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Review

Association between the gut microbiota and diet: Fetal life, early childhood, and further life

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ABSTRACT

Gut microbiota establishment and further microbiota shifts are very important for maintaining host health throughout life. There are some factors, including genetics, the mother's health and diet, delivery mode, breast or formula feeding, that may influence the gut microbiota. By the end of approximately the first 3 y of life, the gut microbiota becomes an adult-like stable system. Once established, 60 to 70% of the microbiota composition remains stable throughout life, but 30 to 40% can be altered by changes in the diet and other factors such as physical activity, lifestyle, bacterial infections, and antibiotic or surgical treatment. Diet-related factors that influence the gut microbiota in people of all ages are of great interest. Nutrition may have therapeutic success in gut microbiota correction. This review describes current evidence concerning the links between gut microbiota composition and dietary patterns throughout life.

Introduction

The human gut microbiota has become a widely discussed topic over the past decade. Gut microbiota plays an important role in the normal functioning of the host organism. This is confirmed by a growing number of studies, which reveal more about mechanisms of interaction between the microorganisms and the human body. A host also may affect its gut microbiota by changing lifestyle; naturally diet is a very important factor. One study showed that an increase in caloric intake from 2400 to 3400 kcal/d (with similar nutrient profile that included 24% protein, 16% fat, and 60% carbohydrates) over 3 d increases *Firmicutes* representation and decreases the representation of *Bacteroidetes* [1]. Inverse changes in the gut microbiota occur while reducing caloric intake [2]. It is difficult to investigate the effects on energy intake. Normal caloric intake differs from person to person and depends on age, habits, metabolism, and so on. For this reason, we have paid more attention to different nutrition compounds.

Dietary habits determine what our bacteria can consume; it is the way we are "feeding" our microbiota. Bacteria metabolic activity is defined mostly by its genome and epigenome. Saccharolytic bacteria are able to metabolize carbohydrates; this bacteria group includes *Bacteroides, Bifidobacterium, Lactobacillus, Eubacterium, Propionibacterium*, *Escherichia, Enterococcus, Peptostreptococcus, Fusobacteria*, and others. Proteolytic bacteria derive energy from protein fermentation and are represented by *Streptococcus, Staphylococcus, Proteus, Escherichia,* and some species of *Clostridium, Fusobacteria, Bacillus, Propionibacterium*, and others. Some of them are strictly proteolytic, whereas others have mild saccharolytic activity or are actively engaged in carbohydrate fermentation. Thus, many bacteria are capable of metabolizing both proteins and carbohydrates. The aim of this

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review was to provide partial answers to at least some questions about the gut microbiota and diet based on published studies; and to identify important gaps in knowledge where further research should be done.

Gut microbiota establishment and diet

Antenatal period and delivery

Gut microbiota colonization begins during the antenatal period [3,4]. Recent studies have proved the presence of bacteria in the amniotic fluid, placenta, cord blood, meconium [5–7]. A mother's diet before and during pregnancy influences the development of the child's gut microbiota [8,9]. For example, excessive maternal intake of trans-fats in rats has been shown to induce a low-grade inflammation in babies, whereas supplementation with Jussara (*Euterpe edulis* Mart.) during pregnancy and lactation reverses the effects of trans-fatty acids and increases *Lactobacillus* spp. in offspring [10]. A maternal gluten-free diet increases the number of *Akkermansia, Proteobacteria*, and *TM7* bacteria in the gut microbiota of mice offspring and reduces the incidence of diabetes and low-grade inflammation [11].

It has been shown in humans that an unhealthy mother's diet during pregnancy as well as poor early childhood nutrition can lead to the establishment of a lean defective intestinal microbiota [12]. This results in further dysfunction of the immune system and in a dysregulation of genes involved in a lipid and glucose metabolism [12,13]. Interestingly, a recent study found that even maternal consumption of the oily fish influences the infant gut microbiota composition [14].

The next step in the microbiota establishment is a delivery. Method of the delivery is of great importance for microbiota colonization. For instance, cesarean delivery is accompanied by lower microbiota diversity and postponed *Bacteroidetes* colonization [15]. In contrast, vaginal delivery is accompanied by an extensive colonization of child's microbiota by vaginal bacteria, mainly represented by *Lactobacillus*. Thus, vaginally delivered infants acquired the microbiota similar to their mother's vaginal microbiota, represented by *Lactobacillus* and *Prevotella*, and babies born by cesarean delivery acquired the microbiota similar to the mother's skin microbiota, dominated by *Staphylococcus, Corynebacterium*, and *Propionibacterium* [16].

Early childhood: breast and formula and complementary feeding

The neonatal and early childhood periods are critical for the formation of a healthy intestinal microbiota in children. Following birth, child's gut microbiota is characterized by a low diversity until 2 to 3 y old [13,17]. It is assumed that initial colonization of the gut microbiota with facultative anaerobes, such as *Staphylococcus, Streptococcus, E. coli*, and *Enterobacterium*, make further obligate anaerobe colonization possible [18,19].

Later, during the breast feeding period, the digestive tract is colonized with *Actinobacteria* and *Firmicutes* [20]. *Actinobacteria* in breast-fed children are represented mainly by *Bifidobacterium* (B.), *B. breve, B. longum, B. dentium, B. infantis, B.* pseudocatenulatum [21]. With regard to *Firmicutes* phylum, it is at most represented by *Lactobacillus, Enterococcus,* and *Clostridium* [17,20]. Breast feeding is considered to be the perfect nutrition for children. Healthy mothers' breast milk contains 10^9 microorganisms/L [22], and a healthy maternal diet is crucial for the child's normal milk composition and proper gut microbiota establishment [23].

The gut microbiota in formula-fed children differs from that of breast-fed infants. Formula-fed infants' microbiota contains more *Bacteroides, Enterobacteriaceae*, including *Klebsiella, Atopobium*, and *Clostridia* [21,24] and lower levels of *Bifidobacterium* [25]. Although, according to some studies, the total number of *Bifidobacterium* but not levels of *Bifidobacterium cantenulatum* and *Bifidobacterium adolescentis* are relatively similar in breast-fed infants and in those fed with formula supplemented with galactooligosaccharides and fructooligosaccharides [22,26].

The composition of the gut microbiota also differs among breast-fed infants. In many respects, it is determined by the maternal nutrition [27]. Findings from one study demonstrated that high-fat maternal diet results in microbiota dysbiosis in primate offspring [28]. Certainly, new studies are required for further development and practical application of this hypothesis.

An adult-like microbiota is established approximately between 2 and 3 y of age, after cessation of breast feeding. Its composition largely depends on the type of complementary feeding [17,24]. For instance, the more polysaccharides a diet contains, the more bacteria in the gut are able to ferment it (e.g., *Prevotella*) [29]. Research conducted in 2014 in Denmark with 330 healthy infants aged up to 3 y found that significant changes in the gut microbiota occurred after weaning. The number of *Bifidobacterium, Lactobacillus,* and *Enterobacteriaceae* decreased, whereas Bacteroidetes phylum members were observed to increase. Regardless of the age of weaning, the number of butyrate-producing bacteria such *as C. leptum*, *Eubacterium Halli,* and *Roseburia* is growing along with microbiota diversity [17,30].

By 36 mo after birth the baby's gut microbiota undergoes last shifts it becomes a stable system mainly represented by *Bacteriodetes, Firmicutes*, and smaller rates of *Actinobacteria, Proteobacteria*, and *Verrucomicrobia* [17,29–31]. "Proper" microbiota establishment is crucial because about 60% to 70% of microbiota bacteria remain unchanged throughout life. Notably, *Bacteroidetes* and *Actinobacteria* rates are much more stable than *Firmicutes* and *Proteobacteria* [32,33].

Nutrients in a diet affecting gut microbiota

We still cannot say what comprises "healthy" microbiota; its composition varies greatly according to the lifestyle, diet, and many other factors [34]. Scientists are attempting to identify major features of the gut microbiota in healthy people to set up a conception of normal gut flora. However, to our knowledge, there are no precise conclusions to date, and microbiota appears to be similar in people living in the same area and having contact with each other [18,35].

In 2011, three enterotypes with a predominance of *Bacteroides, Prevotella*, or *Ruminococcus* were described. *Bacteroides* enterotype is common in people following a Western diet that is rich in fat and protein. *Prevotella* enterotype is common in people who consume a lot of fiber [31]. Protein- and fat-degrading bacteria are more abundantly present in the gut of people who eat more fat and protein (e.g., such a pattern was observed in the US population). In turn, microbiota of Malawi (East Africa) residents contains more polysaccharide-degrading microorganisms [35]. A high-fat diet is associated with high levels of *Bacteroidetes* and *Actinobacteria* in the gut. The same bacteria are in inverse proportion to the plant fiber consumption. *Firmicutes* and *Proteobacteria* have an opposite association with these macronutrients [36]. Although, the relevancy of enterotypes or "fecotypes" is disputed, 30% to 40% of adults' gut microbiota can

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be modified during the lifetime, and diet is one of the most powerful factors we can use (Fig. 1).

Gut microbiota and carbohydrates

Carbohydrates that reach the gut are resistant starches (RS), nonstarch polysaccharides, and oligosaccharides. Short-term changes in carbohydrate consumption can lead to some shifts in the intestinal microbiota composition [37,38], whereas long-term diets are associated with the profound microbiota composition alteration [36]. As mentioned previously, the composition of microbiota is similar in Europeans [39] and Americans who eat a lot of fats, but differs from that in Africa or South America populations that consume more polysaccharides [35]. A landmark study demonstrated that microbiota in Burkina Faso (West Africa) children contains more *Bacteroidetes* (73%) than microbiota of children from Italy (27% *Bacteroidetes* and 51% *Firmicutes*). It should be noted that *Bacteroidetes* is quite a big phylum that includes very different genera (e.g., *Prevotella* and *Xylanibacter* are broadly presented in African children). On the contrary, abundance of these bacteria is severely low in Italian children. Representatives of these genera ferment xylans, cellulose, and other polysaccharides [29].

Fibers intake and gut microbiota

Dietary fibers are polysaccharides mainly composed of ≥10 monosaccharide units that are resistant to digestion by human enzymes. The American Dietetic Association recommends daily consumption of 14 g dietary fiber/1000 kcal, or 25 g for adult women and 38 g for adult men. The World Health Organization recommends eating 25 to 35 g/d of dietary fiber. The therapeutic dose is considered to be ≤40 to 45 g (maximum daily dose 60 g) [40]. Essential dietary fibers needed for proper digestion are RS and nonstarch polysaccharides (Fig. 2).

Starches. There are four types of indigestible RS (Table 1) [41]. These starches also are metabolized differently by intestinal microbiota [42].

Starch is one of the most common carbohydrates contained in rice, wheat, root vegetables, fruits, beans, and the like. Starch generally consists of about 20% to 25% of amylose and 75% to 80% of amylopectin; this proportion may influence the possibility of microbiota species to ferment starches [43–45]. One study looked at the changes in microbiota in 46 healthy adults after switching to a diet rich in RS and demonstrated an increase of *Ruminococcus bromii* abundance (*Clostridia* class) after this dietary intervention [46]. Similar results have been obtained in a

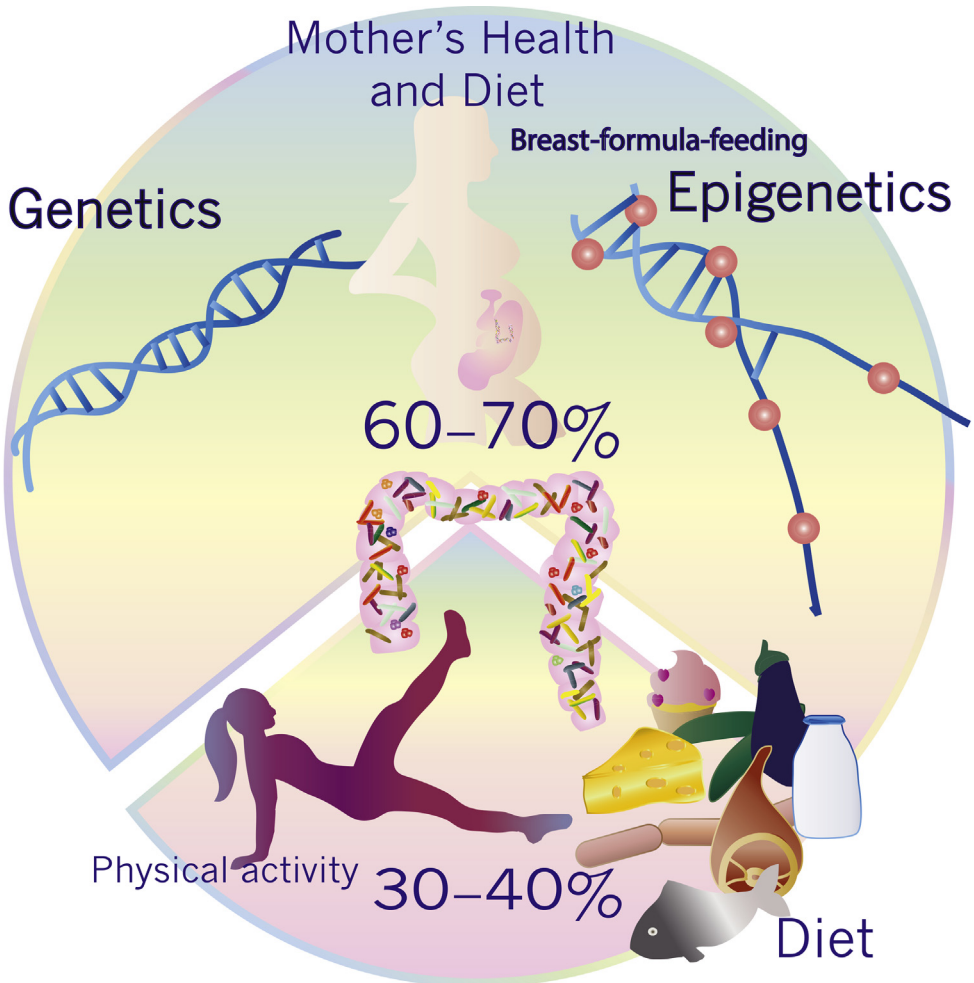

Fig. 1. What influences our gut microbiota?

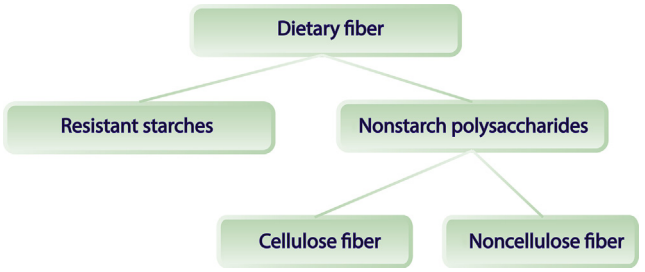

Fig. 2. Dietary fiber types.

recent research conducted in obese men: The levels of *Eubacterium rectale* and *Ruminococcus bromii* (*Firmicutes* phylum) in gut microbiota was increased significantly after only 10 wk on a high-starch diet. Interestingly, two samples in this study had a very low level of *Ruminococcus bromii*, and 69% and 65% of dietary starches was unfermented in these samples (compared with <4% in other samples) [37]. Another study revealed an increase of *Eubacterium rectale* and *Ruminococcus bromii* abundance in participants consuming more RS2 (raw RS), while consuming of RS4 (chemically modified RS) was associated with higher levels of *Bifidobacterium adolescentis* and *Parabacteroides distasonis* [42]. In yet another study, it was reported that *Bifidobacterium adolescentis* and *Ruminococcus bromii* are more likely to ferment RS2 and RS3 (retrograded RS from previously cooked and cooled raw starch) than *Eubacterium rectale* and *Bacteroides thetaiotaomicron* [43]. Thus, all these studies have shown that RS promote the growth of the saccharolitic bacteria, and this effect differs according to the RS type. Interestingly, in a recent study, an intake of maltodextrin (the novel nonviscous dietary resistant fiber) was associated with significant increasing of the *Ruminococcus, Eubacterium, Lachnospiraceae, Bacteroides, Holdemania,* and *Faecalibacterium* levels in the gut [47].

Nonstarch polysaccharides. The nonstarch polysaccharides group contains cellulose and noncellulose fibers including pectins, gums, slimes, glycosaminoglycans, alginates, carrageenans, chitosans, and fucoidans. Cellulose is the most common nonstarch polysaccharide, a basic component of plant cell walls. It is found in whole grain and bran products, vegetables, and fruits. Cellulose is one of the substrates for the short-chain fatty acid (SCFA) production. High cellulose consumption increases the concentration of the potentially beneficial bacteria. One study investigated the influence of the dietary carbohydrate (RS and nonstarch polysaccharides) reduction and detected a significant lowering of *Roseburia/Eubacterium rectale* group along with a lowering of SCFAs in feces after the experiment [48]. Another study found that the prebiotic xylooligosaccharide increases fecal levels of *Bifidobacterium* and *Bacteroides fragilis* and SCFA [49]. The wheat bran extract containing arabinoxylan-oligosaccharides also has been shown to promote *Bifidobacterium* growth in healthy preadolescent children [50].

Table 1
Resistant starch types

RS type	Description	Food sources
RS1	Physically inaccessible undigestible starch	Whole seeds, grains
RS2	Ungelitinized tightly packed starch indigestible due to high amylose content	Raw potatoes, green bananas, plantains, becomes accessible when heated.
RS3	Retrograded cooled gelitinized starch	Bread, cooked and cooled pasta, potatoes, rice, legumescornflakes
RS4	Chemically modified starch	Industrial starch, in processed foods (e.g., cheese, puddings, breads, crackers, etc.).

RS, resistant starch

The gut microbiota members produce SCFAs during the fiber fermentation, 90% of SCFAs is absorbed in the colon and is involved in various essential processes such as lipogenesis and gluconeogenesis [51]. SCFAs bind the G protein-coupled receptors (GPCR), basically GPCR41 and GPCR43, which are suppressing a low-grade inflammation. SCFAs decrease colonic pH locally, increase motor activity, and alter intestinal permeability. Additionally, SCFAs are involved in the processes of water, sodium, chlorine, calcium, and magnesium absorption. Finally, pH decline results in transformation of ammonia, produced during the amino acid fermentation, into ammonium ions. These ions cannot be absorbed into the blood and are mainly excreted in feces as ammonium salts [52]. Thus, diets rich in fiber are supposed to be associated with high abundance of beneficial bacteria, higher levels of SCFAs, and lower levels of protein fermentation products.

Gut microbiota and proteins

Proteins are an integral part of a healthy diet; because some amino acids are not produced in a human organism they must be obtained from food. On the other hand, improper protein consumption may result in different disorders.

About 10% of dietary protein reaches the colon. Proteins are not just a substrate for proteolytic bacteria, but also a source of nitrogen for saccharolytic species. The main proteolytic bacteria are *Streptococcus, Bacillus, Propionibacterium, Staphylococcus*, some species of *Clostridium, Bacteroides*, and others. These bacteria, crucial for protein degradation, live mostly in the distal colon, where carbohydrate sources are too small [53,54].

One of the key steps in amino acid degradation in the colon is the deamination. The products of the protein and amino acid breakdown are SCFAs (acetic, propionic, and butyric acids), branched-chain fatty acids (BCFAs; isobutyrate, isovalerate and 2-methylbutyrate), phenol compounds (phenylpropionate, phenylacetate, *p*-cresol, indole propionate, and indole acetate), amines, sulphides, and ammonia. Microorganisms involved in the deamination are *Clostridium*, some *Bacteroides*, and *Enterobacterium* spp; bacteria involved in the lactic fermentation are *Bifidobacterium* and *Lactobacillus* [55]. All these products have different effects on the human organism and although some are healthy, and others are not (e.g., nitrosamine precursors in the stomach are oncogenic and they form most probably because of the bacterial nitrate-reductase activity) [56,57]. Moreover, proteins are the source of L-carnitine, which has the potential to be fermented by bacteria to trimethylamine *N*-oxide (TMAO). TMAO is supposed to induce atherosclerosis [58].

A high-protein diet does not always lead to toxic damages [59,60], as a rule, disorders are associated with a nutrient imbalance. Dietary fibers enlarge fecal mass, reduce a fecal transit time, and make bacteria “work” with carbohydrates. This results in lower toxic metabolite concentration and reduces the affect of the protein fermentation metabolites on intestinal mucosa [61–63]. Thus, resistant starches may reduce the proportion of the protein fermentation products in humans [64]. A number of studies have proved that prebiotics as well as probiotics reduce the levels of proteolytic markers, such as phenol and *p*-cresol, in the gut [65,66].

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Various proteins affect human organism and gut microbiota differently. As for microorganisms, in vitro it was shown that an abundance of *C. perfringens/histolyticum* was higher in a beef diet compared with fish and chicken diets; *Bifidobacterium* and *Bacteroides* grew better in a chicken diet group. Moreover, it was shown that method of cooking might influence the gut microbiota (e.g., *Clostridium* growth was higher in a fried meat group compared with a group that ate boiled meat) [67]. Glycated plant proteins improve the gut microbiota balance, increase *Lactobacilli* and *Bifidobacteria* growth and SCFAs levels [68]. In turn, dietary glycated bovine protein had an opposite effect on *Eubacteria* and *Bifidobacteria* in one study [69]. To our knowledge there is insufficient evidence to assess the whole microbiota role in the protein degradation. Most of the conducted studies focused on metabolite evaluation, and further studies are necessary.

Gut microbiota and fats

Dietary fats are mostly absorbed in the small intestine, but 7% is excreted with the feces [70]. One study showed that the germ-free mice fed a high-fat diet over a 4-wk period did not gain weight. In the same study scientists revealed that changing to a high-fat diet during a 12-wk period in wild mice resulted in microbiota shifts, although after 10 wk of normal feeding microbiota had returned to previous levels [71]. High-fat diets are associated with low SCFA and low Bifidobacterium concentrations [59]. Actually, it is difficult to compare different studies results due to various nutrition compounds as fat, protein, and carbohydrate types may differ significantly.

There are few studies considering a kind of fats. One study investigated the influence of different oils (olive, palm, and safflower) on microbiota composition. The most dramatic changes in microbiota composition were observed in mice fed a palm oil diet. The diet high in palm oil increased the ratio of *Firmicutes* to *Bacteroidetes* and the abundance of *Clostridium* clusters XI, XVII, and XVIII and reduced microbiota diversity. In mice fed the high-fat olive or safflower oil diets, microbiota shifts were not so prominent [72]. Consequently, saturated and unsaturated fats might affect gut microbiota in various ways. However, this question also requires further study. Interestingly, one study found out that conjugated linoleic acids, contained mostly in meat and dairy products, overrode the negative effects of a high-fat diet and exerted a prebiotic action on *Bacteroidetes/Prevotella* and *Akkermansia muciniphila* levels in mice [73]. Dietary polyphenols also have shown to attenuate high-fat diet-induced influences, promote *Akkermansia muciniphila* growth, and decrease the ratio of *Firmicutes* to *Bacteroidetes* in mice [74], while high-cholesterol diet increased the ratio of *Firmicutes* to *Bacteroidetes* [75].

According to some studies, a high-fat diet results in elevated levels of serum lipopolyssacharide, endotoxemia, and low-grade inflammation [76]. In turn, probiotics reduce cytokine expression and are beneficial in counteracting high-fat diet-induced dysbiosis [77]. Even a moderate high-fat diet may cause metabolic endotoxemia and low-grade inflammation and decrease the representation of *Lactobacilli* [78]. Furthermore, high-fat diets may influence microbiota indirectly by stimulation of bile-acid production. Some bile acids reach the colon and are dehydroxylated by microbiota to carcinogenic secondary bile acids [79,80].

One study supposed that dietary habits might influence the gut microbiota in mice even more than murine genotype. The researchers examined the gut microbiota in inbred, transgenic, and outbred mice and determined that, despite divergent genotypes, gut flora was consistently altered by the diet in these mice [81]. Microbiota fermentation products are schematically displayed in Figure 3.

To summarize this information we highlight some links between gut microbiota composition and dietary habits, namely vegetarian and Mediterranean diets and the appetite.

Gut microbiota and regular diets

Gut microbiota and vegetarian diets

Vegetarian diets are of a great interest nowadays. These diets are thought to be associated with a lower risk for obesity, coronary heart disease, and other disorders. Recent findings on the links between the dietary patterns and microbiota composition differ. For instance, one experiment showed that the gut microbiota composition in healthy human vegans and omnivores

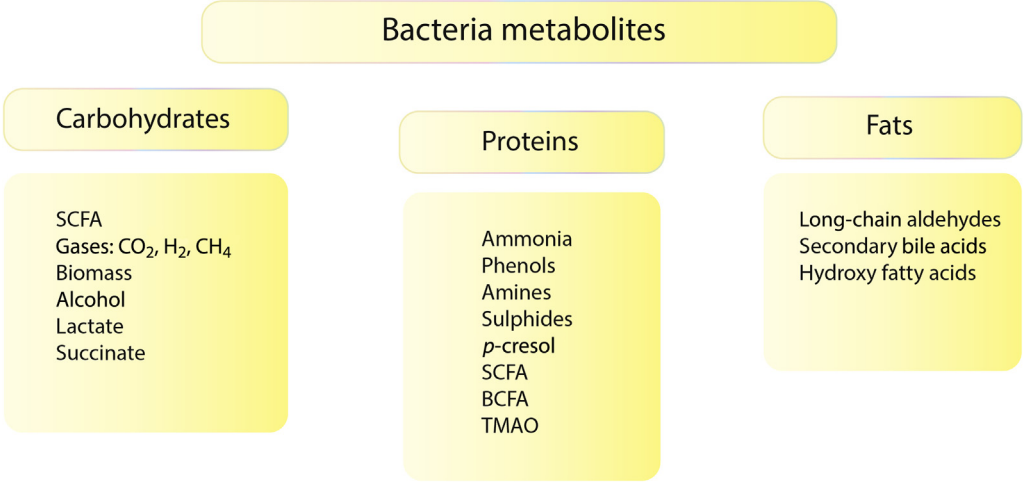

Fig. 3. Carbohydrate, protein, and fat fermentation products. BCFA, branched-chain fatty acid; SCFA, snort-chain fatty acid; TMAO, trimethylamine N-oxide.

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was similar, and the vegan diet was not associated with higher levels of fecal SCFAs, although plasma metabolome was different [82]. Perhaps, such results may be explained by some identical dietary habits (e.g., fast food, high consumption of sugar-containing drinks, pastries, soybean products, and palm oil that is widely used and similar to animal fat). Also, vegetarian diet types vary as widely as omnivore diets. For instance, one group reported an increased level of *Clostridium* cluster XIVa bacteria, specifically *Roseburia* spp.–*Eubacterium rectale* in omnivores. However, this study was conducted with women from South India and Indian dietary patterns differ greatly from Western patterns [83]. According to one study, the vegan diet is associated with lower levels of *Bacteroides, Bifidobacterium, E. coli*, and *Enterobacteriaceae* [84]. Another study reported that the ratio of *Bacteroides* to *Prevotella*is higher in vegetarians [85]. Such contradictory data arouse a profound interest. Certainly, more detailed and systematic studies are necessary.

Gut microbiota and Mediterranean diet

The Mediterranean diet is considered one of the world's healthiest diets and often is recommended by nutrition specialists. The main components of the Mediterranean diet are seafood, whole grain foods, legumes, fruits and vegetables, foods containing unsaturated fatty acids, and red wine in moderation. According to a transcriptome analysis, the Mediterranean-inspired diet resulted in a significant improvement of the gut microbiota composition in patients with Crohn's disease [86]. Actually, to our knowledge no studies have been conducted on the potential effects of the Mediterranean diet on microbiota, but we can find many links between Mediterranean diet components consumption and microbiota composition. As mentioned previously, diets rich in fiber and unsaturated fatty acids are associated with high levels of so-called beneficial bacteria. As for moderate wine consumption, it is thought to increase the number of *Enterococcus, Prevotella, Bacteroides,* and *Bifidobacterium* and to decrease systolic and diastolic blood pressures and triacylglycerol, total cholesterol, high-density lipoprotein cholesterol, and C-reactive protein levels. These prebiotic benefits are associated with the inclusion of red wine polyphenols in the diet [87]. Currently, polyphenols have received special attention from the scientific community due to their ability to reduce free radical formation and to scavenge free radicals. In addition to their antiinflammatory, antioxidant, and anticarcinogenic qualities, some polyphenols have moderate antimicrobial activity against pathogenic microorganisms [88]. Polyphenols are found largely in fruits, vegetables, cereals, tea, coffee, and wine and are an essential part of the Mediterranean diet. Thus, the Mediterranean diet might be a good choice in influencing the gut microbiota. The literature regarding the role of the regular diets in microbiota composition is still lacking.

Gut microbiota and human appetite

It should be mentioned that the gut microbiota may influence the appetite. For instance, gut mucosal cells produce Y3-36 anorexigenic peptide [89]. Expression of this peptide is induced by the binding of GPR41 and GPR43 with acetate and propionate, which are produced by the gut microbiota [90]. Current studies also detected the link between microbiota composition and anorexigenic leptin hormone. High abundance of *Lactococcus, Bifidobacterium*, and *Lactobacillus* is associated with high leptin concentrations in mice, whereas *Clostridium*, *Bacteroides* (genus in *Bacteroidetes* phylum), and *Prevotella* are associated with low leptin levels [91,92].

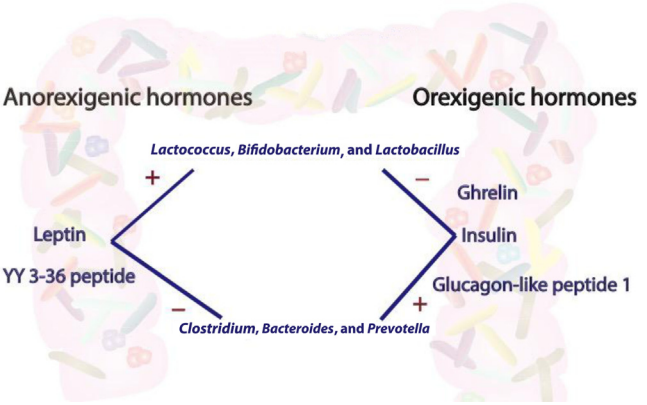

Fig. 4. Microbiota versus appetite.

Thus, a high fecal ratio of *Firmicutes* to *Bacteroidetes* is associated with decreased appetite probably because of leptin and YY peptide stimulation. A recent study demonstrated that leptin plays a role in the regulation of the microbiota composition independently of food intake in mice [93]. Moreover, a low fecal ratio of *Firmicutes* to *Bacteroidetes* was connected to low ghrelin level in this study. Ghrelin is well known as an orexigenic hormone. One study demonstrated that serum ghrelin level correlates negatively with *Bifidobacterium, Lactobacillus,* and *Blautia coccoides–Eubacterium rectale* group levels and positively correlates with the *Bacteroides* and *Prevotella* levels [92]. Similar results were found in another study [94].

Microbiota composition also is purported to be associated with insulin concentrations. In one study, microbiota infusion from lean donors to individuals with metabolic syndrome showed an increase in 16 bacterial groups, including those related to the butyrate-producer Roseburia intestinalis, and an improvement in insulin sensitivity [95]. The intestinally derived hormone glucagon-like peptide (GLP)-1 affects insulin gene expression and insulin secretion [96], and some authors consider that it also is connected to the microbiota composition (Fig. 4) [97,98].

Conclusion

Alterations to the gut microbiota have been observed in numerous diseases, including liver disease, obesity, type 2 diabetes, atherosclerosis, and irritable bowel syndrome. The fascinating research findings concerning the links between gut microbiota composition and brain [99], depression [100], and other disorders [101] were shown here. One of the key factors in determining gut microbiota composition is diet. Cooking methods, nutrient additives, probiotic and prebiotic consumption, and diet changes are likely to be good tools in influencing gut microbiota composition, which is particularly important in people of all ages.

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