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How to feed your microbiome? The role of dietary fibres in shaping microbiome and host health

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Abstract. Feeding our microbiome involves understanding the complex interactions between diet and diverse microbial communities residing in the human gut. The gut microbiota plays a crucial role in maintaining health, and its composition can be influenced by dietary components such as dietary fibres. Therefore, this article presents knowledge on the relationship between different diets and the microbiome and focuses on the current understanding of dietary fibres and their role in shaping the microbiome. The reader will gather information about the role of the microbiome in health and disease status and the composition of the eubiotic and dysbiotic microbiota. Finally, this article focuses on microbial secondary metabolites, particularly short-chain fatty acids, with outstanding effects on health status.

Keywords and phrases: polysaccharides, oligosaccharides, prebiotic, eubiosis, dysbiosis, short-chain fatty acids

1. Introduction

The human microbiome is defined as a characteristic microbial community (viruses, bacteria, and fungi) residing in the human body. The aim of this article is to provide an overview of the current understanding of the role of nutritional fibres in shaping the microbiome and the role of the microbiome in health maintenance.

The question of how to feed our microbiome has become a burning issue today, both in the social and scientific areas. Even though the role of dietary fibre (DF) was recognized in the 1950s, the way we approach the subject today has changed considerably due to its role in shaping the microbiome. Since 2016, when the Human Microbiome Project ended (*NIH Human Microbiome Project – About the Human Microbiome*, n. d., *Lloyd-Price et al.*, 2017), knowledge regarding the composition and role of the human microbiome in our health/disease status has increased enormously. This current knowledge rewrites our understanding of fibres and their role in shaping the microbiome. A healthy microbiome, through its secondary metabolites (short-chain fatty acids), helps maintain a healthy status (*Cronin et al.,* 2021). However, the complexity of these interactions poses challenges, and future perspectives in this field would be personalized dietary recommendations to optimize health outcomes.

2. Nutritional role of dietary fibres

To understand the nutritional role of dietary fibre, we need to look into its history. Hippocrates was the first to recognize the benefits of dietary fibre in 430 BC; unfortunately, this discovery was forgotten at that time (*McBurney et al.*, 2019). As a term, DF first appeared in the 1950s. Initially, it was connected to substances derived from plant cells; later, it was specified that this meant plant-derived polysaccharides are indigestible by humans and cannot be absorbed through the gastrointestinal tract. Gradually, it was found that dietary fibres have more than just nutritional benefits (*Kshirsagar et al.*, 2020).

Modern thinking recognizes that the quality and type of DF influence the gut microbiome, thus affecting the health of the host (*McBurney et al.*, 2019). We know now that DF, consisting of polysaccharides, lignin, and oligosaccharides, helps maintain gut health by aiding digestion, reducing constipation, and other beneficial factors. DF support beneficial gut bacteria by serving as prebiotic substrates (*Timm & Slavin*, 2023). There are several other known health benefits, including lowering plasma lipid levels, stabilizing blood sugar levels, and reducing inflammation. We can also mention protection against diseases such as stroke, type 2 diabetes, and even cancer (*Kim & Je*, 2014). However, they are important in regulating appetite, and studies have shown their role in increasing satiation and reducing hunger, resulting in reduced energy intake and weight loss (*Akhlaghi*, 2024).

In addition to dietary fibre, other nutrients are also important. Because nutrition recommendations are related to calorie intake, they differ between sexes and age classes. The recommended daily intake of dietary fibre is 38 g/day for healthy men, and 25 grams g/day for healthy women (*Slavin*, 2005). The recommendations of Nordic Nutrition in 2012 for healthy people are similar to the previously mentioned amounts, more precisely the same for women and 35 g/day for men (*Carlsen & Pajari*, 2023). According to the United States Institute of Medicine, the current recommended daily dietary fibre consumption for different age classes ranges from 14 to 20 g/day for children, 22–30 g/day for adolescents, and 25–38 g/day for the elderly (*Yusuf et al.*, 2022).

Diet and eating habits have a major impact not only on health but also on the quality of life of the host, which is influenced by geographical, religious, ethical, and cultural factors. Today, one of the most recognized diets is the Mediterranean diet, which is popular for its health benefits such as reducing the risk of infectious diseases. The diet focuses on the consumption of vegetables, fruits, whole grains, nuts, low dairy consumption, moderate fish consumption, and unsaturated fats such as olive oil (*Klement & Pazienza*, 2019). Similarities can be drawn between a vegetarian diet, which typically avoids meat, poultry, and fish, and a vegan diet, which avoids all animal products (*Key et al.*, 2006).

Overall, we could say that despite the initial recognition, which proved difficult, and that the thinking of the time ignored Hippocrates's observations on the physiological effects of dietary fibre (*McBurney et al.*, 2019), today it is becoming an important and essential part of understanding more both personalized diets and research topics.

3. Classification of dietary fibres

Dietary fibres can be identified as carbohydrate polymers and oligomers, which are comprised of sugar units such as glucose, fructose, galactose, xylose, and arabinose (*Cantu-Jungles et al.*, 2021). The main part of plants that has an impact on health is their cell walls. These supramolecular cell walls mostly contain cellulose, hemicelluloses, pectin, and lignin (*Augustin et al.*, 2020). The overly simplistic method for classifying dietary fibres is either soluble or insoluble. This kind of comparison comes from its physicochemical properties, based on the fibre content analysis of foods (*Puhlmann & de Vos*, 2022). One of the most studied soluble fibres in this field is inulin-type fructooligosaccharides (FOS). Additionally, some new studies have also proven that insoluble fibres, such as chitin-β-1,3 glucan, can have a huge impact on the intestinal tract (altering the *Clostridium* cluster) (*Cantu-Jungles et al.*, 2018). However, the physicochemical characterization of fibres is limited. To gain a full understanding of dietary fibre, we must also analyse its functional properties.

The fibres that we consume have specificity, which describes how many bacterial strains are able to use each of them for their life cycle (*Puhlmann & de Vos*, 2022). Dietary fibres can be distinguished based on their low or high specificity (*Figure 1*). *Cantu-Jungles et al.* evaluated the microbiota fermentation of fibres, classifying each with low to high specificity. Dietary fibres with low specificity are fructooligosaccharides because of their simple chemical structure and are often used in the Western diet. Fibres with low-to-intermediate specificity, such as type II resistant starch, also have simple structures and are common in most diets, but they are insoluble in water, which increases their specificity. Pectin belongs to the intermediate specificity group because it has a complex chemical structure. However, it is soluble in water; therefore, it does not belong to the high-specificity group. β-glucan fibres have high specificity because they are insoluble in water and are uncommon in our diet. It has been proven that if we have a specific bacterial strain belonging to the *Anaerostipes* genus or *Bacteroides uniformis*, these communities can be sustained by consuming high-specificity fibres such as β-glucan (*Cantu-Jungles et al.*, 2021). β-glucans are the most studied fibres in this field (*Rahman et al.*, 2023). Overall, eating high-specificity dietary fibres can cause a dramatic shift in the microbial community of the gut (*Cantu-Jungles et al.*, 2021).

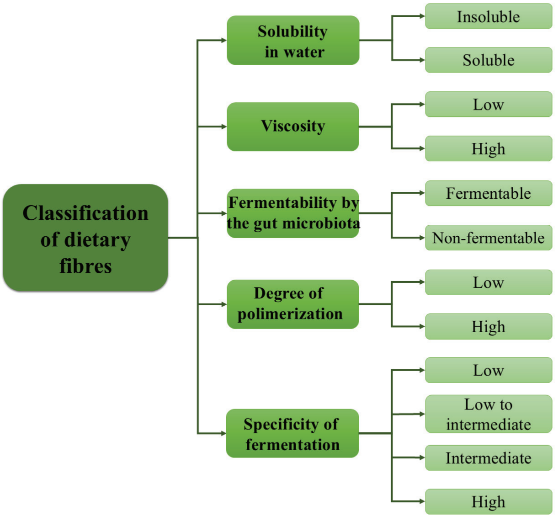

Figure 1. The classification of dietary fibres based on their properties

Dietary fibres can also be differentiated based on their fermentability and viscosity. Whether a fibre is fermentative (inulin and fructooligosaccharides) or non-fermentative (cellulose) depends on whether the bacterial community in the gut can metabolize it. We can say that a fibre is fermentable if the bacteria in the proximal gastrointestinal tract can metabolize it; otherwise, they are non-fermentable (*Rahman et al., 2023*). We can also characterize soluble fibres based on their viscosities. Viscosity is a physicochemical feature, which indicates how resistant the fibre is against the flow we are talking about. This also means how thick or jelly-like will the fibre be after mixing with aqueous solutions (*Rahman et al.*, 2023). If some dietary fibres are mixed with aqueous solutions, they can form a gel, which means that they have gel-forming capacity. The concentration, ionic type, temperature, and chemical composition influence gel-forming capacity *(Cui et al., 2013*). All fibres have different physicochemical features, impacting the body and human health differently through the gut microbiome (*Rahman et al.*, 2023).

The final characterization method is to determine the molecular weight of the fibre. We can distinguish whether they have a high or low molecular weight. Non-starch polysaccharides, resistant starch, and other associated substances, such as lignin, have high molecular weights. Oligosaccharides and inulin have low molecular weights based on their chemical structures.

The presence of dietary fibre in food can be determined using either the Englyst method (NSP) or the Association of Official Analytical Chemists method (AOAC). The soluble and insoluble dietary fibre concentrations of the different foods was determined by *Li et al.* (2002).

Dietary fibre is often used as a synonym for prebiotic substances. *Rezende et al.* classified dietary fibres as prebiotics, candidates for prebiotics, and not recognized prebiotics. Prebiotics should beneficially affect the host by selectively stimulating the growth and metabolic activity of beneficial gut bacteria. Fructooligosaccharides and galactooligosaccharides are considered in literature as prebiotics, fermentable carbohydrates as mannanoligosaccharides, and xylooligosaccharides as prebiotic candidates – based on *in vitro* and preclinical studies (*Rezende et al.*, 2021).

4. Healthy and dysbiotic microbiome

The human microbiome, a complex ecosystem of microorganisms, plays a crucial role in maintaining health and contributes to disease when imbalanced. The human microbiome consists of diverse microorganisms, including bacteria, fungi, archaea, protozoa, and viruses, which are abundant in different organ systems such as the digestive, respiratory, urinary, reproductive, and neural systems (*Link*, 2021; *Xiao et al.*, 2024). The impact of microbiota on health and various diseases has been known since the 17th century. A healthy microbiome, also known as eubiosis, supports metabolic functions, immune modulation, and protection against pathogens. In contrast, dysbiosis, which is an imbalance in microbial communities, is associated with various diseases. In the mid-2000s, progress in modern sequencing technologies and metagenomics made it possible to study the composition and function of the microbiome in depth (*Bresalier & Chapkin*, 2020).

Microbial colonization begins after birth and undergoes gradual transformation. Many influencing factors can affect colonization. These factors include ethnicity, geographical location, economic status, and social status, all of which contribute to the formation and development of this bacterial community. The most important factors influencing the microbiome during pregnancy are the maternal microbiome, mode of delivery (vaginal babies have a more diverse gut microbiota in the first two years than those born by caesarean section), diet, antibiotics, and probiotics. Microbial colonization in infancy undergoes the greatest changes during the first few years of life, and thereafter shows relative stability and constancy depending on environmental factors (*McBurney et al.*, 2019).

These microbes perform essential functions such as aiding digestion, producing vitamins, and protecting against infections. In particular, gut microbiota is crucial for metabolism and immune system activation, influencing the central nervous system and contributing to overall health *(Haripriya et al.*, 2024*; Marano et al.*, 2023). The composition and function of the microbiome, particularly the gut microbiome, dynamically change in response to the actual diet of the host, antibiotic use, and other environmental factors, and resilience is an important characteristic of a healthy microbiome, that is, the ability to return to a state of equilibrium (*Bresalier & Chapkin*, 2020).

The human microbiome is composed of several key phyla, including *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, and *Proteobacteria*. These phyla interact intricately with each other and with the host, thereby influencing health and disease states. *Firmicutes* and *Bacteroidetes* are the dominant phyla in the human gut microbiome. *Firmicutes* are involved in energy metabolism and are known for their role in breaking down complex carbohydrates, whereas *Bacteroidetes* are crucial for the degradation of proteins and polysaccharides (*Ravikrishnan & Raman*, 2021; *Zhang et al.*, 2023). *Actinobacteria*, including *Bifidobacterium*, are important for maintaining gut health and have been associated with anti-inflammatory properties (*Yang et al.*, 2023). *Proteobacteria* are less abundant, include many pathogenic species, and are often associated with dysbiosis and inflammatory conditions (*Ravikrishnan & Raman*, 2021). Microbiota plays a crucial role in an individual's health, and a reduction in its diversity can increase the risk of developing certain diseases.

A diet rich in salt, low in fibre, carbohydrate-oriented, and lacking in physical activity negatively affects the microbiome, which may be associated with the potential development of certain chronic diseases later in life (*McBurney et al.*, 2019). For example, growing evidence suggests that the gut microbiome plays a significant role in the development and progression of colorectal cancer (CRC). CRC is the second leading cause of cancer-related deaths. Increased numbers of *Fusobacterium nucleatum* have been detected in stool samples and tumour tissues of patients with the disease (*Zhang et al.*, 2023). In addition, an imbalance in the gut microbiota, known as dysbiosis, has been associated with weight gain and low levels of inflammation, which impair glucose metabolism. Soluble fibres, such as oligofructose and long-chain inulin, can help restore the balance of gut flora, reduce weight gain, and improve glucose metabolism (*Makki et al.*, 2018). Although the associations between different dietary components and health or disease are strong, further research is required to identify microorganisms with proven therapeutic potential (*Wilson et al.*, 2020).

5. The difference in microbiome composition caused by low and high fibre intake

Dietary fibre consumption is particularly important in shaping the composition of the microbiome. High fibre intake generally promotes a more diverse and beneficial microbiome, whereas low fibre intake can lead to less favourable microbial profiles. The health benefits of dietary fibre are mediated by gut microbiota, as fibre fermentation in the colon promotes the growth of beneficial bacteria, which produce beneficial metabolites, lower pH levels, and inhibit harmful bacteria. High-fibre diets promote an increase in beneficial bacteria, such as *Bacteroides* and *Bifidobacterium*, which are linked to improved immune responses and reduced tumour-promoting genera (*Sharma et al.*, 2024). Inadequate or insufficient fibre intake (which is common in industrialized nations) alters the microbial composition of the gut, which can lead to the development of many chronic diseases *(Kok et al.*, 2023). Low-fibre diets can reduce the abundance of beneficial bacteria and alter the production of regulatory immune molecules, such as IL-10, which is crucial for maintaining intestinal homeostasis *(Rivera-Rodriguez et al.*, 2023). Fibre from fruits and vegetables helps to maintain microbiota diversity, positively influences its structure and function, and leads to the production of short-chain fatty acids (SCFAs) through fermentation (*Tanes et al.*, 2021). Understanding how dietary fibre affects the gut microbiota can be key to the battling of chronic diseases (*Oliver et al.*, 2021).

The individual variability of the gut microbiome responds accordingly to different dietary fibres, which is why personalized diets are becoming increasingly important and popular in improving gut health and metabolic efficiency (*Kok et al.*, 2023). The Western diet, high in red meat, saturated fats, processed grains, and added sugars and low in fruits, fibre, vegetables, nuts, whole grains, and seeds, has a distinct impact on the gut microbiome. Studies have shown that it leads to lower levels of beneficial bacteria, such as *Prevotella copri*, and higher levels of species associated with negative health condition such as *Alistipes* and *Ruminococcus* (*Dahl et al.*, 2020). The Mediterranean diet (consumed in Mediterranean countries such as Spain, Greece, and Italy) is characterized by plant-based foods (fruits and vegetables, whole grains), olive oil, moderate fish and poultry intake, limited dairy, and a joyful, active lifestyle. Research shows that this diet positively influences gut microbiota, particularly boosting beneficial bacteria such as *Faecalibacterium prausnitzii*, which produces butyrate, and reducing potentially harmful bacteria such as *Ruminococcus gnavus*. Additionally, lower adherence to this diet is linked to higher levels of urinary trimethylamine-N-oxide (TMAO), a compound associated with cardiovascular and other chronic diseases (dementia and hypertension), which may signal the development of insulin resistance. These findings suggest that the Mediterranean diet may reduce disease risk through its effect on gut health (*Dahl et al.*, 2020). The typical American diet is low in fibre, with less than 10% of Americans meeting the recommended daily fibre intake. In contrast, most, although not all, vegetarians and vegans consume higher amounts of dietary fibre (*Tanes et al.*, 2021). Vegetarian and vegan diets are often considered beneficial for health because of their higher intake of plant-based foods, which typically results in greater fibre consumption. Studies have found variations in specific microbiota components, such as reduced levels of *Collinsella* and *Holdemania*, but increased levels of *Roseburia* and *Lachnospiraceae* in vegetarians. Plant-based diets influence microbiota function, including higher microbial gene and protein abundance involved in polysaccharide and protein breakdown, and vitamin synthesis (*Kok et al.*, 2023). Human studies involving controlled diets have demonstrated that vegetables high in inulin can increase the levels of *Bifidobacterium*, promote a feeling of fullness, and aid in weight reduction (*Armet et al.*, 2022). A ketogenic diet, which is characterized by fats and is very low in carbohydrates, induces body ketosis and relies on fat for energy. Research on this diet has shown varying effects on gut microbiota, including reduced *Firmicutes* and increased *Bacteroidetes*. Some findings have indicated that a ketogenic diet may lead to decreased microbiome diversity. Furthermore, a modified Mediterranean-ketogenic diet has been associated with changes in microbiota composition and a reduction in Alzheimer's disease biomarkers in the cerebrospinal fluid (*Dahl et al.*, 2020). The Paleolithic diet imitates the eating habits of ancient humans, emphasizing meats, fish, nuts, seeds, healthy oils, fresh fruits, and vegetables, while avoiding legumes, dairy, grains, refined sugars, and processed foods. Research has indicated that this diet supports a diverse microbiome (*Dahl et al.*, 2020).

There is growing evidence that microbial responses are individualized. When comparing dietary fibre studies, it is important to consider all the aspects. For example, in a group of obese patients, different changes in body mass index (BMI) were noted after three months of inulin supplementation. Responders who experienced a decrease in BMI had higher baseline levels of *Akkermansia* and *Butyricicoccus* and lower levels of *Anaerostipes*. Responders in this group showed increased levels of *Prevotella copri* and genes related to β-glucan degradation, which in subsequent mouse studies were linked to greater glycogen storage in the liver (*Kok et al.*, 2023). In murine models on a high-fat diet, the benefits of inulin, including promotion of the incretin hormone glucagon-like peptide 1 and protection against metabolic syndrome, were diminished when antibiotics were used, suggesting a role for the gut microbiota (*Armet et al.*, 2022).

Studies on the importance of dietary fibre and the microbiome emphasize the complexity and variability of the gut microbiome, which can result in significant differences in individual responses to dietary interventions (*Oliver et al.*, 2021).

6. Metabolic function of gut microbiome

The gut microbiota is a “living metabolic organ” that can interact with the human body and influence its state of health. Human hosts can use these metabolites as energy sources (*Schippa & Conte*, 2014). The microbiota can produce many metabolites, including vitamins (*Soto-Martin et al.*, 2020) and short-chain fatty acids (SCFA) (*Fusco et al.*, 2023), influence ion absorption (*Engevik & Engevik*, 2021), and synthesise amino acids (*Ashniev et al.*, 2022).

In the intestinal tract, we can distinguish microbial-accessible carbohydrates (MACs), which are complex polysaccharides and oligosaccharides that the gut microbiome can degrade by carbohydrate-active enzymes (CAZymes). CAZymes are microbial enzymes for degrading endogenous and exogenous, simple to complex carbohydrates with high specificity. Since 1999, the Carbohydrate-Active Enzymes database (CAZy; http://www.cazy.org) coupled with the CAZypedia encyclopedic resource has been available, which offers updated classification data of CAZymes (*Lombard et al.*, 2014). *Bacteroidetes* can degrade different kinds of polysaccharides with the help of glycan-binding proteins because they have polysaccharide utilization loci (PUL), which encode the degrading system for them (*Cheng et al.*, 2022). *Firmicutes*, *Roseburia* spp., and *Eubacterium rectale* possess carbohydrate-active enzymes (CAZymes) *(Sheridan et al.*, 2016) and are crucial members of the metabolism of fibre substrates in the gut microbiome (*Kok et al.*, 2023). They specialize in the use of different carbohydrate substrates. The *Roseburia/E. rectale* group can utilize starch and fructooligosaccharides. However, not all members of *Roseburia* genus are capable of completely using these dietary fibres; for example, *R. hominis* is less capable (*Sheridan et al.*, 2016). *Proteobacteria* is one of the most abundant phyla in the human gut (*Rizzatti et al.*, 2017). In 2018, *Méndez-Salazar et al.* proved that a relatively high abundance of phyla can predict gut dysbiosis (*Méndez-Salazar et al.*, 2018). However, many bacteria in the gut are anaerobic, and members of the *Proteobacteria* phyla are facultative or obligate anaerobes in humans and other mammals. Therefore, they also use oxygen in their life cycle, which lowers the redox potential in the gut. They also produce a relatively high range of metabolites (*Moon et al.*, 2018).

The microbial community can also produce bioactive polyphenols from dietary substrates such as fruits, vegetables, and cereals. The five-carbon and six-carbon monosaccharides can also be degraded by the classical pentose phosphate pathway or the Embden–Meyerhof–Parnas pathway (*Krautkramer et al.*, 2021).

7. The role of dietary fibres in microbial SCFAs production and host health

Dietary fibres affect the microbes of the gastrointestinal tract and the metabolic profile of the bacterial community. Several studies have shown that consuming dietary fibre has a positive effect on host health through the stabilization of blood glucose concentration, reduction of cholesterol levels, and gastrointestinal tract disorders (*Williams et al.*, 2017). Short-chain fatty acids (SCFAs) are produced by the gut microbiome as a result of dietary fibre fermentation. These organic compounds cannot be produced by human enzymes and can only be metabolized by specific microbes, mainly bacteria in the gut (*Fusco et al.*, 2023). The average SCFAs produced in the colon were 40 mM acetate, 15 mM propionate, and butyrate for a normal adult. These numbers are lowered if the individuals follow a Western diet and are raised by consuming a high dietary fibre diet (*Tan et al.*, 2023). As shown in *Figure 2*, SCFA molecules can affect health state, mood, and behaviour (*Fusco et al.*, 2023). However, most studies have shown that SCFAs have a significant positive impact on human health. Some studies have demonstrated side effects of SCFA production such as increasing hepatic lipid accumulation or inducing brain neurochemistry impairment (*Xiong et al.*, 2022).

In this section, we discuss different SCFA profiles based on dietary fibre consumption. *Chen et al.* published a study about the effect of arabinogalactan on the gut microbiome. They proved that supplementation of arabinogalactan by 30 healthy adults at 15 g each day decreased the level of isovaleric, valeric, and hexanoic acid production (*Chen et al.*, 2021). In 2012, *Damen et al.* investigated the effects of eating bread containing arabinoxylan oligosaccharides (AXOS). AXOS is the main dietary fibre component of cereals. In their study, they examined 27 volunteers aged between 18 and 46 years old. They showed that the consumption of *in situ* baked bread can increase butyrate concentration in faeces, and they also measured increased levels of acetate and propionate – but not significantly (*Damen et al.*, 2012). However, the effect of inulin on the gut microbiome remains unclear. Several studies have demonstrated changes in the SCFA profile after the daily utilization of inulin, but these changes were not significant. For example, *Reimer et al.* compared 50 healthy adults with low dietary fibre consumption (< 15 g/day in women, < 18 g/day in men) in their study. They examined subjects'

SCFA profiles based on inulin intake. The subjects were categorized into two groups. The first group consumed 7 g/day, and the second group consumed 3 g/day. There were no significant differences between the two groups compared to the placebo groups. However, some significant changes were detected in the faecal butyrate concentration, but after including the baseline concentration, the significance was eliminated (*Reimer et al.*, 2020). In their systematic review, *Vinelli et al.* analysed 42 studies on the effects of dietary fibre on SCFA production in the gut microbiome. From these 42 studies, seven demonstrated that dietary fibre consumption can significantly increase SCFA production (*Vinelli et al.*, 2022). Dietary fibre can also protect the intestinal barrier. The gut microbiome degrades several types of dietary fibres and produces butyrate, which can be an energy source for enterocytes. Enterocytes help to maintain the integrity of the epithelium (*Zhang et al.*, 2022).

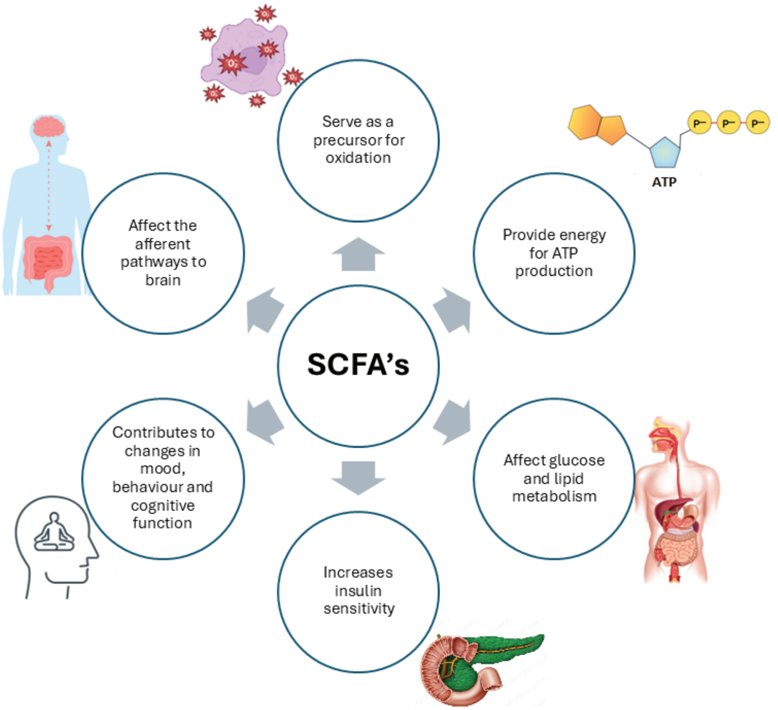

Figure 2. The benefits of SCFA molecules for host health

In 2021, *Medawar et al.* published an article that compared healthy and overweight adults. They examined the subjects' eating behaviour, BMI, microbiome composition, and SCFA profile from serum and faeces. Their results showed that higher dietary fibre intake was significantly associated with lower body fat mass. In addition, they could correlate participants eating less with higher faecal propionate levels. In addition, they demonstrated that patients with lower body fat mass had higher serum acetate and butyrate levels. Based on these results, they stated that dietary fibre intake may modify unfavourable microbiota genera and thus the SCFA profile (*Medawar et al.*, 2021).

Some studies have attempted to combine dietary fibres to determine their impact on host health. *Peng et al.* fed mice with four different types of dietary fibres (pectin 98%, cellulose 99%, type II resistant starch 98%, and fructooligosaccharides 98%) for four weeks. They created three types of testing groups: single dietary fibre, a mixture of two dietary fibres, and a mixture of multiple dietary fibres. The mixture of fructooligosaccharides and cellulose resulted in higher total acid, lactic acid, and butyric acid concentrations, as well as in one of the highest concentrations of propionic and acetic acid in the gut (*Peng et al.*, 2013).

8. Concluding remarks and future perspectives

There is an intricate relationship between diet and the gut microbiota to promote health and manage diseases. For example, through fibre fermentation, the gut microbiota produces SCFAs, which improve metabolism-related disease conditions and potentially reverse metabolic dysfunctions associated with low-fibre diets. Despite the well-documented benefits of dietary fibre, individual responses to fibre supplementation can vary. Understanding the specific interactions between different types of fibres and the microbiome is essential for optimizing health outcomes. Therefore, personalized dietary recommendations for shaping the microbiome are emerging. However, complex host–microbiome interaction networks and their metabolic impacts require further exploration. Cutting-edge technologies, such as engineered organoids, high-throughput cultivation methods, and microfluidic assays, have enhanced the effectiveness and precision of microbiome studies. These technological advancements, combined with an expanding molecular understanding of how gut microbes interact with nutrients, are poised to deepen our understanding of the dietary effects on host health and disease, paving the way for individualized nutritional strategies and treatments. As this field evolves, it is essential to combine data from these innovative techniques with functional metabolic profiles and biomarkers to create more accurate and reliable dietary guidelines. However, upcoming studies in nutrigenomics could shed light on the mechanisms by which prebiotics interact with human genes to affect health outcomes. This research may lead to tailored dietary guidelines that incorporate prebiotic supplements based on the unique genetic profiles of individuals. Continued research and technological advancements are essential to fully realize the potential of personalized nutrition in shaping the microbiome to improve health outcomes.

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