Gut microbiota dysbiosis and the role of its person-to-person transmission in the development of non-communicable diseases

Disbiosis de la microbiota intestinal y el papel de su transmisión de persona-a-persona en el desarrollo de enfermedades no transmisibles

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Palabras clave

Obesidad; disbiosis; microbiota; salud; dieta.

Resumen

La microbiota intestinal desempeña un papel integral en la realización de los procesos de digestión, además de tener profundas implicaciones para la salud. Su composición y su impacto en el huésped dependen de diversos factores ambientales, tales como el tipo de dieta que consume un individuo. La alteración del microbioma intestinal provoca su disbiosis. Algunas enfermedades actualmente consideradas no transmisibles están relacionadas con la microbiota intestinal disbiótica. En los últimos años ha habido un interés creciente en estudiar la transmisión persona-a-persona de la microbiota intestinal y su papel en los efectos asociados a la salud. En esta revisión, se proporciona una visión sobre estos temas; además, se propone estudiar más a fondo los efectos de factores como la cohabitación y la dieta personal en la velocidad de transmisión.

Keywords

Obesity; dysbiosis; microbiota; obesity; health; diet.

Abstract

The gut microbiota plays an integral role in carrying out digestion processes as well as having profound health implications. Environmental factors such as the type of diet an individual consumes dictate its composition and its impact on the host. The disruption of the gut microbiome causes dysbiosis. Some presently considered non-communicable diseases are related to dysbiotic gut microbiota In recent years, there has been increasing interest in studying gut microbiota's person-to-person transmission and its role in health associated effects. In this review, an insight is provided into these topics; additionally, a proposition is made to further study the effects of factors such as cohabitation and personal diet on transmission rate speed.

Introduction

The diverse microbial community colonizing the human gastrointestinal (GI) tract gathers more than 100 trillion organisms and is termed as the gut microbiota [1]. The co-evolution of the gut microbiota and the host has formed a tangled symbiotic interaction [2]. These organisms include bacteria, yeasts, viruses, and parasites [3]; however, the major focus of current gut microbiota studies lie on bacteria [4].

Intestinal microbiota has been alluded to be a key determinant factor influencing the digestion, absorption, metabolism, and storage of indigested nutrients, with profound effects on the host physiology; therefore, gut dysbiosis, understood as reduced diversity and an imbalance of gut microbiota community structure [5], [6] has been associated with obese state, diabetes, and gastrointestinal diseases such as inflammatory bowel disease [7].

Non-communicable diseases (NCDs) such as obesity [8], heart disease and diabetes are some of the leading causes of death worldwide [9] and represent an emerging global health threat [10]. Deaths from NCDs now exceed all communicable disease deaths combined; they represent 41 million of them each year (7 out of 10 deaths worldwide) [10]. Growing evidence suggests that individuals with noncommunicable diseases have intestinal microbiota dysbiosis

[11]. Moreover, the occurrence and progression of obesity, comprehended as a metabolic disease, is significantly contributed by the gut microbiota, which influences mechanisms like energy homeostasis, lipid synthesis and storage [12], and gut permeability [13].

There are limitations to establish what constitutes a healthy gut microbiome common to all individuals, as many environmental factors shape its composition (Table 1), more than host genetics do [14], [15]. These factors include inflammation [16], diet, exercise, sleep pattern, smoking, alcohol intake, radiation, air pollution, exposure to antibiotics, and various co-morbidities [6], [17]. Furthermore, depending on a specific strain, its location in the body, the relative abundance of other bacteria, and many other conditions, a discrimination between health-associated bacteria and harmful pathogenic bacteria is not always clear [18], [19]. It is presently considered that the most abundant phyla in gut microbiota are Firmicutes and Bacteroidetes (90%) [20]. An increased Firmicutes/Bacteroidetes (F/B) ratio has been linked to obesity and could be a marker of dysbiosis [5], [21].

Table 1. Some environmental factors and their effects on gut microbiota.

Factor	Effects	References
Smoking	Neonates exposed to environmental smoke had a higher relative abundance of *Ruminococcus* and *Akkermansia*, and infants exposed to environmental smoke during pregnancy or postnatal period showed increased *Firmicutes* levels at 3 months of age, along with higher odds of obesity at 1 and 3 years of age.	[22]
Excessive alcohol consumption	Increases gut permeability, alters gut microbiota communities, and influences the pathogenesis of diseases including alcoholic liver disease.	[23], [24]
	Even a low dose of alcohol, such as 0.8 g/kg/day, altered the gut microbiota composition in mice.	[25]
	Gut microbiota composition differs between alcohol-related liver disease and non-alcoholic fatty liver disease, indicating an effect of alcohol intake on the gut microbiota.	[25]
Exercise	Exercise frequency tended to be negatively associated with the amount of *Enterobacteriaceae*, and positively correlated with the amount of *Prevotella*, in feces.	[26]
	Rapid increase in microbiota diversity before and after competition in a world-class ultramarathon runner.	[27]
	Exercise-induced alterations in the gut microbiota were closely associated with improvements in glucose homeostasis, insulin sensitivity, anti-inflammatory effects, increased microbiota diversity, and increased amount of commensal bacteria.	[28], [29]
Air pollution	Fine particulate matter (<10 μM) induces alterations in the microbiota diversity throughout the gastrointestinal tract.	[17], [30]
	Microbial diversity of spontaneously hypertensive rats was shown to be inversely associated with pollutants exposure.	[31]

Native core microbiota is shaped during early life: the profile of intestinal microbiota in the pregnancy term (birth gestational age), type of birth delivery, methods of milk feeding, the introduction of solid food, termination of milk feeding age, and use of antibiotics, are some of the major determinants, most of them being heavily influenced by the mother's own gut microbiome [1]. Another factor in the shaping of the gut microbiota is host genetics, which has a role in the selection of commensal bacteria; for example, the expression of fecal microRNA (miARN) genes by gut epithelial cells can regulate bacterial gene expression and growth [32].

However, maternal seeding alone cannot account for the large diversity of microorganisms found in adults [33]. How members of the microbiome are acquired and transmitted by individuals and spread in populations, and how this shapes the personal microbiome genetic makeup, remain largely unexplored, especially in humans [33], [34], [35]. Recent findings have brought to light the importance of inter-host transmission and its influence on microbiome composition and dynamics [36].

Diet is another fundamental factor that shapes gut microbiota composition and function [7]. The diversity of the microbiota gained through food depends on diet [18], as it is one of the major lifestyle factors responsible for microbiome changes [37], [38]. Commensal bacteria provide health benefits to the host that are a result of their colonization; whereas, depending on their virulence and infectious dose, pathogen colonization can cause disease [18].

The colon is the most densely populated microbial body location [39]; there, undigested food acts as a substrate for bacterial metabolism [7]. Dietary macronutrient composition dictates the source and amount of fermentable substrate by the microbiota, which releases different classes of metabolites [40]. These products can induce a series of physiological functions on hosts and other bacteria [41]. Short-chain fatty acids (SCFAs) are one of the most extensively studied gut microbiota metabolites, and account for specific functions such as regulation of gut microbiota composition [41]; however, their production is decreased under Western-style diets (WSD), which are low in fibers and high in fats and simple sugars [42].

Hereinafter, the influence of dietary patterns, particularly WSD, in the gut microbiota is discussed, as well as the factors determining the person-to-person transmission dynamics of the microbiota, in an attempt to explore the influence of diet-induced dysbiotic gut microbiota in the transmission of diseases currently considered non-communicable.

Dietary fibers as primordial microbial substrates

Dietary fibers are carbohydrates mainly from plant foods, like whole grains, fruits, vegetables and legumes [43]. Based on physiological properties, dietary fiber can be subdivided into three types: non-starchy polysaccharides (NSPs), resistant starches (RS) and resistant/nondigestible oligosaccharides (ROS) [43], [44]. Dietary fiber is fermented by fiber-degrading bacteria, producing beneficial microbial metabolites, such as SCFAs [43]. Generally, SCFAs are considered beneficial to gut health [7].

Dietary fibers evade breakdown in the upper gastrointestinal tract and are fermented by bacteria in the colon, where fiber serves as a substrate for microbial carbohydrate-active enzymes (CAZymes), like glycoside hydrolases (GHs) and polysaccharide lyases. Some bacterial strains can share dietary fibers synergistically through cross-feeding, i.e., primary degraders can partially hydrolyze polysaccharides and these breakdown products can be used by secondary degraders [40], [43].

Among the metabolites produced by gut microbial degradation of nutrients, SCFAs have a weighty importance as they are essential for microbial population and intestinal homeostasis; these metabolites are mainly produced by anaerobic fermentation of dietary fibers in the intestine [45]. SCFAs contain less than six carbon atom numbers; acetate, propionate and butyrate account for 90% of SCFAs produced by gut microbiota [46], which are a major energy source for the intestinal epithelial cells [47]. Besides, SCFAs impact host health by mechanisms related to gut barrier function, glucose metabolism, immunomodulation, and obesity [21].

The processes by which the SCFAs are biosynthesized involve specific bacterial taxa. *Bifidobacterium* species are characteristic acetate producers [48], which is also secreted by *Akkermancia muciniphila* along with propionate [49]. *A. muciniphila* has an important role

promoting the synthesis of SCFAs by regulating the gut microbiota [50]. *Roseburia inilivorans* and *Coproccocus spp.,* which belong to the Lachnospiraceae family, together with Bacteroidetes such as P*revotella spp.*, and Bacillota (*Phascolarctobacterium succinatutens* or *Veillonella spp.*), are examples of bacteria that can release propionate [48]. Most butyrate-producing bacteria pertain to the Clostridia class of the Firmicutes phylum, including *Faecalibacterium prausnitzii*, *Roseburia spp.*, *Eubacterium spp.*, *Anaerostipes spp.,* and *Coprococcus spp.* Of importance, *Faecalibacterium prausnitzii* is the most abundant butyrate producer in the human gut [51]. Furthermore, in obese individuals, the levels of *F. prausnitzii* have been found to be reduced [5], [52]. Interestingly, species like *Eubacterium hallii* utilize acetate and lactate produced by *Bifidobacterium spp.* for butyrate generation, which in turn supports *Bifidobacterium spp.* abundance, evidencing the cross-feeding between SCFAs-producing bacteria [48], [51].

The Western-Style diet and gut health

Despite the known fiber requirements for gut health, the WSD lacks dietary fiber [44] and it is rich in saturated and trans fats, while low in health-promoting fats such as mono and polyunsaturated fats [53]. The development of obesity and other metabolic diseases is contributed by changes from a diet rich in fibers and low in fats to a diet low in fibers and high in saturated fats [54], [55]. There are major differences in gut microbiota composition among individuals adhering to a WSD and those with a diet high in fiber [17].

Some diets may affect the gut microbiota by promoting the growth of some bacterial strains and inducing dysbiosis. For example, greater permeability of the inner mucus layer and a slower mucus growth rate were observed in mice fed a WSD, compared with chow-fed mice, together with a gradual decrease of *Actinobacteria* (*Bifidobacterium*) and *Bacteroidetes*, while *Firmicutes* increased in relative abundance in the colonic luminal content [56]. In another study, greater colonic damage and decreased expression of tight junction proteins (TJPs) in colonic tissue was observed in rodents fed a high fat diet (HFD), compared to the low-fat diet treatment [57]. Likewise, the F/B ratio was higher in HFD-fed mice following a 16-week intervention, compared to chow-fed mice, also showing lower expressions of TJPs (occludin and claudin-1) [58], which compromise the regulation of the intestinal barrier permeability [59]. Futhermore, a decreased abundance of probiotics like *Faecalibacterium, Dubosiella,* and *Muribaculaceae* was reported in the HFD-fed mice, while the relative abundance of harmful bacteria such as *Erysipelatoclostridium, Romboutsia,* and *Acetatifactor* increased [58]. Similarly, under a whole-grain diet, healthy, overweight adults with high *Prevotella* abundance in their gut microbiota lost more weight than in the refined-grain diet (lower in dietary fiber) [60].

Interestingly, “good” bacteria intake has shown promising potential for ameliorating WSD negative effects. For example, the oral administration of *Lactiplantibacillus plantarum* strain CNCM I−4459 on male mice improved the metabolic parameters that were compromised by HFD treatments, such as hepatic lipid and glucose metabolism [8]. Likewise, in HFD-induced obese mice treated with *Lactobacillus plantarum* K50, the fat mass and body weight were significantly reduced, compared to the HFD-fed control mice; the (F/B) ratio was notably higher in the HFD-fed control mice than in *L. plantarum* K50-treated mice; and the concentration of SCFAs such as butyrate and valerate had a significant increase in the *L. plantarum* K50-treated mice, showing how this probiotic could ameliorate obesity and even reverse HFD-induced gut microbiota dysbiosis [61]. In a like manner, body weight gain in HFD-induced diabetic mice was reduced after being fed with *Akkermancia muciniphila*-derived extracellular vesicles, showing increased expression of major TJPs (occludin, zonal occludens and claudin-5) in the intestinal epithelial layer [62].

The person-to-person transmission dynamics of the gut microbiota

For the transmission of commensal and pathogenic bacteria, the bacteria must exit the host, typically through fecal matter, then they must persist in the external space and survive environmental stresses such as the toxic effects of atmospheric oxygen, ultraviolet radiation, a lack of nutrients, adverse temperatures and desiccation [18].

Once the bacteria persist in the environment and are ingested by a host, they must colonize it, which entails establishing a niche in the intestinal environment, using available nutrients, and replicating to a level that will ensure stability and survival; for all of that to happen, the bacteria must compete against the resident microbiota, and this colonization resistance has important roles in preventing invasion by pathogenic bacteria and in maintaining intestinal homeostasis [18]. Resident bacteria can fend off pathogenic bacteria by using the available nutrients and by secreting toxins that target neighboring bacteria [18], [63]. The reservoirs of commensal bacteria are food, water, animals, the built environment (furniture, objects, structures, and surfaces), and humans as the main reservoir [18], [64].

There's also a hypothetical model that explains the different transmission dynamics of spore-forming and non-spore-forming bacteria. For people who are in close contact and proximity with each other, for example co-residents, both non-spore-forming and spore-forming bacteria have the same transmission efficiency; in contrast, with a colleague or an acquaintance, one might get in close contact less frequently and more physically distant, which leads to the spore-forming bacteria to have prevalence in transmission since they can remain viable in the environment for longer periods of time [17].

However, the extent to which interpersonal relations shape the individual makeup of the microbiome and its transmission within and across populations remains largely unknown. Valles-Colomer *et al.* [33] used a robust metagenomic dataset to detect extensive bacterial strain sharing across individuals, with distinct transmission patterns among mother-to-infant, intra-household and intra-population. Around 50% of the same strains were shared in mother-to-infant transmission, while 12% were shared in cohabitating individuals, with time since the start of cohabitation having a larger role in strain sharing than age or genetics did. Moreover, diet, drug consumption, access to health institutions, and hygiene practices had little influence on microbiome transmission, referring to the transmission rate itself and not the types of microbiota composition transmitted [33]. These results might point to similar colonization resistance across populations potentially having greater importance than the rates of transmission events; and suggest that, given that the gut microbiome can be inherited and even transmitted, some diseases categorized as non-communicable should be reevaluated [33].

The interindividual differences in disease evolution, incomplete comprehension of the mechanisms integrating microbiota-derived signals into host signaling pathways, and microbial communities' heterogeneity, considerably represent current limitations when understanding the contribution of the gut microbiota to disease causality [65]. The interaction between diet, gut microbiota, and human health are complex and multidirectional, which also poses a challenge in establishing causality for the gut microbiome's role in the predisposition to human diseases [66].

The possible transmission of non-communicable diseases (NCDs) through dysbiotic gut microbiota

There is growing evidence suggesting that NCDs are associated with some transmissible components, one of them being the gut microbiota [67], [68], [69]. For example, in a study of fecal microbiota transplant from obese and lean co-twin mice to separate groups of germ-free mice, significantly greater increases in body mass, as well as obesity-associated metabolic

phenotypes, were conveyed from the obese co-twins' bacterial component than those from the lean mice, where SCFAs fermentation was increased; moreover, cohousing mice harboring a lean twin's microbiota with mice containing obese co-twin's microbiota prevented the aforementioned effects in obese cage mates and transformed their microbiota's metabolic profile to a lean like state [70].

The spread of NCDs may be promoted as people socialize more frequently, since this can multiply the risk of gut microbiota exchange among individuals in a population [11]. In a study conducted by Huang *et al.* [17], several questions were addressed related to the hypothesis that NCDs are in fact communicable via dysbiosis, some of them being: can environmental factors such as diet, smoking, alcohol intake, exercise, and air pollution influence the microbiota (Table 1), and how dysbiosis can be induced by the transmission of the microbiota from person to person [17]?

In 1890, Robert Koch published a set of postulates that have served well for establishing the causative agent of most infectious diseases. Applying a version of Koch's postulates adapted to NCDs could determine whether the collective microbiota can be considered an "infectious agent," which would support the hypothesis of communicable NCDs [69]. First, transmissible dysbiotic microbiota (TDM) should be found in individuals with NCDs. Second, TDM can be isolated from the host and grown in culture. Third, TDM can cause NCDs when transferred into a healthy host. Finally, TDM can again be isolated from the inoculated diseased host [71].

However, another issue concerns the definition of transmissible dysbiotic microbiota. The composition of TDM may differ among various NCDs, as well as at the population level due to heterogeneity among individuals. In fact, these pathogen or causative agent in NCDs patients could be induced to a higher abundance or prevalence under some environmental factors such high-fat diet and smoking. These may not simply alter the gut microbiota composition but could also induce microbiota dysbiosis in the gut [17].

The role of colonization resistance in the transmission of the gut microbiota

Colonization resistance is a phenomenon whereby the gut microbiota has the capacity to resist the invasion of the exogenous pathogens and the expansion of the resident pathobionts [71]. The diversity and richness of gut microbiome is key to immune system regulation and colonization resistance against pathogens [72].

The determination of who becomes the donor and who becomes the recipient is dependent on each individual's gut microbiota state [18]. A person with a healthy non-dysbiotic microbiota possesses a high colonization resistance [73] and is presumed to be the usual donor which can therefore provide commensal bacteria to the environment, which can then colonize a dysbiotic recipient, characterized by having a low colonization resistance [18]. In theory, donors that have the greatest diversity of commensal bacteria are most likely to replenish the depleted microbiota of potential recipients [74]. Suboptimal donors may have once been healthy donors, but antibiotic exposure or other disease conditions caused a decrease in the diversity of their gut microbiota, and they could potentially include higher levels of pathogens, which may be transmitted at a higher frequency than from healthy donors [18].

Conclusion

A Western-style diet is capable of inducing gut microbiota dysbiosis which can then cause pathophysiological effects on the host, such as an increase in weight, eventually leading to overweight and obesity. Assuming that dysbiotic gut microbiota is transmittable, through the routes of transmission previously expanded upon, additional studies are necessary to establish

the links and causalities between the person-to-person transmission of a dysbiotic gut microbiota and the development of a disease presumed to be non-communicable, taking into account the colonization resistance of each person.

Assembling and maintaining a healthy intestinal microbiota may depend not only on one's diet but also on the diet-induced state of others' microbiota. The health status of the donors that people acquire the microbiota from may affect the composition of one's own intestinal microbiota.

Further investigations should focus on studying the effects on transmission dynamics in more specific social contexts, such as following a household change, and if factors such as the amount of time since the start of cohousing or personal diets affect the speed of transmission rate.

References

[1] E. Rinninella *et al.*, "What is the Healthy Gut Microbiota Composition? A Changing Ecosystem across Age, Environment, Diet, and Diseases," *Microorganisms*, vol. 7, no. 14, Jan. 2019, doi: 10.3390/microorganisms7010014.

[2] E. Thursby and N. Juge, "Introduction to the human gut microbiota," *Biochemical Journal*, vol. 474, no. 11, pp. 1823–1836, Jun. 2017, doi: 10.1042/BCJ20160510.

[3] M. De Siena *et al.*, "Gut and Reproductive Tract Microbiota Adaptation during Pregnancy: New Insights for Pregnancy-Related Complications and Therapy," *Microorganisms*, vol. 9, no. 3, p. 473, Feb. 2021, doi: 10.3390/microorganisms9030473.

[4] C.-H. Tseng and C.-Y. Wu, "The gut microbiome in obesity," *Journal of the Formosan Medical Association*, vol. 118, pp. S3–S9, Mar. 2019, doi: 10.1016/j.jfma.2018.07.009.

[5] T. U. Maioli *et al.*, "Possible Benefits of Faecalibacterium prausnitzii for Obesity-Associated Gut Disorders," *Front Pharmacol*, vol. 12, no. 740636, Dec. 2021, doi: 10.3389/fphar.2021.740636.

[6] J. E. Martinez *et al.*, "Unhealthy Lifestyle and Gut Dysbiosis: A Better Understanding of the Effects of Poor Diet and Nicotine on the Intestinal Microbiome," *Front Endocrinol (Lausanne)*, vol. 12, no. 667066, Jun. 2021, doi: 10.3389/fendo.2021.667066.

[7] P. Zhang, "Influence of Foods and Nutrition on the Gut Microbiome and Implications for Intestinal Health," *Int J Mol Sci*, vol. 23, no. 17, p. 9588, Aug. 2022, doi: 10.3390/ijms23179588.

[8] E. Jacouton, S. Mondot, P. Langella, and L. G. Bermúdez-Humarán, "Impact of Oral Administration of Lactiplantibacillus plantarum Strain CNCM I–4459 on Obesity Induced by High-Fat Diet in Mice," *Bioengineering*, vol. 10, no. 10, p. 1151, Oct. 2023, doi: 10.3390/bioengineering10101151.

[9] World Health Organization, "Noncommunicable diseases," World Health Organization . Accessed: Apr. 05, 2024. [Online]. Available: https://www.who.int/data/gho/data/themes/noncommunicable-diseases#:~:text=They%20include%20tobacco%2C%20harmful%20use,be%20overcome%20using%20existing%20knowledge.

[10] Centers for Disease Control and Prevention, "About Global NCDs," Centers for Disease Control and Prevention. Accessed: Apr. 05, 2024. [Online]. Available: https://www.cdc.gov/globalhealth/healthprotection/ncd/global-ncd-overview.html

[11] F. Bu *et al.*, "Pathogenic or Therapeutic: The Mediating Role of Gut Microbiota in Non-Communicable Diseases," *Front Cell Infect Microbiol*, vol. 12, no. 906349, Jul. 2022, doi: 10.3389/fcimb.2022.906349.

[12] Z. Cheng, L. Zhang, L. Yang, and H. Chu, "The critical role of gut microbiota in obesity," *Front Endocrinol (Lausanne)*, vol. 13, no. 1025706, Oct. 2022, doi: 10.3389/fendo.2022.1025706.

[13] P. Portincasa *et al.*, "Intestinal Barrier and Permeability in Health, Obesity and NAFLD," *Biomedicines*, vol. 10, no. 83, p. 83, Dec. 2021, doi: 10.3390/biomedicines10010083.

[14] M. I. McBurney *et al.*, "Establishing What Constitutes a Healthy Human Gut Microbiome: State of the Science, Regulatory Considerations, and Future Directions," *J Nutr*, vol. 149, no. 11, pp. 1882–1895, Nov. 2019, doi: 10.1093/jn/nxz154.

[15] E. R. Leeming, P. Louca, R. Gibson, C. Menni, T. D. Spector, and C. I. Le Roy, "The complexities of the diet-microbiome relationship: advances and perspectives," *Genome Med*, vol. 13, no. 10, Jan. 2021, doi: 10.1186/s13073-020-00813-7.

[16] Z. Al Bander, M. D. Nitert, A. Mousa, and N. Naderpoor, "The Gut Microbiota and Inflammation: An Overview," *Int J Environ Res Public Health*, vol. 17, no. 20, p. 7618, Oct. 2020, doi: 10.3390/ijerph17207618.

[17] R. Huang, Z. Ju, and P.-K. Zhou, "A gut dysbiotic microbiota-based hypothesis of human-to-human transmission of non-communicable diseases," *Science of The Total Environment*, vol. 745, p. 141030, Nov. 2020, doi: 10.1016/j.scitotenv.2020.141030.

[18] H. P. Browne, B. A. Neville, S. C. Forster, and T. D. Lawley, "Transmission of the gut microbiota: spreading of health," *Nat Rev Microbiol*, vol. 15, no. 9, pp. 531–543, Sep. 2017, doi: 10.1038/nrmicro.2017.50.

[19] D. Patra, D. Banerjee, P. Ramprasad, S. Roy, D. Pal, and S. Dasgupta, "Recent insights of obesity-induced gut and adipose tissue dysbiosis in type 2 diabetes," *Front Mol Biosci*, vol. 10, no. 1224982, Sep. 2023, doi: 10.3389/fmolb.2023.1224982.

[20] E. Amabebe, F. O. Robert, T. Agbalalah, and E. S. F. Orubu, "Microbial dysbiosis-induced obesity: role of gut microbiota in homoeostasis of energy metabolism," *British Journal of Nutrition*, vol. 123, no. 10, pp. 1127–1137, May 2020, doi: 10.1017/S0007114520000380.

[21] O. Lange, M. Proczko-Stepaniak, and A. Mika, "Short-Chain Fatty Acids—A Product of the Microbiome and Its Participation in Two-Way Communication on the Microbiome-Host Mammal Line," *Curr Obes Rep*, vol. 12, no. 2, pp. 108–126, May 2023, doi: 10.1007/s13679-023-00503-6.

[22] C. McLean, S. Jun, and A. Kozyrskyj, "Impact of maternal smoking on the infant gut microbiota and its association with child overweight: a scoping review," *World Journal of Pediatrics*, vol. 15, no. 4, pp. 341–349, Aug. 2019, doi: 10.1007/s12519-019-00278-8.

[23] V. B. Dubinkina *et al.*, "Links of gut microbiota composition with alcohol dependence syndrome and alcoholic liver disease," *Microbiome*, vol. 5, no. 141, Dec. 2017, doi: 10.1186/s40168-017-0359-2.

[24] A. Lenhart and W. D. Chey, "A Systematic Review of the Effects of Polyols on Gastrointestinal Health and Irritable Bowel Syndrome," *Advances in Nutrition*, vol. 8, no. 4, pp. 587–596, Jul. 2017, doi: 10.3945/an.117.015560.

[25] J. P. Arab, M. Arrese, and V. H. Shah, "Gut microbiota in non-alcoholic fatty liver disease and alcohol-related liver disease: Current concepts and perspectives," *Hepatology Research*, vol. 50, no. 4, pp. 407–418, Apr. 2020, doi: 10.1111/hepr.13473.

[26] T. Shima *et al.*, "Association of life habits and fermented milk intake with stool frequency, defecatory symptoms and intestinal microbiota in healthy Japanese adults," *Benef Microbes*, vol. 10, no. 8, pp. 841–854, Dec. 2019, doi: 10.3920/BM2019.0057.

[27] G. J. Grosicki, R. P. Durk, and J. R. Bagley, "Rapid gut microbiome changes in a world-class ultramarathon runner," *Physiol Rep*, vol. 7, no. 24, Dec. 2019, doi: 10.14814/phy2.14313.

[28] Y. Liu *et al.*, "Gut Microbiome Fermentation Determines the Efficacy of Exercise for Diabetes Prevention," *Cell Metab*, vol. 31, pp. 77–91, Jan. 2020, doi: 10.1016/j.cmet.2019.11.001.

[29] V. Monda *et al.*, "Exercise Modifies the Gut Microbiota with Positive Health Effects," *Oxid Med Cell Longev*, vol. 2017, pp. 1–8, 2017, doi: 10.1155/2017/3831972.

[30] E. A. Mutlu *et al.*, "Inhalational exposure to particulate matter air pollution alters the composition of the gut microbiome," *Environmental Pollution*, vol. 240, pp. 817–830, Sep. 2018, doi: 10.1016/j.envpol.2018.04.130.

[31] D. Chen *et al.*, "Exposure to atmospheric pollutants is associated with alterations of gut microbiota in spontaneously hypertensive rats," *Exp Ther Med*, vol. 18, no. 5, pp. 3484–3492, Aug. 2019, doi: 10.3892/etm.2019.7934.

[32] S. Liu *et al.*, "The Host Shapes the Gut Microbiota via Fecal MicroRNA," *Cell Host Microbe*, vol. 19, pp. 32–43, Jan. 2016, doi: 10.1016/j.chom.2015.12.005.

[33] M. Valles-Colomer *et al.*, "The person-to-person transmission landscape of the gut and oral microbiomes," *Nature*, vol. 614, no. 7946, pp. 125–135, Feb. 2023, doi: 10.1038/s41586-022-05620-1.

[34] A. Sarkar *et al.*, "Microbial transmission in animal social networks and the social microbiome," *Nat Ecol Evol*, vol. 4, no. 8, pp. 1020–1035, Jun. 2020, doi: 10.1038/s41559-020-1220-8.

[35] S. Samartino, D. Christie, A. Penna, P. Sicotte, N. Ting, and E. Wikberg, "Social network dynamics, infant loss, and gut microbiota composition in female Colobus vellerosus during time periods with alpha male challenges," *Primates*, vol. 65, no. 4, pp. 299–309, Jul. 2024, doi: 10.1007/s10329-024-01132-w.

[36] C. D. Robinson, B. J. Bohannan, and R. A. Britton, "Scales of persistence: transmission and the microbiome," *Curr Opin Microbiol*, vol. 50, pp. 42–49, Aug. 2019, doi: 10.1016/j.mib.2019.09.009.

[37] V. Lazar *et al.*, "Gut Microbiota, Host Organism, and Diet Trialogue in Diabetes and Obesity," *Front Nutr*, vol. 6, no. 21, Mar. 2019, doi: 10.3389/fnut.2019.00021.

[38] P. Illiano, R. Brambilla, and C. Parolini, "The mutual interplay of gut microbiota, diet and human disease," *FEBS J*, vol. 287, no. 5, pp. 833–855, Mar. 2020, doi: 10.1111/febs.15217.

[39] P. I. Costea *et al.*, "Enterotypes in the landscape of gut microbial community composition," *Nat Microbiol*, vol. 3, pp. 8–16, Dec. 2017, doi: 10.1038/s41564-017-0072-8.

[40] K. A. Krautkramer, J. Fan, and F. Bäckhed, "Gut microbial metabolites as multi-kingdom intermediates," *Nat Rev Microbiol*, vol. 19, no. 2, pp. 77–94, Feb. 2021, doi: 10.1038/s41579-020-0438-4.

[41] J. Liu, Y. Tan, H. Cheng, D. Zhang, W. Feng, and C. Peng, "Functions of Gut Microbiota Metabolites, Current Status and Future Perspectives," *Aging Dis*, vol. 13, no. 4, p. 1106, 2022, doi: 10.14336/AD.2022.0104.

[42] G. Birchenough, B. O. Schroeder, F. Bäckhed, and G. C. Hansson, "Dietary destabilisation of the balance between the microbiota and the colonic mucus barrier," *Gut Microbes*, vol. 10, no. 2, pp. 246–250, Mar. 2019, doi: 10.1080/19490976.2018.1513765.

[43] J. Fu, Y. Zheng, Y. Gao, and W. Xu, "Dietary Fiber Intake and Gut Microbiota in Human Health," *Microorganisms*, vol. 10, no. 12, p. 2507, Dec. 2022, doi: 10.3390/microorganisms10122507.

[44] K. Makki, E. C. Deehan, J. Walter, and F. Bäckhed, "The Impact of Dietary Fiber on Gut Microbiota in Host Health and Disease," *Cell Host Microbe*, vol. 23, no. 6, pp. 705–715, Jun. 2018, doi: 10.1016/j.chom.2018.05.012.

[45] P. Portincasa *et al.*, "Gut Microbiota and Short Chain Fatty Acids: Implications in Glucose Homeostasis," *Int J Mol Sci*, vol. 23, no. 3, p. 1105, Jan. 2022, doi: 10.3390/ijms23031105.

[46] R.-G. Xiong *et al.*, "Health Benefits and Side Effects of Short-Chain Fatty Acids," *Foods*, vol. 11, no. 18, p. 2863, Sep. 2022, doi: 10.3390/foods11182863.

[47] J. G. LeBlanc, F. Chain, R. Martín, L. G. Bermúdez-Humarán, S. Courau, and P. Langella, "Beneficial effects on host energy metabolism of short-chain fatty acids and vitamins produced by commensal and probiotic bacteria," *Microb Cell Fact*, vol. 16, no. 1, p. 79, Dec. 2017, doi: 10.1186/s12934-017-0691-z.

[48] W. Fusco *et al.*, "Short-Chain Fatty-Acid-Producing Bacteria: Key Components of the Human Gut Microbiota," *Nutrients*, vol. 15, no. 9, p. 2211, May 2023, doi: 10.3390/nu15092211.

[49] A. P. Lakshmanan, S. Murugesan, S. Al Khodor, and A. Terranegra, "The potential impact of a probiotic: Akkermansia muciniphila in the regulation of blood pressure—the current facts and evidence," *J Transl Med*, vol. 20, no. 1, p. 430, Sep. 2022, doi: 10.1186/s12967-022-03631-0.

[50] J. Shen *et al.*, "*Akkermansia muciniphila* attenuated lipopolysaccharide-induced acute lung injury by modulating the gut microbiota and SCFAs in mice," *Food Funct*, vol. 14, no. 23, pp. 10401–10417, 2023, doi: 10.1039/D3FO04051H.

[51] V. Singh *et al.*, "Butyrate producers, 'The Sentinel of Gut': Their intestinal significance with and beyond butyrate, and prospective use as microbial therapeutics," *Front Microbiol*, vol. 13, no. 1103836, Jan. 2023, doi: 10.3389/fmicb.2022.1103836.

[52] R. Martín, L. G. Bermúdez-Humarán, and P. Langella, "Searching for the Bacterial Effector: The Example of the Multi-Skilled Commensal Bacterium Faecalibacterium prausnitzii," *Front Microbiol*, vol. 9, no. 346, Mar. 2018, doi: 10.3389/fmicb.2018.00346.

[53] R. K. Singh *et al.*, "Influence of diet on the gut microbiome and implications for human health," *J Transl Med*, vol. 15, no. 1, p. 73, Dec. 2017, doi: 10.1186/s12967-017-1175-y.

[54] D. Statovci, M. Aguilera, J. MacSharry, and S. Melgar, "The Impact of Western Diet and Nutrients on the Microbiota and Immune Response at Mucosal Interfaces," *Front Immunol*, vol. 8, no. 838, Jul. 2017, doi: 10.3389/fimmu.2017.00838.

[55] A. Agus *et al.*, "Western diet induces a shift in microbiota composition enhancing susceptibility to Adherent-Invasive E. coli infection and intestinal inflammation.," *Sci Rep*, vol. 6, no. 1, p. 19032, Jan. 2016, doi: 10.1038/srep19032.

[56] B. O. Schroeder *et al.*, "Bifidobacteria or Fiber Protects against Diet-Induced Microbiota-Mediated Colonic Mucus Deterioration," *Cell Host Microbe*, vol. 23, no. 1, pp. 27–40, Jan. 2018, doi: 10.1016/j.chom.2017.11.004.

[57] G. Chompre *et al.*, "A one month high fat diet disrupts the gut microbiome and integrity of the colon inducing adiposity and behavioral despair in male Sprague Dawley rats," *Heliyon*, vol. 8, no. 11, p. e11194, Nov. 2022, doi: 10.1016/j.heliyon.2022.e11194.

[58] X. Zhu *et al.*, "A High-Fat Diet Increases the Characteristics of Gut Microbial Composition and the Intestinal Damage Associated with Non-Alcoholic Fatty Liver Disease," *Int J Mol Sci*, vol. 24, no. 23, p. 16733, Nov. 2023, doi: 10.3390/ijms242316733.

[59] F. Schreiber, I. Balas, M. J. Robinson, and G. Bakdash, "Border Control: The Role of the Microbiome in Regulating Epithelial Barrier Function," *Cells*, vol. 13, no. 6, p. 477, Mar. 2024, doi: 10.3390/cells13060477.

[60] L. Christensen *et al.*, "Prevotella Abundance Predicts Weight Loss Success in Healthy, Overweight Adults Consuming a Whole-Grain Diet Ad Libitum: A Post Hoc Analysis of a 6-Wk Randomized Controlled Trial," *J Nutr*, vol. 149, no. 12, pp. 2174–2181, Dec. 2019, doi: 10.1093/jn/nxz198.

[61] H. Joung, J. Chu, B.-K. Kim, I.-S. Choi, W. Kim, and T.-S. Park, "Probiotics ameliorate chronic low-grade inflammation and fat accumulation with gut microbiota composition change in diet-induced obese mice models," *Appl Microbiol Biotechnol*, vol. 105, no. 3, pp. 1203–1213, Feb. 2021, doi: 10.1007/s00253-020-11060-6.

[62] C. Chelakkot *et al.*, "Akkermansia muciniphila-derived extracellular vesicles influence gut permeability through the regulation of tight junctions," *Exp Mol Med*, vol. 50, no. 2, pp. e450–e450, Feb. 2018, doi: 10.1038/emm.2017.282.

[63] F. Spragge *et al.*, "Microbiome diversity protects against pathogens by nutrient blocking," *Science (1979)*, vol. 382, no. 6676, Dec. 2023, doi: 10.1126/science.adj3502.

[64] S. T. Kelley and J. A. Gilbert, "Studying the microbiology of the indoor environment," *Genome Biol*, vol. 14, no. 2, p. 202, 2013, doi: 10.1186/gb-2013-14-2-202.

[65] A. Metwaly, S. Reitmeier, and D. Haller, "Microbiome risk profiles as biomarkers for inflammatory and metabolic disorders," *Nat Rev Gastroenterol Hepatol*, vol. 19, no. 6, pp. 383–397, Jun. 2022, doi: 10.1038/s41575-022-00581-2.

[66] A. M. Armet *et al.*, "Rethinking healthy eating in light of the gut microbiome," *Cell Host Microbe*, vol. 30, no. 6, pp. 764–785, Jun. 2022, doi: 10.1016/j.chom.2022.04.016.

[67] A. Kumar *et al.*, "Communication in non-communicable diseases (NCDs) and role of immunomodulatory nutraceuticals in their management," *Front Nutr*, vol. 9, no. 966152, Sep. 2022, doi: 10.3389/fnut.2022.966152.

[68] Z. Huang *et al.*, "Unveiling and harnessing the human gut microbiome in the rising burden of non-communicable diseases during urbanization," *Gut Microbes*, vol. 15, no. 1, Dec. 2023, doi: 10.1080/19490976.2023.2237645.

[69] B. B. Finlay, "Are noncommunicable diseases communicable?," *Science (1979)*, vol. 367, no. 6475, pp. 250–251, Jan. 2020, doi: 10.1126/science.aaz3834.

[70] V. K. Ridaura *et al.*, "Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice," *Science (1979)*, vol. 341, no. 6150, Sep. 2013, doi: 10.1126/science.1241214.

[71] I. Khan *et al.*, "Mechanism of the Gut Microbiota Colonization Resistance and Enteric Pathogen Infection," *Front Cell Infect Microbiol*, vol. 11, no. 716299, Dec. 2021, doi: 10.3389/fcimb.2021.716299.

[72] A. M. Seekatz, N. Safdar, and S. Khanna, "The role of the gut microbiome in colonization resistance and recurrent *Clostridioides difficile* infection," *Therap Adv Gastroenterol*, vol. 15, pp. 1–18, Jan. 2022, doi: 10.1177/17562848221134396.

[73] D. Podlesny *et al.*, "Identification of clinical and ecological determinants of strain engraftment after fecal microbiota transplantation using metagenomics," *Cell Rep Med*, vol. 3, no. 8, p. 100711, Aug. 2022, doi: 10.1016/j.xcrm.2022.100711.

[74] V. Horrocks, O. G. King, A. Y. G. Yip, I. M. Marques, and J. A. K. McDonald, "Role of the gut microbiota in nutrient competition and protection against intestinal pathogen colonization," *Microbiology (N Y)*, vol. 169, no. 8, Aug. 2023, doi: 10.1099/mic.0.001377.