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THE ROLE OF THE INTESTINAL MICROBIOTA IN THE PATHOGENESIS OF OBESITY: CURRENT UNDERSTANDING AND THERAPEUTIC PERSPECTIVES

Abstract: *One of the major public health issues of the twenty-first century is obesity, which is linked to an increased risk of cardiovascular and metabolic disorders. The gut microbiota's function as a crucial regulator of energy balance has drawn a lot of scientific attention in recent decades. The methods by which the gut microbiota affects the development of obesity are summarized in this article. These mechanisms include energy extraction, the creation of short-chain fatty acids, metabolic endotoxemia, the regulation of the gut barrier, the metabolism of bile*

acids, and the interaction between the stomach and the brain. There is also discussion of the potential for microbiota-oriented treatment approaches.

***Key words**: obesity, gut microbiota, dysbiosis, short-chain fatty acids, metabolic endotoxemia, probiotics.*

***Language**: English*

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Introduction

A chronic metabolic condition, obesity has become an epidemic on a global scale. Over 650 million adults worldwide suffer from obesity, which has more than quadrupled since 1975, according to the World Health Organization [1,2]. Type 2 diabetes, cardiovascular disease, several types of cancer, and a markedly reduced quality of life and life expectancy are all linked to this chronic metabolic disorder [3]. The pathophysiology of obesity has traditionally been understood as an imbalance between energy intake and expenditure brought on by low physical activity, high-calorie foods, and genetics. However, the understanding of the crucial role played by the gut microbiota-a complex ecosystem of bacteria that live in the human gastrointestinal tract-has led to a considerable expansion of this paradigm during the past 20 years.

Trillions of species, including bacteria, viruses, fungus, and archaea, make up the complex and dynamic human gut microbiota. The most researched part of the microbiota is the bacterial component, which comprises over 1,000 distinct species that are only found in the Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria taxa. With around 3 million genes-150 times the number of genes in the human genome-the microbiota (microbiome) collectively create a host organism with vast metabolic capacity [4].

According to current research, the microbiota is a functionally independent "virtual organ" that regulates immune responses, energy metabolism, nutrition metabolism, and neuroendocrine regulation [5,6]. Obesity and associated metabolic problems are directly linked to "dysbiosis," or disruption of its composition and functional activities [7].

Historical facets of researching the connection between obesity and microbiome

Backhed et al.'s groundbreaking study from 2004 showed that, despite consuming more food, germ-free mice had lower body weight and fat deposits than conventional animals. Within two weeks of colonizing germ-free mice with conventional mice's microbiota, the mice's body weight increased by 60% and they developed insulin resistance, demonstrating the microbiota's causative role in regulating energy metabolism [8]. Turnbaugh and colleagues' later research demonstrated that the Firmicutes/Bacteroidetes ratio was changed in genetically obese mice (ob/ob), and that transplanting the microbiota of obese animals to recipients who were germ-free resulted in a more noticeable buildup of fat. The translational importance of these findings was confirmed by the discovery of similar abnormalities in obese humans [9]. The gut microbiota composition of obese and normal-weight people differed significantly, according to parallel investigations conducted on fluid samples. Compared to lean people, obese people showed comparatively low levels of Bacteroidetes and a persistent rise in Firmicutes, according to Ley and co-authors (2006). It's interesting to note that the microbiota's composition somewhat returned to normal when body weight was decreased while following a low-calorie diet, seemingly to match the profile of slim individuals [10].

The main mechanisms of the influence of the intestinal microbiota on body weight Energy release and nutrient enrichment

The gut microbiota's capacity to bind extra molecules from indigestible dietary components is one of the basic ways it affects energy balance. In order to break down complex plant-derived polysaccharides (dietary fiber) that are resistant to the action of efficient human enzymes, the microbiota has developed a set of enzymes [9].

According to research findings, obese people's microbiota has a higher capacity to obtain energy from food. Turnbo and his colleagues have demonstrated that the microbiota of obese mice has an enriched gene profile for production and facilitates more effective dietary calorie consumption [10].

Mice colonized with microbiota from fat people had lower residual energy content in their feces, indicating more thorough calorie extraction in the intestine, according to calorimetric investigations of fecal matter [11]. Additionally, obese people have higher energy extraction efficiency. The quantity of calories absorbed from food and the degree of increase in Firmicutes content, which was linked to a more effective energy supply, were found to be correlated with changes in the microbiota's composition by Jumpertz and colleagues [12]. People with "obesogenic" microbiota can therefore manufacture and absorb more calories even when they eat the same quantity of food, which leads to excessive weight gain.

Short-chain fatty acids (SCFAs)

Short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate, are produced when bacteria ferment food fiber in the large intestine. These fatty acids are important mediators of the relationship between the host's metabolism and the microbiota [13]. SCFAs have a variety of roles and affect energy homeostasis in different ways. First, up to 10% of the daily calories consumed by humans come from SCFAs, which aid in the synthesis of energy [20]. While acetate and propionate are absorbed into the portal stream and metabolized in the liver and peripheral organs, butyrate is the conventional energy source for colonocytes. Obese people may have a favorable energy balance due to increased production of SCFA-producing microbiota [14]. Second, the intestinal epithelium, muscular tissue, immunological cells, and other tissues contain distinctive G protein-coupled receptors such GPR41 (FFAR3) and GPR43 (FFAR2), which are activated by GCCs [16].

Intestinal hormones, including as glucagon-like peptide-1 (GLP-1) and peptide YY (PYY), which control hunger, satiety, and insulin secretion, are modulated when these receptors are activated [17].

It's interesting to note that SCFAs have a dual, context-dependent function in controlling body weight. On the one hand, lipogenesis and fat storage may be encouraged by excessive acetate synthesis [15]. Propionate and butyrate, on the other hand, offer advantageous metabolic benefits, such as decreased hunger, enhanced insulin sensitivity, and anti-inflammatory properties [18]. According to research on animals, feeding butyrate to obese mice results in weight loss and a stable metabolic profile [14].

Inflammation and metabolic endotoxemia

One of the hallmarks of obesity and metabolic syndrome is chronic low-intensity feeding, and the gut microbiota is essential for both starting and sustaining this inflammatory state. The occurrence of metabolic endotoxemia, initially reported by Kani et al. [19], is a crucial mechanism.

Gram-negative bacteria's cell walls include lipopolysaccharide (LPS), which is a powerful stimulating agent. LPS is translocated into the systemic circulation and causes metabolic endotoxemia when coronary intestinal permeability (increased intestinal permeability) is disturbed, which is frequently seen in dysbiosis [19]. Increased levels of circulating LPS cause immune cells and adipocytes to activate their Toll-like receptors 4 (TLR4), which sets off a chain reaction of pro-inflammatory signals that results in the release of cytokines like TNF-α, IL-6, and IL-1β [20].

According to experimental research, mice given low doses of LPS over an extended period of time replicate the primary characteristics of obesity, such as increased body weight, adipose tissue, insulin resistance, and solid liver infiltration. On the other hand, mice lacking TLR4 were shielded against obesity and metabolic disorders brought on by food. Humans who are obese have higher levels of systemic inflammatory markers including circulating LPS [20]. A relative rise in LPS-producing bacteria and a decline in intestinal barrier-strengthening bacteria, like Akkermansia muciniphila, are signs of dysbiotic microbiota in obesity [21].

Control of the intestinal barrier

One important measure of the extent of bacterial translocation and metabolic endotoxemia is the intestinal barrier's integrity. Through a number of ways, the intestinal microbiota is essential to preserving the intestinal barrier function [22]. Some commensal bacteria, particularly those that produce butyrate, maintain intimate contact with epithelial cells, induce goblet cells to create mucin, and regulate the immunological response. Particularly advantageous effects on the intestinal barrier and metabolism have been shown for A. muciniphila, a Gram-negative bacteria that colonizes the intestinal mucous layer [23]. Research has demonstrated an inverse relationship between body weight, obesity, and metabolic diseases and the relative content of A. muciniphila. The metabolic profile persisted, body weight decreased, secretion decreased, and the intestinal barrier was restored when A. muciniphila was added at certain levels. The endocannabinoid system is modulated, tight junction proteins are expressed more frequently, and mucin synthesis is stimulated [21].

Pilot investigations have demonstrated that adding pasteurized A. muciniphila to patients with metabolic syndrome and excess weight in humans results in decreased cholesterol, activity indicators, and prolonged insulin sensitivity [23].

The metabolism of bile acids

Historically, bile acids have only been thought of as short-term lipid digestion and absorption detergents. But it has recently been established that bile acids serve as crucial signaling molecules that control body weight, energy expenditure, and the metabolism of fats and carbohydrates [24, 25]. By deconjugating bile acids and changing primary bile acids—which are produced in the liver—into secondary bile acids, the gut microbiota plays a crucial part in the metabolism of bile acids [17]. Certain nuclear receptors, such as farnesoid X receptors (FXR) and Takeda receptors associated with G protein 5 (TGR5), which control the expression of genes involved in glucose, lipid, and energy metabolism, are activated by these altered bile acids [26].

TGR5 activation in muscles and brown adipose tissue promotes thermogenesis and energy expenditure, which aids in weight loss [2]. Furthermore, intestinal L cell TGR5 activation

promotes GLP-1 production, which enhances satiety and glycaemic control [17].

Obesity-related dysbiosis is linked to poor bile acid metabolism, which may exacerbate metabolic diseases. Bile acid pools can return to normal and metabolic parameters can be improved by restoring the normal microbiota composition through dietary changes or probiotics [27, 28].

The brain-gut axis

As the gut-brain axis spreads, the gut microbiota actively communicates in both directions between the central nervous system and the gastrointestinal tract [28, 30]. Numerous channels, including as the vagus nerve, immunological signals, gut hormones, and neuroactive metabolites, are involved in this communication.

Serotonin, dopamine, γ-aminobutyric acid (GABA), noradrenaline, and other neurotransmitters and neuroactive substances can be produced or their synthesis modulated by the microbiota [31]. In the colon, enterochromaffin cells produce about 90% of the body's serotonin under the influence of microbial metabolites [29].

The blood-brain barrier can be crossed by CCP, particularly acetate and propionate, which can then influence the activity of neurons in the hypothalamus, a crucial organ for controlling hunger and energy balance. Acetate administered centrally decreases food intake by stimulating anorexigenic neurons, according to animal studies [15].

Furthermore, the microbiota controls the release of intestinal hormones such GLP-1, PYY, ghrelin, and leptin that control hunger and fullness [32]. Impaired secretion of these hormones is linked to dysbiosis in obesity, which may lead to positive energy balance and hyperphagia [23].

Intestinal microbiota characteristics in obesity

Complex taxonomic and functional alterations that impact the species composition of microorganisms as well as their metabolic activity characterize the gut microbiota in obesity. The development and maintenance of metabolic diseases are greatly aided by these alterations, which show a breakdown in the symbiotic interaction between the microbiota and the host organism [33, 34].

Reduced diversity of microorganisms

A decrease in α-diversity, which reflects the quantity and uniformity of bacterial taxonomic distribution in the colon, is one of the most frequently repeatable features of the microbiota in obesity. The functional stability of the microbial ecology is reduced in obese people due to a decline in commensal species and the predominance of a small group of bacteria [22].

Increased intestinal permeability, chronic low-intensity inflammation, dyslipidemia, and more severe insulin resistance are all linked to a decline in microbial diversity. Furthermore, a reduction in β-diversity suggests that comparable "dysbiotic" microbial profiles are formed in many obese patients, indicating the existence of shared pathophysiological pathways [35].

Changes at the phylum level

Patients with obesity frequently exhibit a rise in the relative proportion of Firmicutes and a fall in Bacteroidetes at the level of major bacterial phyla, which raises the Firmicutes/Bacteroidetes ratio. By enhancing the enzymatic pathways for the breakdown of complex carbohydrates, this change is linked to the microbiota's improved capacity to extract energy from food [22]. Since some population studies have not supported this pattern, it should be noted that this ratio is not a universal biomarker of obesity. This demonstrates how the microbiota varies greatly from person to person and how lifestyle, nutrition, and genetics affect its makeup [36].

Pro-obesity and protective taxa of the intestinal microbiota

Gram-negative microorganisms with high lipopolysaccharide-producing activity, which contributes to the formation of metabolic endotoxemia, activation of the innate immune response, and maintenance of chronic low-intensity inflammation [38], some members of the genus Lactobacillus (particularly Lactobacillus reuteri, which has a context-dependent effect on energy metabolism), and bacteria of the genera Clostridium and Staphylococcus [37] are among the microbiota in obesity, which is characterized by systemic taxonomic shifts reflecting the predominance of microorganisms associated with a pro-inflammatory metabolic profile and pro-obesity. At the same time, a metabolically favourable, "healthy" phenotype is characterised by a relative enrichment of the intestinal ecosystem with taxa such as Akkermansia muciniphila, a specialised mucin-degrading bacterium that plays a key role in maintaining the integrity of the intestinal barrier and modulating inflammatory processes [39], Faecalibacterium prausnitzii, one of the dominant producers of butyrate, which has pronounced anti-inflammatory, insulin-sensitising and immunoregulatory effects, as well as representatives of the Christensenellaceae family [40], which are characterised by a high degree of heritability and a stable inverse association with body mass index, visceral obesity and the risk of developing metabolic disorders [41].

Functional changes in the microbiota

The intestinal microbiota in obesity is marked by significant functional alterations that represent a

change in its metabolic capability towards more effective energy extraction and use, in addition to noticeable taxonomic changes [42]. According to metagenomic and metabolomic research, there is an increase in the enzymatic breakdown of complex dietary polysaccharides, an enrichment of microbial genes involved in lipid and carbohydrate metabolism, and the biosynthesis of short-chain fatty acids with a relative predominance of acetate over butyrate. The production of metabolites with anti-inflammatory and barrier-strengthening qualities, especially butyrate, is also declining. This results in increased intestinal permeability, a disturbance of energy homeostasis, and the activation of systemic low-intensity inflammation, all of which are important factors in the pathophysiology of obesity and related metabolic disorders [43].

Key microbial markers of metabolic health

Akkermansia muciniphila, Faecalibacterium prausnitzii, and members of the Christensenellaceae family are thought to be the most consistent and promising microbial markers of a metabolically healthy phenotype based on a combination of clinical and experimental findings. Their decrease in obesity is a result of both an imbalance in the microbial population and the loss of defense mechanisms that maintain immunological and energy homeostasis [39, 40, 41].

Even while research on the gut microbiota's role in the pathophysiology of obesity has advanced significantly, certain basic features are still not well understood. Complex relationships between the microbiota, host metabolism, and the onset of obesity are shown by current research; nevertheless, the data's mostly associative character restricts their clinical interpretation and usefulness [45]. First, it is still unknown how the gut microbiota contributes to the development of obesity. We are unable to ascertain whether metabolic illnesses are the cause or result of increased body weight because the majority of research merely show correlations between changes in microbiota composition and these conditions. Our knowledge of the dynamics of the microbiota at various phases of the development of obesity is severely limited by the paucity of longitudinal and interventional investigations in humans [46].

Second, because of the significant inter-study variability, the use of prominent taxa as universal indicators of obesity is still debatable, even in light of the observed shifts in their ratio [47]. Because their effects rely on the metabolic context, the significance of microbial metabolites, such as secondary bile acids, lipopolysaccharides, and short-chain fatty acids, is also unclear [47].

Moreover, little is known about the molecular mechanisms underlying the interactions between the microbiota and the host that control insulin resistance, inflammation, and energy metabolism. More molecular clarification is needed regarding the microbiota's suspected role in immunological and endocrine modulation [48]. Furthermore, the construction of universal microbiome models of obesity and the extrapolation of results are greatly complicated by the considerable interindividual heterogeneity of the microbiota, which is caused by diet, age, genetic, and ethnic factors [49]. Long-term cohort studies are necessary since there is a lack of information on the long-term sustainability of microbiome changes and the part early microbiome programming plays in the development of adult obesity [49].

A crucial precondition for the creation of efficient and individualized methods for the prevention and treatment of obesity is the identification of information gaps, which highlight the need for thorough multidisciplinary research integrating metagenomic, metabolomic, and clinical approaches.

Therapeutic strategies aimed at modulating the microbiota by Probiotics

Probiotics are live microorganisms that, when provided in sufficient quantities, positively influence the host's health and are seen as a potential approach for rectifying intestinal dysbiosis and regulating body weight [45,46]. Multiple experimental research in animal models and clinical trials in people have evidenced the efficacy of specific probiotic strains concerning obesity and related metabolic disorders. Specifically, anti-obesity properties have been recognized in some strains of Lactobacillus and Bifidobacterium. The application of Lactobacillus gasseri correlated with a decrease in visceral adipose tissue and overall body weight, Lactobacillus plantarum enhanced metabolic parameters and diminished systemic inflammation, whereas Bifidobacterium breve and B. longum exhibited the capacity to decrease fat mass and enhance glycaemic control. Akkermansia muciniphila is notably significant, as numerous studies demonstrate its substantial beneficial impact on intestinal barrier integrity and the body's metabolic profile [47].

The mechanisms by which probiotics operate are multifaceted, encompassing competitive inhibition of pathogenic microorganisms, fortification of the intestinal epithelial barrier and its permeability reduction, modulation of the immune response with diminished pro-inflammatory cytokine production, augmentation of short-chain fatty acid synthesis and other biologically active metabolites, as well as influence on bile acid metabolism and regulation of gene expression pertinent to lipid and carbohydrate metabolism [45]. Simultaneously, it is imperative to underscore that the effects of probiotics are completely strain-specific, and not all probiotic microorganisms exhibit anti-obesity properties. Furthermore, in specific instances, particular

Lactobacillus strains may facilitate weight growth contingent upon physiological and nutritional factors. This situation underscores the necessity for meticulous selection, molecular characterization, and clinical validation of probiotic strains prior to their application as a therapeutic intervention for obesity management [48].

Prebiotics and dietary fibers

Prebiotics are indigestible food constituents that selectively promote the growth and/or metabolic activity of the intestinal microbiota, regarded as an efficient non-pharmacological method for its manipulation. The primary prebiotic substrates comprise dietary fiber, such as inulin, fructooligosaccharides, galactooligosaccharides, and resistant starch, which operate as a nutritional source for commensal microbes in the colon. The beneficial effects of prebiotics are achieved through various interconnected pathways. Initially, they advocate for the targeted enhancement of metabolically significant bacteria, including Bifidobacterium, Lactobacillus, and Akkermansia muciniphila, resulting in the reestablishment of microbial equilibrium. The fermentation of prebiotic fibers results in an elevated generation of short-chain fatty acids, chiefly butyrate, which possesses significant anti-inflammatory and barrier-enhancing attributes. Simultaneously, there is a reduction in the pH of the intestinal contents, which establishes adverse conditions for the proliferation of pathogenic microbes, alongside an increase in fecal volume and enhanced intestinal motility.

Furthermore, prebiotics affect the neuroendocrine regulation of energy metabolism by altering the secretion of intestinal hormones such as glucagon-like peptide-1 (GLP-1) and peptide YY (PYY), thereby enhancing satiety, diminishing appetite, and lowering food intake.

Clinical studies indicate that the consistent incorporation of prebiotics into the diet may result in mild weight reduction, enhanced glycaemic regulation, and decreased systemic inflammation in overweight and obese populations. Cani and collaborators specifically shown that the incorporation of inulin-type fructans enhances the relative abundance of Akkermansia muciniphila and correlates with improved metabolic parameters in obese individuals [47].

Faecal microbiota transplantation (FMT)

Fecal microbiota transplantation (FMT), which entails the transfer of fecal matter from a healthy donor to a recipient, is the most extreme and direct approach of altering the intestinal microbiota. This method has shown significant clinical effectiveness in treating recurrent Clostridium difficile infection; nevertheless, its application in obesity and related metabolic disorders is presently in the first phases of research. Results from pilot clinical investigations in people suggest the potential efficacy of FMT, although remain inconclusive. A study by Vrieze et al. shown that microbiota transplantation from lean donors to males with metabolic syndrome resulted in a statistically significant enhancement in insulin sensitivity six weeks post-procedure. The long-term consequences of this intervention were constrained, as the metabolic enhancements attained were not maintained without subsequent transplants. The efficacy of FMT varied considerably based on the specific traits of both the donor and recipient, encompassing the initial microbiota composition, metabolic condition, and lifestyle factors [51]. Notwithstanding the potential of this method, the application of FMT in obesity treatment is fraught with many limits and problems. This encompasses the necessity for stringent, multi-phase donor screening to avert the spread of infectious pathogens, significant interindividual heterogeneity in clinical responses, inadequate investigation of long-term safety, and ethical and regulatory concerns. A further issue is the absence of cohesive and standardized protocols for FMT. Consequently, while its considerable therapeutic promise, the application of faecal microbiota transplantation for obesity treatment necessitates additional extensive, randomized, controlled clinical trials to assess its efficacy, refine methodologies, and verify long-term safety [51,52,53].

The effect of diet on the gut microbiota

Diet is one of the most potent and direct elements that has the ability to modulate the composition of the gut microbiota as well as the functional qualities of what it produces. A variety of dietary patterns and individual nutrients each have their own unique impacts on the microbiota and the metabolic status that is related with one another.

It has been found that the Mediterranean diet, which is characterized by a high content of dietary fiber, polyphenols, and unsaturated fatty acids, is associated with increased microbial diversity, an increase in the number of short-chain fatty acid (SCFA) producers, a decrease in the proportion of bacteria that promote inflammation, and improved metabolic parameters [59].

A high-fat diet, sometimes known as the "Western diet," is associated with a reduction in the diversity of microorganisms, an increase in the number of Gram-negative bacteria and endotoxin levels, a reduction in the generation of butyrate-producing bacteria, and a disruption in the integrity of the intestinal barrier [60]. A diet that is mostly composed of plant foods has been shown to improve the variety of microbiota, boost the production of short-chain fatty acids (SCFA), and reduce levels of trimethylamine N-oxide (TMAO), a metabolite that has been linked to an elevated risk of cardiovascular disease [59, 60]. In the recent years, there has been a

significant amount of focus placed on the impact that artificial sweeteners have on the microbiota. According to the findings of a study conducted by Suez and colleagues, the consumption of saccharin, sucralose, and aspartame can lead to dysbiosis of the intestinal microbiota and decreased glucose tolerance in both mice and humans. This alteration in the microbiota is the mechanism that causes these effects.

Therefore, nutrition is an important tool for the prevention and repair of metabolic disorders since it has a significant impact on the composition of the gut microbiota as well as the functional condition of the species that lives there.

Existing constraints and deficiencies in understanding

Notwithstanding considerable advancements in comprehending the function of gut microbiota in body weight management, numerous unsolved inquiries and methodological obstacles persist [61]:

1. Causal links: The majority of human research are observational, complicating the establishment of causal relationships between microbiome and obesity. The relationship between dysbiosis and obesity remains ambiguous regarding causation and outcome.

2. Individual variability: The microbiota's composition exhibits significant interindividual heterogeneity, complicating the identification of universal indicators and treatment targets [62,63].

3. Functional characterization: Additional research is required to comprehend the functional capacities of the microbiota, rather than solely its taxonomic composition. Metagenomic, metatranscriptomic, and metabolomic methodologies may yield a more comprehensive understanding [64].

4. The molecular mechanisms by which certain bacteria affect human metabolism necessitate additional investigation [55, 57].

5. Durability of intervention efficacy: The majority of research on probiotics, prebiotics, and dietary modifications is of a short-term nature. Extended investigations are required to evaluate the sustainability of effects [55, 56].

6. Standardization of methodologies: The absence of standardized microbiota analysis techniques, bioinformatic strategies, and clinical protocols complicates the comparison of outcomes across studies [54].

7. Personalized approaches: The formulation of tailored techniques for microbiota modulation, including individual features (genetics, baseline microbiota composition, food, lifestyle), is a significant topic for future research [65].

CONCLUSION

The gut microbiota is a crucial regulator of energy homeostasis and metabolic functions in the body, significantly contributing to the development of obesity. Recent data suggest that dysbiosis, defined as an alteration in the composition and functional activity of the microbiota, correlates with heightened energy extraction from food, variations in short-chain fatty acid production, metabolic endotoxemia, compromise of intestinal barrier integrity, bile acid imbalance, and disruption of the gut-brain axis. Collectively, these processes facilitate the onset of excessive body weight, insulin resistance, and persistent low-grade inflammation.

The characterization of the microbiota in obesity demonstrated a reduction in bacterial diversity, an alteration in the Firmicutes/Bacteroidetes ratio, a prevalence of pro-obesity and pro-inflammatory taxa, and a decline in the quantity of metabolically protective microorganisms, including Akkermansia muciniphila, Faecalibacterium prausnitzii, and members of the Christensenellaceae family. These alterations are associated with functional modifications in the microbiota, encompassing enhanced energy extraction and diminished synthesis of barrier-strengthening and anti-inflammatory compounds.

Therapeutic approaches designed to modify the microbiota, such as probiotics, prebiotics, dietary modifications, and fecal microbiota transplantation, demonstrate potential for rectifying dysbiosis and enhancing metabolic indices. It is essential to take into account the strain specificity of probiotics, the particular characteristics of the microbiota, and the insufficient data regarding the long-term efficacy of FMT. Diet is a significant element in influencing the microbiota. Mediterranean and plant-based diets enhance microbial diversity and the synthesis of advantageous metabolites, but Western diets and artificial sweeteners may induce dysbiosis and metabolic problems.

Notwithstanding considerable advancements in microbiota and obesity research, persistent challenges endure, such as causal linkages, interindividual variability, functional mechanisms of microbial action, long-term efficacy of therapies, and methodological standardization. The development of personalized strategies for regulating the microbiota, considering the genetic, metabolic, and nutritional traits of each patient, is a viable avenue.

Consequently, the gut microbiota becomes a prospective therapeutic target for the prevention and treatment of obesity. Additional clinical and experimental investigations are required to establish safe, effective, and personalized strategies for microbiota modulation that can enhance metabolic health and alleviate the prevalence of obesity in the community.

Conflict of Interest

The author declares that there is no conflict of interest regarding the publication of this scientific review article.

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