, PG, Lydersen, S., & Valeur, J. 2019	Cross section	Sweeteners can antagonize the effects of butyric acid and do not reduce weight in people with obesity.
Hermes G, Reijnders D, Kootte RS, Goossens GH, Smidt H, Nieuwdorp M, Blaak EE, & Zoetendal EG 2020	Cross section	The microbiota of obese and insulin-resistant male individuals have predictive potential.
Nogacka AM, Salazar N., Arboleya S., Ruas-Madiedo P, Mancabelli L., Suarez A., Martinez-Faedo C., Ventura M., Tochio T., Hirano, K., Endo, A., G de Los Reyes-Gavilán, C., & Gueimonde, M. 2020	Experimental study	1-kestose was the fructose oligomer that showed the highest gas accumulation and the highest modulating activity of the microbiota together with GO.
Davis, SC, Yadav, JS, Barrow, SD, & Robertson, BK 2017	Cross section	Consumption of processed food has a strong influence on the structure of the microbiota and was associated with lower species diversity in relation to BMI.
López-Moreno A., Suarez A., Avanzi C., Monteoliva-Sánchez M., & Aguilera M. 2020	Systematic review and meta-analyses	The positive modulation of the microbiota seems to be related to BMI and biomarkers. Due to the small number of studies, it was not clear if they correlate with other glycemic, inflammatory, and gut hormone parameters.
Carrera-Quintanar, L., OrtuñoSahagún, D., Franco-Arroyo, NN, Viveros-Paredes, JM, Zepeda-Morales, AS, & LopezRoa, RI 2018	Systematic review	Knowledge of the study of the microbiota opens the possibility of considering fecal transplantation as a relevant therapeutic alternative for obesity and other treatments for metabolic diseases.
Horvath A, Leber B, Feldbacher N, Tripolt N, Rainer F, Blesl A, Trieb M, Marsche G, Sourij H, & Stadlbauer V. 2020	Randomized controlled trial	Glucose metabolism as a primary endpoint remained unchanged during intervention with a multispecies symbiotic in patients with diabetes. However, symbiotics improved some symptoms and biomarkers of type 2 diabetes and aspects of quality of life.
Janczy A, AleksandrowiczWrona E, Kochan Z, & Małgorzewicz S. 2020	Randomized controlled trial	There were no significant relationships between body mass, BMI, and changes in gut microbiota or zonulin concentrations.
Kassaian N., Aminorroaya A., Feizi A., Jafari P., & Amini M. 2017	Randomized clinical trial	Supplementation of prebiotics and probiotics may be a successful strategy to improve metabolic health, and insulin resistance and prevent T2DM, which may be useful in the management of metabolic disorders in pre-diabetics.

Continue...

Table 1

Continuation.

Author	Kind of study	Main result
Guo Y., Luo S., Ye Y., Yin S., Fan J., & Xia M. 2021	Controlled clinical trial/ Etiology study/ Observational study/ Risk factors	Intermittent fasting induces a significant alteration of the intestinal community and functional pathways in a way that is closely associated with the mitigation of cardiometabolic risk factors.
Ejtahed HS, Soroush AR, Siadat SD, Hoseini-Tavassol Z., Larijani B., & HasaniRanjbar, S. 201	Systematic review	The alteration of the intestinal microbiota after interventions was affected by the basal composition of the intestinal microbiota. Consumption of plants can have beneficial effects in restoring a healthy gut microbiome, in addition to reducing body fat.
Forbes, JD, Azad, MB, Vehling, L., Tun, HM, Konya, TB, Guttman, DS, Field, CJ, Lefebvre, D., Sears, MR, Becker, AB, Mandhane, PJ, Turvey, SE, Moraes, TJ, Subbarao, P., Scott, JA, Kozyrskyj, AL 2018	Controlled clinical trial	Breastfeeding may be protective against overweight, and the intestinal microbiota may contribute to this effect.
Reiter M, Krebs C, Lopes B, Nichelatti B, Moeller F, Screpec I. 2018	Literature review	A decrease in processed foods and an increase in natural foods reduced chronic diseases, intestinal transit, and improved immunity.
Amabebe E, Robert FO, Agbalalah T, Orubu ESF. 2020	Literature review	The synergism between a high-fat diet and dysbiosis leads to increased adiposity and poor glycemic control.
Zhao L, Zhang F, Ding X, Wu G, Lam YY, Wang X, et al. 2018	Randomized clinical trial	Short-chain fatty acids decrease the production of harmful compounds, such as indole and hydrogen sulfide, in addition to improving glycosylated hemoglobin levels.
Cancello R, Turrone S, Rampelli S, Cattaldo S, Candela M, Cattani L, et al. 2019	Cohort study	Diet and probiotics led to a decrease in weight and <i>Collinsella</i> , in addition to an increase in <i>Akkermansia</i> , a mucin degrader with benefits on host metabolism.

DISCUSSION

The intestinal microbiota is made up of trillions of bacteria and has a metabolic and protective function, acting in the maintenance of energy homeostasis and host immunity.⁶ Quantitative and qualitative changes in its constitution are called dysbiosis. According to the articles, it was observed that diet, administration of probiotics, and chronic diseases generate effects on the diversity of the microbiota and may be associated with the development of diabetes and obesity. Western diet, for example, favors the prevalence of *Bacteroides*, *Bifidobacterium*, *Escherichia*, and *Lachnospiraceae*; the latter two are related to increased anthropometric measurements and blood pressure, in addition to inflammation and insulin resistance. The sweetener, in turn, increases the prevalence of *Ruminococcus gnavus* and *Streptococcus* spp., and decreases butyrate production, leading to glucose intolerance, increased

appetite, and weight gain. Consumption of processed food decreases species diversity, while consumption of natural food restores microbiota, reduces body fat, and improves immunity. A high-fat diet generates increased adiposity and poor glycemic control, while a high-fiber diet increases the prevalence of *Bifidobacterium* and the amount of short-chain fatty acids, in addition to improving glycosylated hemoglobin levels. The administration of probiotics, such as 1-kestose and galacto-oligosaccharide, generates an increase in the production of colonic gases and those of the genus *Faecalibacterium*, which decrease the inflammatory state; there is also an increase in *Bacteroides*, responsible for the increase in short-chain fatty acids. Still, regarding probiotics, they generate an increase in the production of colonic and *Faecalibacterium* gases, which decrease the inflammatory state; there is also an increase in *Bacteroides*, responsible for the increase in short-chain fatty acids. Regarding probiotics, they generate an

increase in the production of colonic and *Faecalibacterium* gases, which reduce the inflammatory state; there is also an increase in *Bacteroides*, responsible for the increase in short-chain fatty acids. Regarding probiotics, the *Lactobacillus rhamnosus* causes a decrease in glucose and insulin biomarkers. Finally, individuals with chronic diseases have less diversity in the microbiota, with a decrease in *Bacteroides*, *Prevotella*, *Ruminococcus*, and *Bifidobacterium*, in contrast to the increase in Proteobacteria.

Changes in the microbiota depending on the diet

Changes in the microbiota generated by small dietary changes, such as a high-fiber diet, may be reversible. However, prolonged eating habits, such as a Western diet, can have lasting changes in the intestinal flora.⁷ Studies have shown that the consumption of processed and high-fat foods, present in the Western diet, has more deleterious effects on the diversity of the microbiota than being overweight and obesity.⁷

The fiber-rich diet increases the abundance of *Bifidobacterium* and the total amount of short-chain fatty acids (SCFA), in addition to improving glycated hemoglobin (Hb1Ac) levels.^{8,9} SCFA are formed through bacterial fermentation of dietary carbohydrates and proteins. Most SCFA constituents (95%) are acetate, propionate, and butyrate, the others (5%) are represented by isobutyrate, valerate, isovalerate, and caproate. SCFA act as an energy source for the colonic epithelium and are also responsible for modulating appetite and inflammation. *Bifidobacterium pseudocatenuatum*, an acetate-producing anaerobic bacteria, is one of the most significant SCFA producers. The increase in their population decreases the production of substances such as indole and hydrogen sulfide, which are harmful to metabolism.^{8,9}

The use of sweeteners led to dysbiosis, with a reduction in *Faecalibacterium prausnitzii* and *Bacteroides fragilis*, and an increase in *Ruminococcus gnavus* and *Streptococcus* spp.¹⁰ Intestinal flora imbalance was associated with a decrease in butyrate production. This, in turn, is one of the main components of SCFA and has multiple benefits,

such as reduced appetite, feeling of satiety, reduced insulin resistance, among others. Therefore, its decrease caused glucose intolerance, increased appetite, and weight gain, in addition to neurophysiological and brain dysfunctions.¹⁰

The study that seeks to compare the non-Western microbiota of Colombians with the microbiota of Western populations showed that Colombians have in their microbiota the genus *Treponema* and a large number of bacteria from the Ruminococcaceae family and the genus *Methanobacteriaceae*.¹¹ In the western population, the presence of *Bacteroides*, *Bifidobacterium*, *Escherichia*, and Lachnospiraceae is common, in addition to the abundance of the genus *Barnesiella*. Some members of the Lachnospiraceae family are associated with an increased risk of cardiometabolic diseases, obesity, and type 2 diabetes mellitus, as they cause changes in BMI, waist circumference, blood pressure, among others. The genus *Escherichia* plays an essential role in obesity since lipopolysaccharides present in the outer membrane of these Gram-negative bacteria generate toxicity responsible for inducing inflammation, obesity, and insulin resistance.¹¹ In contrast to bacteria from western populations, the Ruminococcaceae family decreases the risk of cardiometabolic diseases and obesity.¹¹ The abundance of gene *Bifidobacterium* is linked to healthier phenotypes, in addition to improving glucose homeostasis and lipid metabolism and decreasing inflammatory markers.¹²

Consumption of plant-based products can have beneficial effects in restoring a healthy gut microbiome in addition to reducing body fat. High polyphenol supplementation reduced body weight gain in animal studies, inhibited harmful species such as Clostridia and Enterobacteria, and increased beneficial bacteria such as lactic acid and *Akkermansia muciniphila*.¹³

Another study sought to compare the effects of exclusive breastfeeding to those of supplementation with infant formulas in a sample of 1087 children.¹⁴ Children fed exclusively with formula up to 3 months of age were at increased risk of being overweight; from 3 to 4 months of age, a decrease in the abundance of Bifidobacteriaceae and abundance of Enterobacteriaceae was observed. Breastfeeding, in turn, seems to be protective against overweight. Thus, early childhood

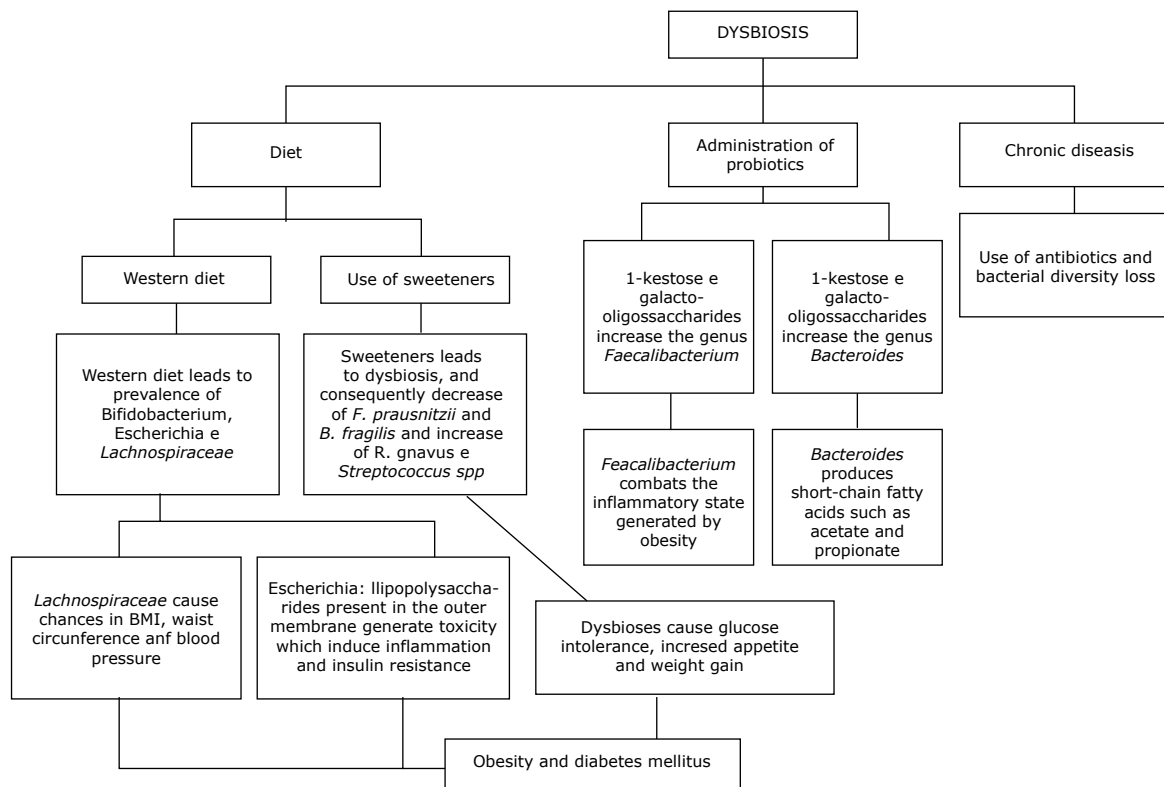


Figure 2: Flowchart representing the main data present in the discussion. The impact of intestinal microbiota imbalance on the development of obesity.

is understood as a critical period in which transient intestinal dysbiosis can lead to an increased risk of being overweight.¹⁴

Finally, one study included adult patients aged 30 to 50 years with metabolic syndrome.¹⁵ From this sample, it was found that intermittent fasting induced significant changes in gut microbiota communities, increased the production of short-chain fatty acids, and decreased circulating levels of lipopolysaccharides. The latter being responsible by the toxicity that induces inflammation, obesity, and insulin resistance.¹⁵

Changes in the microbiota after administration of probiotics

Probiotics are beneficial and harmless microorganisms capable of stimulating the growth of other microorganisms, establishing the balance

of the intestinal microbiota. Among the genera of probiotics, we can mention the *Lactobacillus*, *Bifidobacterium*, *Saccharomyces*, *Streptococcus*, among others.

There are at least 18 comorbidities associated with overweight and obesity, such as type 2 diabetes mellitus, cardiovascular disease, Alzheimer's disease, and cancer. Therefore, obesity can be considered an emerging public health problem, currently affecting more than 24% of children and adolescents.¹⁶ The use of probiotics maintains the balance of the intestinal flora and can help prevent obesity. A study that aimed to compare the effects of using probiotics in a total of 37 children, 20 of them overweight and 17 with normal weight, demonstrated that there were significant impacts on beta diversity, but not on alpha diversity.¹⁶ Beta diversity consists of the difference in composition and species between different sites or samples; alpha diversity is the diversity of

each site or sample, which is related to species richness and taxonomic distribution.¹⁶

Fecal cultures were collected from healthy adults of normal weight and from adults with morbid obesity.¹⁷ These were supplemented with inulin-type fructans (such as 1-kestose, inulin, among others) and galacto-oligosaccharide. The impact of such supplements was monitored by the production of gases and the evaluation of changes in the composition of the microbiota. Colonic gases produced by anaerobic fermentation, such as H₂ and CH₄, can increase anti-oxidation and anti-apoptosis processes, which contribute to the reduction of inflammation.¹⁷ In the context of obesity, an inverse relationship was observed between BMI and the production of these gases. The use of 1-kestose and galacto-oligosaccharides in individuals with morbid obesity was responsible for the increase in the genus *Faecalibacterium*, known to have anti-inflammatory properties, which are essential in combating the inflammatory state generated by obesity. In addition, there was also an increase in the genus *Bacteroides*, responsible for a large production of short-chain fatty acids, such as acetate and propionate. Thus, the mentioned probiotics generated beneficial effects in individuals with morbid obesity by modulating the microbiota and increasing the production of colonic gases.¹⁷

A systematic review was performed based on the pattern of probiotic administration and effective doses for obesity-related disorders according to their ability to positively modulate key biomarkers and dysbiosis.¹⁸ High doses of single or multispecies *Lactobacillus* and *Bifidobacterium* improved related parameters to obesity. Species of different strains of *Lactobacillus rhamnosus*, when administered, caused beneficial effects such as decreased glucose and insulin biomarkers, but without effect on weight.¹⁸ Despite the numerous benefits, inadequate consumption of probiotics can generate undesirable effects on the immune response, generation of genes related to antibiotic resistance, alterations in the integrity of the intestinal barrier, and harmful metabolic activities.¹⁸

In turn, a study using a sample of 60 patients with excess body mass, sought to determine the effects of weight loss through diet and

the use of symbiotics on the intestinal microbiota and the concentration of zonulin (a protein that reversibly regulates intestinal permeability).¹⁹ The use of symbiotics, formed by the association of one or more probiotics with one or more prebiotics, for 3 months increased the diversity of the microbiota and decreased the amount of zonulin in fecal samples. In addition, a diet associated with the use of symbiotics improved the condition of the microbiota and the intestinal barrier.¹⁹

Twenty-six obese patients with type 2 diabetes received daily doses of multispecies symbiotics for 6 months, with the aim of testing their effectiveness on glucose metabolism, intestinal microbiota, intestinal permeability, neutrophil function, and quality of life of these patients.²⁰ During the intervention, glucose metabolism remained unchanged. However, there was an improvement in anthropometric parameters, such as waist circumference, reduction of intestinal permeability after 3 months of intervention by observing serum levels of zonulin, improvement in glycemic control.²⁰

Furthermore, a survey was carried out to determine the effects of probiotic or symbiotic supplementation on metabolic syndrome indices and the composition of the intestinal microbiota over 6 months in pre-diabetic individuals.²¹ Bacteria, Archaea, and Eukarya present in the gastrointestinal tract have been associated with chronic inflammation and may participate in the pathogenesis of obesity and events related to cardiovascular disease. Therefore, early interventions are essential in preventing type 2 diabetes. Still, the potential benefits of using symbiotics in pre-diabetic individuals at high risk of developing type 2 diabetes mellitus and experiencing cardiovascular events have received little attention, requiring further studies.²¹

Changes in the microbiota in the presence of chronic diseases and obesity

Chronic diseases, such as cardiovascular diseases, obesity, asthma, inflammatory bowel diseases, among others, have suffered a significant increase in their prevalence. Genetic and

environmental factors and dysbiosis can contribute to the manifestation of such diseases.²² The microbiota of individuals with chronic diseases, compared to the microbiota of healthy individuals, showed a significant loss of species diversity. The genera *Bacteroides*, *Prevotella*, and *Ruminococcus* showed the highest depletions in sick individuals compared to healthy ones. Furthermore, there was an association between the use of antibiotics and the occurrence of chronic diseases, with the use of such substances associated with loss of bacterial diversity one year after their use.²²

A recent study involving the microbiota of elderly obese women living in Italy demonstrated a decrease in biodiversity, in addition to a reduction in SCFA producers belonging to the Lachnospiraceae family.²³ Furthermore, an inversely proportional relationship was observed between the abundance of Lachnospiraceae and BMI and waist circumference.²³ There was a significant increase in the phylum Proteobacteria in the microbiota of obese people compared to the microbiota of normal-weight subjects.²⁴

In the microbiota of overweight and obese children, there was a predominance of the genus *Clostridium*, while in children with normal weight, these bacteria were reduced by about 14%.²⁵ In the microbiota of children with normal weight, there was a predominance of the genus *Bacteroides* and *Bifidobacterium*, which were decreased by around 20% and 18%, respectively, in the overweight and obese groups. These results indicate that overweight and obese children have a decrease in SCFA concentrations compared to those with normal weight.²⁵

The study of the microbiota and its role in the development of obesity and metabolic disorders opened the possibility of considering it as a potential treatment for obesity and other inflammatory diseases. Numerous studies have been carried out on the intestinal microbiota and its effects on host metabolism.²⁶ However, the relationship between the microbiota and obesity remains complex. A survey includes data from animal models, methodologies, and previous studies to understand the relationship between the intestinal microbiota and metabolic diseases, which allowed consideration of fecal transplantation as a

therapeutic alternative for patients with obesity and metabolic disorders. However, more clinical trials are needed to consider this alternative as safe and effective.²⁶

CONCLUSION

In view of the review carried out, it was observed that diets rich in fiber and non-Western and the use of probiotics can generate beneficial changes in the diversity of the intestinal flora, with an increase in bacteria of the genus *Faecalibacterium* and *Bacteroides* and the Ruminococcaceae family. On the other hand, the use of sweeteners and the Western diet could cause an increase in bacteria that are harmful to the body, such as *Ruminococcus gnavus* and *Streptococcus* spp, and the genus *Escherichia*, respectively. Finally, there was an association between the use of antibiotics and the occurrence of chronic diseases, with this pharmacological class causing a loss of bacterial diversity about a year after its use. In view of the findings, the need for a deeper understanding of the impact of different factors on the intestinal microbiota is emphasized since its imbalance can favor the emergence of numerous metabolic disorders. Thus, in-depth knowledge of the causal factors of intestinal dysbiosis may support the development of health strategies aimed at combating and controlling this condition, as well as the health conditions resulting from it.

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