

THE ROLE OF GUT MICROBIOTA IN OBESITY

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Abstract: Obesity is a disease which is currently one of the most serious problems affecting approximately 650 million people worldwide. Improper lifestyle is considered the primary cause of the disease; however, many other factors contribute to the problem. In recent years, attention has been drawn to the role of gut microbiota in developing and controlling obesity and overweight. Microorganisms in the gastrointestinal tract are responsible for the fermentation of certain nutrients, causing efficient digestion, stimulation of intestinal transit, vitamin production, and modulation of the host's immune system. Numerous studies have demonstrated that gut microbiota composition differs between obese individuals and those with a normal body mass index (BMI). It has also been shown that altering gut microbiota can influence the phenotype of the host organism, promoting metabolic changes, including BMI reduction. Recent studies aimed at using probiotics to modify gut microbiota composition to reduce body weight are still inconclusive.

1. Introduction. 2. Obesity. 3. Gut microbiota. 4. Diet and microbiota. 5. Dysbiosis. 6. Microbiological assessment. 7. Gut microbiota in patients with obesity and normal body weight. 8. Use of probiotics in obese patients. 9. Conclusions. 10. References

Keywords: gut microbiota, obesity, probiotics

1. Introduction

In recent years, the problem of being overweight and obese has been increasing and affecting even younger individuals. This disease is diagnosed in all ages and socioeconomic groups, mainly in developed and developing countries (NCD-RisC 2017). The most common cause of obesity is excessive energy intake compared to its expenditure. Lifestyle factors (such as improper diet and lack of physical activity) play a significant role in the pathogenesis of this phenomenon, along with genetic, socioeconomic, and mental factors. Recently, more attention has been given to the role of gut microbiota in the pathogenesis of obesity, both in diagnosis and treating the disease.

2. Obesity

Obesity is characterized by excessive accumulation of adipose tissue in the body. Due to its close location to internal organs and hormonal activity, visceral fat has

a multifactorial and detrimental impact on the human body (Górska *et al.* 2015). The body mass index (BMI) is the most common parameter for assessing obesity. It is calculated by dividing body mass (in kilograms) by the square of height (in meters). Diagnosis of overweight or distinct degrees of obesity are demarcated according to specified BMI thresholds – Stage I obesity is designated by a BMI of 30–34.9 kg/m², Stage II by 35–39.9 kg/m², and Stage III by a BMI surpassing 40 kg/m². The extreme manifestation – class III obesity – is commonly referred to as “massive obesity” or “morbid obesity”. Obesity can underlie or exacerbate many health problems and diseases, such as hypertension, dyslipidemia, carbohydrate metabolism disorders, obstructive sleep apnea, depression, fertility disorders, and many others (Zhang *et al.* 2023). The scale of the obesity problem is particularly significant in Western countries with particular feeding patterns. It is estimated that the current number of obese individuals worldwide has reached 650 million, and the prevalence of obesity continues to rise, according to

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the World Health Organization (WHO). The significant dynamics of this problem in recent decades are worth noticing. Since 1975, the number of obese patients has tripled, leading to frequent references to the contemporary “obesity epidemic”. It is anticipated that by the end of 2030, one in five women and one in seven men will have obesity-related issues, equivalent to approximately 1 billion people (data from IASO) (Lobstein *et al.* 2022).

Currently, the treatment of obesity primarily focuses on lifestyle changes, followed and accompanied by pharmacological treatment. Recommended interventions include modifying dietary habits, particularly reducing calorie intake, and incorporating physical activity (Bischoff and Schweinlin 2020). Pharmacotherapy has also become available for obesity treatment in the last decades. In the Polish market, there are currently three registered drugs: a combination of bupropion and naltrexone, liraglutide, and orlistat. In the United States of America and some countries in Europe (United Kingdom, Denmark), there are also some other drugs used for obesity treatment, like phentermine or semaglutide (Table I). Nevertheless, the lack of registration of some agents on local markets limits the treatment options (Richelsen *et al.* 2007; Smith *et al.* 2013; Wadden *et al.* 2013; Bello 2019; Azuri *et al.* 2023). For patients with a BMI > 40 kg/m² or a BMI > 35 kg/m² with obesity-related comorbidities (for example, cardiovascular diseases, diabetes, osteoarthritis), bariatric surgery is also a recommended alternative. The most offered and considered safe bariatric surgery is sleeve gastrectomy (SLG) (Rosen *et al.* 2009). The other types of operation, like gastric bypass or ingastric balloon, are less effective or burdened with more possible complications (Lager *et al.* 2017; Singh *et al.* 2020). One of the newest hypotheses regarding obesity suggests the potential therapeutic use of probiotics, which will modify the composition of gut microbiota, improve obesity treatment, and increase the pace of the weight reduction process (Bischoff and Schweinlin 2020).

Table I. Obesity treatment options.

Non-pharmacological treatment of obesity	Pharmacological treatment of obesity
Reduction diet	GLP 1 analogs (liraglutyd, semaglutyd)
Physical activity	Bupropion and naltrexone
Bariatric surgery	Orlistat
	Phentermine

3. Gut microbiota

The gut microbiome is a complex ecosystem with numerous microorganisms inhabiting the human digestive tract. The number of bacteria and fungi in the

gastrointestinal system is immense – it is estimated that the human gut is colonized by approximately 10 billion microorganisms (Karney 2017). Moreover, gut microbiota is also comprised of viruses – DNA and RNA. It is estimated that gut virome even outnumber bacterial cells, including eucaryotic viruses, endogenous retroviruses, bacteriophages, and archaeal viruses. Less than 1% of human gut virome is estimated to be sequenced (Mukhopadhy *et al.* 2019). Metagenomic studies of the human gut microbiota have identified over 1000 species of bacteria (Zhu *et al.* 2010). Until recently, it was believed that the gut microbiota outnumbered the body’s cells by ten. However, current research suggests a more likely ratio of 1:1 (Sender *et al.* 2016). The majority of bacteria in the human intestines belong to four phyla of microorganisms: Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria (according to the International Committee on Systematics 2021: Bacillota, Bacteroidota, Psuedomonadota and Actinomycetota), with Firmicutes and Bacteroidetes being the most dominant bacteria (Pokrzywnicka and Gumprecht 2016; Frank *et al.* 2007, Oren and Garrity 2021)

The gut microbiome begins to form from birth, although some study indicates the presence of gut microbiota during the prenatal period. Bacterial presence has been detected in the placenta and amniotic fluid, characterized by low diversity and a predominance of Proteobacteria. A study noted common gut microbiota characteristics detected in the placenta, amniotic fluid, and infant meconium, suggesting microbial transfer even during the fetal period (Collado *et al.* 2016). The mechanism of this process is not fully explained. It is possible that the transition of bacteria results from the translocation of microbiota located near the mother’s reproductive organs (Panasiuk and Kowalińska 2023). Various factors are believed to influence the composition of gut microbiota. These include breastfeeding/formula feeding, antibiotic therapy administered by the mother during pregnancy, and antibiotic therapy for the child after birth (Karney 2017; Petrov *et al.* 2021). One of the main factors significantly influencing the composition of gut microbiota is the mode of delivery – newborns delivered by cesarean section do not have contact with the maternal vaginal flora, resulting in a higher likelihood of their gastrointestinal tract being colonized by bacteria such as *Clostridium*, *Enterococcus*, *Staphylococcus*, as well as hospital-acquired bacteria present in the air or on the skin of individuals the baby had contact with during the labor procedure. In comparison, stool samples from infants born vaginally predominantly contain *Enterobacterales* and bacteria from the genera *Bifidobacterium* and *Bacteroides*, which naturally come from the mother’s feces (Karney 2017; Panasiuk and Kowalińska 2023). In a study conducted by Mueller *et al.*, 436 mothers and their children

were assessed to examine the influence of the mode of delivery and maternal antibiotic use during pregnancy on the development of obesity in offspring (Mueller *et al.* 2015). The results obtained indicate that children who were exposed to antibiotic treatment during the prenatal period had an 84% higher risk of obesity. Regardless of antibiotic use, it was also demonstrated that the mode of delivery, specifically cesarean section, was associated with a 46% increased risk of obesity in children (Mueller *et al.* 2015). Early colonization of the gastrointestinal tract may have implications for future gut microbiota differentiation and indirectly impact human health, possibly even influencing tendencies toward altered nutrient absorption profiles and, consequently – abnormal body weight.

So far, the dynamics of gut microbiota changes in toddlers are not fully known, mainly as high-interindividual variability is observed. At the age of 3 years, the gut microbiota pattern becomes more adult-like (D'Argenio and Salvatore 2015). The gut microbiota in adults also changes with age. An impact of this is a modification of lifestyle, diet, drugs, some diseases and even environmental factors, e.g. comparing older people living in their own houses with those living in nursing homes, more diversity is observed in the first group (Panasiuk and Kowalińska 2023).

4. Diet and gut microbiota

Diet is one of the fundamental factor influencing gut microbiota composition (Leeming *et al.* 2019). In a study conducted by Wu *et al.*, changes in gut microbiota were examined before and after the introduction of two different diets by study participants. Patients were given a high-fat, low-fibre diet and a low-fat, high-fibre diet. Changes in gut microbiota composition were observed as early as 24 hours after starting the new diet. However, the study results showed significant individual variability in both subgroups despite having the same diet (Wu *et al.* 2011). Differences in metabolism and gut microbiota composition have also been observed between vegetarians and non-vegetarians, suggesting a significant impact of the diet on the gut microbiome (Wu *et al.* 2016). Xiao *et al.* conducted research on the modification of gut microbiota in humans – in 93 volunteers with central obesity, a specific pattern of whole grain and prebiotic-based diet was introduced. This dietary modification resulted in a change in the profile of gut microbiota, with a decrease in opportunistic bacteria (*Enterobacteriaceae* and *Desulfovibrionaceae*) accompanied by an increase in beneficial gut barrier-forming bacteria like *Bifidobacteriaceae* (Xiao *et al.* 2014). Thus, it can be concluded that the percentage of macronutrients, including carbohydrates, protein,

fats, and fibre influences the individual variability of the gut microbiota. Changes in dietary habits towards the unification and westernization of diets are characterized by increased consumption of monosaccharides and fats and reduced fibre intake, which can negatively affect the gut microbiota. It appears that fibre, especially its insoluble fraction, could potentially influence the diversity of the gut microbiota because it undergoes fermentation after consumption, thus providing nutrition for the microorganisms living in the intestines (Chassaing *et al.* 2017). Other functions of gut microbiota include not only the fermentation of certain food components, which aids in efficient digestion and stimulates intestinal transit but also the production of vitamins and immunomodulatory effects that influence the host's immune system (Tokarz-Deptuła *et al.* 2016; DiBaise *et al.* 2008).

On the other hand, some of the gut microbiota and products of their metabolism may have carcinogenic potential (Mima *et al.* 2017; Honjo *et al.* 2023). There is no confirmed explanation of how the microbiome influences cancer development. Still, one of the most probable hypotheses is that microorganisms modify the immune response by producing substances that affect cell division rate and apoptosis (Al-Ishaq *et al.* 2022).

5. Dysbiosis

Dysbiosis disrupts the microbial community (De Gruttola *et al.* 2016). It can be caused by an improper diet, the use of xenobiotics, antibiotics, or groups of medications used in the treatment of chronic diseases (e.g., methotrexate, proton pump inhibitors, non-steroidal anti-inflammatory drugs). Furthermore, disorders of the gastrointestinal tract, intestinal infections (bacterial, viral, or fungal), as well as certain chronic diseases such as liver diseases, metabolic and endocrine disorders, and psychiatric conditions (chronic stress, anxiety disorders) can also influence the abnormal composition of gut microbial (Shanahan and Murphy 2011; Baohong *et al.* 2017). Dysbiosis leads to impaired intestinal barrier functioning, exacerbating local inflammation and increasing systemic inflammation risk (Lin *et al.* 2022). Moreover, repeated exposure to antibiotics during infancy is linked with a higher risk of obesity (Kesavelu and Jog 2023, Duong *et al.* 2022).

6. Microbiological assessment

The standard method for assessing gut microbiota is still the conventional bacterial culture (Karlsson *et al.* 2013, D'Argenio and Salvatore 2015). However, this method is somewhat limited because it may favor

the selection of some species. And in addition, some microbes are uncultivable (D’Argenio and Salvatore 2015). Moreover, genetic analysis methods based on PCR testing are more accurate and preferable due to the many species involved. Such tests allow for a collective identification of the gut microbiota genome based on extracted DNA samples (Sarangi *et al.* 2019). In recent years, a new technology has become preferred – Next Generation Sequencing (NGS). The method represents an innovative approach applied to the sequencing of DNA and RNA, as well as the identification of variants and mutations. NGS can rapidly sequence hundreds or thousands of genes or an entire genome. The identified sequence variations and mutations through NGS are extensively utilized in disease diagnosis, prognosis, therapeutic decision-making, and patient follow-up. Its extensive parallel sequencing capacity opens up new possibilities for personalized precision medicine, simultaneously reducing sequencing costs (D’Argenio and Salvatore 2015, Behjati and Tarpey 2013). It is important to note that the gut microbiome differs depending on the segment of the digestive tract. This is due to varying conditions present in each segment. The main factors determining these changes include the pH of the environment, the speed of peristalsis, and the types of digestive enzymes and intestinal hormones secreted. The most densely colonized segment by microorganisms is the terminal part of the digestive tract – the large intestine (Canny and McCormick 2008).

7. Gut microbiota in patients with obesity and normal body weight

Previous studies indicate that the microbiota initially differs between obese individuals and those with a normal body mass (Ley *et al.* 2006; Dominianni *et al.* 2015; Bervoets *et al.* 2013). These studies showed that individuals with a normal body mass have more Bacteroidetes bacteria than Firmicutes. Examples of these bacteria species can be found in Table II. Additionally, it has been observed that the gut microbiota of individuals with higher BMI is characterized by a lower abundance of *Rikenellaceae*, *Alistipes finegoldii*, and *Alistipes senegalensis* bacteria (Zhernakova *et al.* 2016). In another study, a 20% increase in the abundance of Firmicutes bacteria and a decrease in Bacteroidetes bacteria were

Table II
Examples of Firmicutes and Bacteroidetes affecting the body mass alteration.

Species of bacteria FIRMICUTES (examples)	Species of bacteria BACTEROIDETES (examples)
<i>Faecalibacterium prausnitzii</i>	<i>Bacteroides fragilis</i>
<i>Clostridium</i> spp.	<i>Bacteroides vulgaris</i>
<i>Roseburia intestinalis</i>	<i>Bacteroides uniformis</i>
<i>Blautia obeum</i>	<i>Prevotella</i> spp.
<i>Lactobacillus reuteri</i>	<i>Alistipes finegoldii</i>
<i>Enterococcus faecium</i>	<i>Parabacteroides distasonis</i>
<i>Staphylococcus leei</i>	

associated with an increased energy harvest from food by up to 150 kcal (Jumpertz *et al.* 2011). Furthermore, in individuals whose diet is fibre-rich, their gut microbiota can produce more short-chain fatty acids (SCFA) such as acetate, propionate, and butyrate (Hur *et al.* 2015). The presence of those substances promotes lower weight gain by influencing metabolic pathways and intestinal hormone activity (Hur *et al.* 2015). SCFA, despite being an energy substrate, also influences the regulation of hunger and satiety by affecting hormones responsible for these sensations – mainly ghrelin and peptide YY (Fig. 1). The development of obesity may also be influenced by Pseudomonadota (Proteobacteria) (e.g. family *Enterobacteriaceae*), which are responsible for producing pro-inflammatory substances and predispose to increased energy storage in the form of fat (Rinninella *et al.* 2019; Bai *et al.* 2019; Rizzatti *et al.* 2017).

A study by Kalliomäki *et al.* demonstrated that an abnormal composition of gut microbiota precedes the development of overweight and obesity. The study found that the number of *Bifidobacteria* in fecal samples from infancy was higher in 7-year-old patients with a normal body mass compared to children who are overweight. Additionally, abnormalities were observed in the increased presence of *Staphylococcus aureus* in fecal samples from infancy in patients who were overweight compared to patients with normal weight (Kalliomäki *et al.* 2008).

Turngbauh *et al.* demonstrated that differences in energy extraction from consumed food may depend on the type of gut microbiota. Mice that received transplants of bacteria from obese individuals gained weight

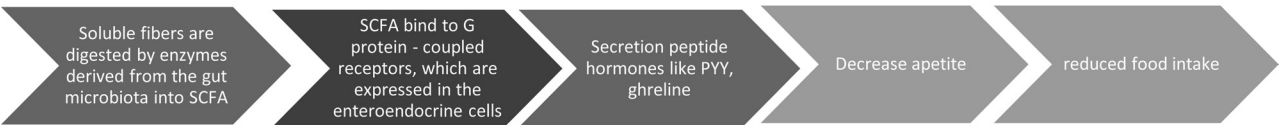


Fig. 1. Correlation of diet fibre intake and SCFA (short-chain fatty acids) production leading to food intake control.

Table III
Bacteria promoting obesity and normal Body mass.

Gut microbiota corresponding with obesity/overweight	Ref	Gut microbiota in normal BMI	Ref
<i>Firmicutes/Bacteroidetes</i> ratio increased	(Turnbaugh <i>et al.</i> 2006)	Supplementation with <i>Akkermansia muciniphila</i> reduced body weight	(Depommier <i>et al.</i> 2019)
Lower level of two species from the family Rikenellaceae, <i>Alistipes finegoldii</i> and <i>Alistipes senegalensis</i>	(Zhernakova <i>et al.</i> 2016)	Increased levels of <i>Bifidobacterium animalis</i> , <i>Lactobacillus paracasei</i> , <i>Lactobacillus plantarum</i>	(Million <i>et al.</i> 2012)
Reduced level of <i>Methanobrevibacter smithii</i>	(Million <i>et al.</i> 2012)	<i>Lactobacillus</i> and <i>Bifidobacterium</i> showed results in reducing body weight	(Álvarez-Arraño <i>et al.</i> 2021)
Higher levels of <i>Lactobacillus reuteri</i>	(Million <i>et al.</i> 2012)	<i>Bifidobacterium infantis</i> , <i>L. acidophilus</i> reducing body weight	(Chang <i>et al.</i> 2011)

more quickly than mice that received gut microbiota transplants from individuals with a normal starting body mass (Turnbaugh *et al.* 2006). In another study on gut microbiota, twins with different body masses (obese vs. normal BMI) were examined. Fecal samples were taken from both female twins and were transplanted into mice. It was followed by introducing those animals to an identical diet containing low fat and high fibre content. The study showed that mice receiving fecal transplants from a woman with a normal BMI had a greater tendency towards a normal body mass than mice receiving gut microbiota from an obese patient (Ridaura *et al.* 2013). Therefore, it appears that gut microbiota may influence the phenotype of the host organism (Ridaura *et al.* 2013; Walker and Parkhill 2013).

In Table III, some examples of bacteria that promote obesity or normal body mass are presented. It is demonstrated that the perturbed ratio of Bacteroidetes/*Firmicutes* phylum is linked with increased intestinal permeability, triggering subsequent inflammation characteristic of diabetes (Iatcu *et al.* 2021). People who suffer from obesity and type 2 diabetes have lower level of *Faecalibacterium prausnitzii* (phylum *Firmicutes*) than individuals with obesity but without diabetes (Pokrzywnicka and Gumprecht 2016). Larsen *et al.* also showed that obesity patients with diabetes mellitus have lower level of *Firmicutes* compared to obesity patients without diabetes (Larsen *et al.* 2010).

8. Use of probiotics in obese patients

Based on the studies conducted so far regarding the correlation of modifying the gut microbiota with body mass reduction, it can be speculated that specific bacterial strains could potentially promote or treat obesity. Therefore, attempts have been made to implement new therapeutic strategies involving probiotics in obesity treatment (Cerdó *et al.* 2019; Abenavoli *et al.* 2019). According to The International Scientific

Association for Probiotics and Prebiotics, probiotics are “live microorganisms that, when administered in adequate amounts, confer a health benefit on the host” (Hill *et al.* 2014). Sources have mainly focused on the bacteria strains of *Lactobacillus* (primarily *L. casei*, *L. gasseri*, *L. rhamnosus*, *L. plantarum*) and *Bifidobacterium* (*B. infantis*, *B. longum*, *B. breve*) (Ejtahed *et al.* 2019). These strains are characterized by low pathogenicity and low antibiotic resistance, making them highly potential with a favorable safety profile (Cerdó *et al.* 2019). Cerdó *et al.* mentioned that in most studies, rodents (both mice and rats) supplemented with these bacterial strains exhibited less weight gain (Cerdó *et al.* 2019). In a survey conducted by Luoto *et al.*, the impact of a perinatal probiotic intervention on the later risk of overweight and obesity in children was evaluated over a 10-year observation period (Luoto *et al.* 2010). The study involved 159 women randomly given probiotics (colony-forming units of *Lactobacillus rhamnosus*) or a placebo for four weeks before the expected delivery date. Anthropometric measurements (height, weight, and BMI) were taken on the newborns at 3, 6, 12, 24 months, and 4, 7, and 10 years. It was found that probiotic administration resulted in a reduction in excessive weight gain until the 24–48-month period, particularly noticeable in children who were overweight. Thus, modifying the maternal gut microbiota during pregnancy may influence the child's growth pattern. In another study, the effects of *Lactobacillus acidophilus*, *Lactobacillus casei*, and *Bifidobacterium bifidum*, given in combination with isoflavones, on weight reduction were assessed (Zhao *et al.* 2012). After the supplementation, a decrease in body weight and a reduction in fat tissue accumulation were observed. However, a similar effect was not achieved with probiotic supplementation alone. The bacterium *Pediococcus pentosaceus* LP28 can also have a beneficial impact on obesity treatment. In a study conducted on obese mice, administration of this strain reduced body weight gain and liver lipid content (Zhao *et al.* 2012). In Table IV,

Table IV
Current research regarding the use of probiotics in body mass reduction

Current research regarding the use of probiotics in body mass reduction	
<i>Bifidobacterium infantis</i> , <i>L. acidophilus</i> ^H	(Chang <i>et al.</i> 2011)
<i>L. acidophilus</i> in combination with <i>L. casei</i> and <i>Bifidobacterium</i> ^H	(Hadi <i>et al.</i> 2019)
<i>Akkermansia muciniphila</i> ^H	(Depommier <i>et al.</i> 2019)
<i>L. curvatus</i> HY7601, <i>L. plantarum</i> KY1032 ^H	(Jung <i>et al.</i> 2015)
<i>Pediococcus pentosaceus</i> LP28	(Zhao <i>et al.</i> 2012) ^M
<i>L. casei</i> , <i>L. gasseri</i> , <i>L. rhamnosus</i> , <i>L. plantarum</i> ^M	(Ejtahed <i>et al.</i> 2019)
<i>Lactobacillus acidophilus</i> , <i>Lactobacillus casei</i> , and <i>Bifidobacterium bifidum</i> were given in combination with isoflavones ^M	(Ali <i>et al.</i> 2004)

M – Mice Studies, H – Human Studies

some examples of probiotics that were studied in body mass reduction are mentioned.

When considering gut microbiota in obesity, attention should also be paid to the bacterium *Akkermansia muciniphila* (Derrien *et al.* 2004). This microorganism primarily resides in the colon’s mucus layer, and its leading role is the breakdown of mucus. It constitutes about 1–4% of the gut microbiota (Macchione *et al.* 2019). The presence of this bacterium is inversely correlated with the body weight of rodents and humans (Everard *et al.* 2013). In a study conducted on obese mice, a lower number of *A. muciniphila* bacteria was observed. Improvements in metabolic health were achieved in these individuals by modifying the gut microbiota and increasing the abundance of *A. muciniphila* (Everard *et al.* 2013). Other sources have shown that supplementation with this bacterium is associated with increased insulin sensitivity and higher levels of propionic acid (Panasiuk and Kowalińska 2023). An increase in the number of these bacteria in the intestines has also been observed during the use of metformin, which enhances

insulin sensitivity (Panasiuk and Kowalińska 2023). Schneeberger *et al.* demonstrated that the number of *A. muciniphila* bacteria depends on the diet. A high-fat diet leads to a decrease in the number of this bacterium in mice. The study also proved that the level of *A. muciniphila* is inversely proportional to certain indicators of insulin resistance and inflammatory markers (Schneeberger *et al.* 2015).

Unfortunately, studies on the impact of probiotics on weight reduction have not always yielded the expected results. In a study on mice subjected to a high-fat diet (HFD), an attempt to use probiotics *Lactobacillus plantarum* DSM 15313 even increased body weight (Cedró *et al.* 2019; Andersson *et al.* 2010). Table V summarizes some studies on the influence of probiotics on body weight.

One potential target of treatment obesity was Fecal Microbiota Transplantation (FMT). This treatment consists of attempting stool of a healthy lean donor and transplanting it into the patient’s duodenum or large intestine using endoscopy methods (Pokrzywnicka and

Table 5
Summary of effects of probiotics on body weight

Source	No. of subjects	Study subject	Duration	Bacteria	Delta weight
1. Depommier <i>et al.</i> (2019)	32	Human	3 months	<i>Akkermansia muciniphila</i>	–2,27 kg +/- 0,92 kg
2. Jung <i>et al.</i> (2015)	120	Human	12 weeks	<i>Lactobacillus curvatus</i> HY7601, <i>Lactobacillus plantarum</i> KY1032	–0,65 kg +/- 0,23 kg
3. Andersson <i>et al.</i> (2010)	20	Mice	20 weeks	<i>Lactobacillus plantarum</i> DSM 15313	+21,5 g +/- 1,1 g
4. Chang <i>et al.</i> (2011)	101	Human	8 weeks	mixture of <i>Streptococcus thermophilus</i> , <i>Lactobacillus acidophilus</i> , <i>Bifidobacterium infantis</i> and extra-ingredients containing <i>Bifidobacterium breve</i> (CBG-C2), <i>Enterococcus faecalis</i> FK-23	–0,24 kg +/- 1,5 kg
5. Yin <i>et al.</i> (2010)	48	Rats	6 weeks	<i>Bifidobacteria</i> M13 –4	+51,72 g
6. Hadi <i>et al.</i> (2019)	60	Human	8 weeks	<i>Lactobacillus acidophilus</i> , <i>Lactobacillus casei</i> , <i>Bifidobacterium bifidum</i> + inulina	–4,01 +/- 4,05 kg

Gumprecht 2016). Sources mentioned that FTM results were slight improvements in insulin sensitivity, lipid metabolism and abdominal adiposity but haven't significantly impacted body weight (Lahtinen *et al.* 2022).

9. Conclusions

The obesity epidemic is a significant problem in modern society. Since the primary causes of obesity are primarily related to unhealthy dietary habits and associated disorders, the fundamental form of treatment involves modifying these factors. The differences in gut microbiota composition between obese and normal-weight individuals suggest that microbiome diagnostics and procedures aimed at altering it may serve as co-factors in obesity treatment. However, a definitive recommendation for this therapy should be withheld due to the inconclusive nature of studies on using specific bacterial strains for treating or assisting in weight management and the lack of high-quality data. Currently, based on the results of the available studies, the use of probiotics in the treatment of obesity can not be recommended. Nevertheless, the potential lying within the study of gut microbiota is substantial and promising, which may lead to a significant increase in interest in this field and a tremendous amount of data soon.

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Conflict of interest

The authors do not report any financial or personal connections with other persons or organizations, which might negatively affect the contents of this publication and/or claim authorship rights to this publication.

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