Impact of Ethnicity and Diet on Host Gut Microbiota: A Review

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Abstract

The health and disease of human beings are affected by the gut microbiota. The association of the disease with the microbiota has been explored in the populations. However, this baseline of the gut microbiota is absent in the whole nation. The gut microbial formation depends on microbial metabolism, but association with the microbiota present in distinct diets of humans has not been discovered. In this manner, the fecal microbiota of children could compare, and the high fiber content is found in it. This would be the same as that of the early settlements of humans at the birth time of agriculture. There is an important enhancement in gut microbiota in these two groups through 16S rDNA sequencing and biochemical analyses. First, there is the identification of the four enterotypes. The three are enhanced for prevotella, Bacteroides, and Escherichia. But there is no dominant genus of the fourth one. Then, there is an imposing collaboration among the gut microbiota and many variables connected to the six kinds: diet, demography, geography, urbanization, etc. Then, there is discovered that the types of largest microbiota are demonstrated by geography. After that, there is a clarification of the different patterns in collaboration with food staple, ethnicity, and residential areas. Finally, there is the observation of the consumption of wheat by individuals as chief food, having more variety of microbiota. This is composed of the 1,3beta-glucosidase and S-adenosyl-L-methionine. This is responsible for biosynthesis in those individuals who are consuming the rice, depending on the prognostic function.

Keywords: Gut Microbiota; Ethnicity; GI Tract; Review Article; Diet Role

Introduction

Microbes play a vital role in animal digestion, endogenous and exogenous compound metabolism, modulation of the immune system for defense, and many other mechanisms as they secrete such enzymes that a host cannot produce and are beneficial for human health. Some species of microbiota can induce systematic immune responses along with their metabolites [32]. The gastrointestinal tract (GI) of humans is the largest interface, with a length of almost $250 – 400$ m^2, among the host, antigens, and the environmental factors. 60 tons of food pass through the GI tract in a human's average lifetime [29] and a huge number of microbes will also enter the body. The overall collection of microbes like archaea and bacteria in the human gut tract is known as "Gut Microbiota."

The total estimate of the GI tract inhabiting microbes exceeds 10^{14}; and this number is 10 times more than the number of human cells. The recent studies suggested that the ratio of host and gut microbes is 1:1 [33]. A bacterial population inhabits the human gut along the length of the oral cavity to the rectum. A number of factors affect the gut microbiota density and composition, including environmental

conditions, substrate availability and secretions of the host, body mass index (BMI), ethnicity, drug use, and smoking [27]. "Core Microbiome" is a common set of the microbe taxa that occurs in individuals, and they have a variety of dietary habitats and geographic origins. There are billions of bacterial cells in the human gut, which are about equal in number to our cells [33].

As a result, there has been a drive to classify the microbiota as a new organ of the human body. Their close proximity to the intestinal mucosa, which is biologically active and has a high cellular turnover rate, makes them physiologically active. In humans, the prevention or precipitation of illness [21]. The gut microbiota has a symbiotic relationship with the host, generating a number of compounds that aid in the maintenance of health and metabolic balance. The metagenome is a collection of bacteria genomes found in the gut. In healthy people, the gut microbiome develops from birth and is mostly complete within three years. Still, it may be altered by environmental variables, including food composition and volume, as well as antibiotic prescription [26].

Microbial cells provide many of the enzymes necessary for carbohydrate and protein digestion in the colon, which are not produced by human host cells [23]. Diet, environmental variables such as temperature and location, and the genetics of the human host have a substantial influence on microbial composition and diversity. With 150 - 400 bacterial species believed to exist in the human gut, it is a unique and complex microbial ecosystem. The gut microbiota profoundly influences human health by forming a barrier against pathogens, producing bioactive metabolites, and regulating immunological activity [8]. The gut ecosystem's homeostasis is maintained in the absence of large influencing factors by a few core species that are commonly shared among different individuals [13]. In healthy people, the gut microbiota is essentially constant (e.g., dietary changes or antibiotic treatment) [34].

Inflammatory bowel disease, obesity, allergies, and autoimmune illnesses have all been related to dysbiosis (an imbalance of the gut microbiota) [2]. As a consequence of extensive disease-targeted microbiota research, several microbial components have been linked to a range of disorders and can thus theoretically serve as biomarkers. The use of faecal microbial markers for colorectal cancer screening, for example, has been studied extensively [6]. Microbiota-based metabolic illness models generated in one region could not be extrapolated to other places, according to a study involving 7009 people from 14 geographic districts in one Chinese province. The efficacy of interpolated models dropped as the geographic scale rose. This highlighted the impact of geography on the composition of the gut microbiota and the use of illness models [13].

Gut microbiota composition differs in individuals and is explained by ethnicity factor considering operational taxonomic units (OTUs) having three main poles, which are classified as Prevotella (Moroccans, Turks, Ghanaians), Bacteroides (consisting African Surinamese, South-Asian Surinamese) and Clostridial with Dutch; it showed greatest alpha diversity in gut microbiota. In addition to geography, we have discovered many different variables of gut microbiota, including ethnicity, food, lifestyle, etc [6]. For example, enterotypes which are basically stratification of gut microbiota linked to the intake of particular fibers and carbohydrates; increase in inter-variations, and reduction in the number of species having high fiber potential are linked to urbanization [3], and chronic diseases have a link with taxa which is differentially distributed across ethnicities. So, it is critical to understand the gut microbiota and its role in a etiopathogenesis, but personal diet control or having a good diet can improve health more effectively. Moreover, we are still unable to know the actual variation in gut microbiome's composition and reactivity worldwide, especially in those having a traditional lifestyle [28].

Types of food affecting the gut microbiota diversity

The dietary habit of organisms is determined by which type of food they usually consume, plus the span of consumption. Nutritional contents of the human diet are proteins, carbohydrates, fats, minerals, fibers, and vitamins. These components are not only the main source of energy but also diversify our gut microbiota. The composition of gut microbiota can be varied by changing dietary composition and lifestyle. The diversity of gut microbiota has been determined by DNA sequence analysis, and their relationship with human diet has

been compared but still needs further research from different human populations. The studies have shown that microbiota composition is mainly get affected by three nutritional components; proteins, lipids, and carbohydrates, as they provide energy to gut microbes making intestinal flora [22].

The most abundant organic nutrient found in plants and animals as an energy source is carbohydrates. They are found in most plants like fruits, legumes, vegetables, and cereals. Starches are digestible to humans, while complex polysaccharides cannot be digested in the small intestine but get partly digested by microorganisms in the large intestine, which provides them with energy. Lipids are found in plants like seeds and in animals' flesh. It has been estimated that high lipid diet leads to an increase in Firmicutes species (*Eubacterium rectale* and *Blautia* coccoides) than *Bacteiodete* [3,30]. examined the ethnic diet of westerns (having high fat and sugar) and found single prototype culture of *Firmicutes* class (*Mollicutes*). The diet increased obesity in mice *In vitro.* A predominant increase in a single class (*Mollicutes*) has reduced the culture of others like the *Bacteroides* genus. Turnbaugh., *et al.* [30] also observed that switching the high carb and fat diet to low sugar, high fiber diet increase *Bacilli* and *Erysipelotrichi,* resultantly changing the composition of microflora. The study of the impact of oils on the gut microbiota of mice by Unger *et al.* [31] 16S RNA gene sequencing demonstrated that increased palm oil content increases Firmicute/Bacteriodetes (F/B) value in mice gut.

The sources of protein**s** are animals' flesh, fish, milk, plants like legumes and nuts, etc. a diet rich in protein contains *Bacteroides culture* in contrast to *Prevotella,* which is found in protein and carb-rich diet. An experiment done by Sprong., *et al.* [24] demonstrated that a cheese (casein) protein fed to rats showed fecal matter with a high level of *Lactobacilli* and *Bifidobacteria*. On the other hand, milk extracted protein showed *Lactobacillus*, *Bifidobacterium*, *Rikenella*, *Peptostreptococcus*, *Desulfovibrio,* and *Mucispirillum* genera in rats' fecal matter and low level of *Clostridium* by Pilvi., *et al.* [19]. Gut microflora can be impacted by using additional supplements like the use of prebiotics. A control experiment was performed by Fouhy., *et al.* [11] using qPCR (quantitative polymerase chain reaction) on mice. It was observed that *Roseburia* spp. and *Bacteroides-Prevotella* spp. were present in controlled diet mice, while a decreased value of this specie in high diet mice. The use of prebiotics like *Arabinoxylan* with a high diet incremented *Bifidobacteria*. The addition of prebiotics and probiotics in the diet helps to provide energy to intestinal microflora that has a significant effect on gut microbiota. In China, varieties of foods are being eaten by people belonging to different regions worldwide [12].

Moreover, China has 56 ethnic groups, and each group has a different lifestyle and customs [16], which is why diversity in gut microbiota can be observed in the Chinese population. Studies show that environmental factors, including diet and lifestyle, affect more than 20% of the variance in the beta-diversity-containing microbiome [20].

Two major groups are found in humans, which are vegetarians and omnivores. Omnivores are those who eat meat and vegetable in their diet. Humans eat a diet that does not consist of meat and only eat vegetables. Lacto-Ovo vegetarian, Semi vegetarian, Pesco vegetarian is on the basis of meat, fish, eggs, and milk [14]. Now the modern sciences have included the research on the relationship between dietary habits and microbiota diversity. The relationship makes the study of DNA recombination and DNA sequencing easier to show us about the vegetarians and omnivores [17]. The studies reveal that the microbial counts are different in different vegetarian subgroups. We can also say that the diet affects gut microbiota. [10], using Glutamate starch red agar, showed the microbial differences between the ovo-Lacto vegetarian and vegan groups. Some groups of microbes like *pseudomonas spp*. have more counts in ovolacto vegetarian than in the vegan group. Some microbiotas are abundant in both groups, and some are more abundant in one group in respect of the other group. There is a huge difference between *Proteobacteria* abundant in omnivores and *verrucomicrobiota* higher in vegetarian groups [22].

Geographical impact: within same and different countries

Geographical barrier among people not only modify culture and tradition but also has a role in gut microbiome modification as the ultimate dependence on the diet figure 1 and 2. Diet varies from east to west. Western diet mainly contains animal products like eggs, meat, fish, milk, and other items. The food contains low fibers, high carbs, and fat contents. On the other hand, the eastern population

uses meat and vegetables that have high fiber and a low-fat diet. Countries consuming Mediterranean diet consuming population eat vegetables, cereals, nuts, fruits, and high fiber food. Despite the geographical distribution among people, humans living in the same area have modified microflora [22]. A study done by De Filippo., *et al.* [4] on the microbiota of the kids of Italy and a small rural area of Africa called Burkina Faso showed a high amount of *Bacteroidetes*, *Actinobacteria,* and *Enterobacteriaceae* in Burkina Faso kids and *Firmicutes* in Italian kids. This showed that the difference in the microbiota composition was because of the different dietary habits of people.
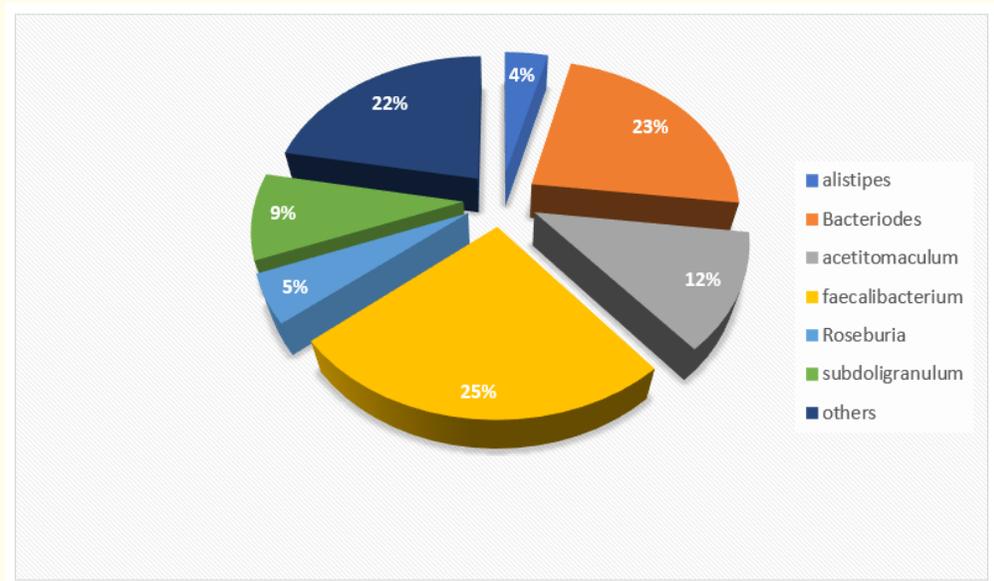

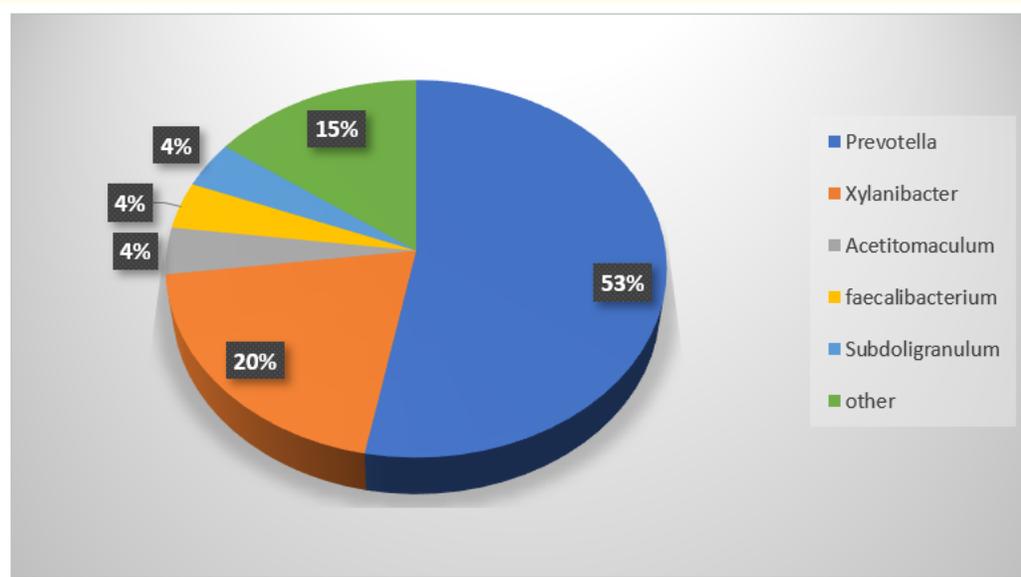*Figure 1: Percentage of various gut microbiota.*

Figure 2: Percentage of gut microbiota reported in European union.

Most microbes in the gut of people in the country have similar microbiota due to almost the same type of food. However, socio-economical and a few geographical differences may have a significant impact. The examination of different localities of India (Assam, Telangana, Sikkim, and Manipur) by Dehingia., *et al.* [5] suggested this difference within the same country. Analysis by NGS demonstrated that *Firmicutes* to *Bacteroidetes* were present in low numbers in the tribes of Manipur than in Telangana and Assam tribes, while Sikkim had high *Actinobacteria*. The tribes of Sikkim had a low level of *Enterobacter*, *Klebsiella,* and *Pantoea,* while Assam had a higher level of *Escherichia* in microbiomes than other tribes.

Impact of ethnic groups on gut microbiota

Gut microbiota helps in immune function and metabolism. It is variable among elders and kids and can be impacted by age, food type, geography, ethnicity, and lifestyles. [9] studied the impact of ethnicity on different ethnic groups of Malaysia, Malay, and Jakun; and compared it with the areas of China and India. The statistical analysis of different researches and demographic analysis showed a dominant culture of *Prevotella* was found in Jakun while *Bacteroides* was found in China. In Malay and India, both first and second types were equally distributed. *Prevotella* to *Bacteroides* (P/B) ratio also showed that Malay and China have the lowest while China and Jakun have the highest ratio. It also included those areas' population structure, dietary, health, and hygiene level. Those factors were considered covariates and also played a major role in modifying the gut microbiota. There was a difference between the pairing of Indian-Malay and Jakun-Indian as an ethnic group. *Clostridiales* were found in Malay [9].

On the other hand, *Klebsiella quasipneumoniae* was found in Jakun and *Bifidobacterium longum* in India. The variation among these four ethnic groups was related to hygiene and lifestyle. The food of the Chinese substantially contained pork, while Malay and jakun had ulam, an ethnic diet. Jakun people had no access to water from pipes and no proper toilet access, while the Chinese had access to toilets. Indian group varied them as a higher proportion of the diabetic population [9].

Lu., *et al.* [16] studied the microbiota of the Chinese ethnic group and analyzed the fecal matter of 2678 volunteers from 63 cities. The stool sample was examined under 16S rRNA gene examination. The results showed *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, and *Actinobacteria* as the major genera. Ethnic groups were determined geographically, which is hard to cast out, and showed that a rich in single gut microbial culture (alpha diversity) was found lowest in Bai. At the same time, Tibetan had the highest alpha diversity. To distinguish between the ethnic group, ethnic minorities were formed as Uygur, Hui, Mongolian, and Tibetan, but also Han samples from the same site. It was observed that the ethnic group from the same sit had no difference except between Han and Yugur. DESeq2 analysis compared the samples of Han to other groups and observed a decreased level of *Clostridium XVIII* genera in Uygur, low level of *Prevotella*, *Fecalibacterium*, and *Alistipesin* in Hui, during a high level of *Holdemanella* and *Enterococcus* in Mongolian group. *Escherichia* was found in the lower level of the Mongolian group [15].

Ali., *et al.* [1] distinguished the alpha and beta diversity of gut microbiota of school students. They showed that the ethnic groups possess a higher alpha diversity (microbes of a single kind) than the beta one. 143 students from Chinese schools volunteered in the experiment between grades 5-7. The information included their sex, diet, family background, body mass index (BMI), and ethnic background. PCR did DNA analysis of the fecal sample, and statistics were done accordingly. Tibetan, Han, and Hui were the three ethnic groups. Results showed much diversity among ethnic groups with the richness of specie (alpha diversity) from Tibetan to Hui and then Han. The analysis of beta diversity among the ethnic group showed Tibetan group had *Porphyromonadaceae*, *Catabacteriaceae*, *Christensenellaceae*, *Bdellovibrionaceae*, and *Anaeroplasmataceae*, *Porphyromonadaceae*, *Catabacteriaceae*, *Christensenellaceae*, *Bdellovibrionaceaein* Han and some *Bacteroidetes incertaesedis* in Hui samples. [25] examined the microflora of Canadian infants of different ethnic groups separated geographically.

The stool of infants of Caucasian and south Asian people residing in Canada was examined. It found South Asian mothers had more chance of getting GIT diabetes and were mostly vegetarian than Canadian mothers. The stool samples of breast-fed infants did this

analysis. Bifidobacterium, Lactococcus, *Streptococcus*, and *Enterococcus* (lactic acid bacteria) were mostly found in South Asian infants [18]. Also, they possess the Atopobium cluster of *Actinobacteria* found in fiber-rich diet-consuming people. Caucasian babies showed *Firmicutes* from the order *Clostridiales* were found in a protein and fat-rich diet. This showed that race has a prominent role in shaping the microflora of an organism, even in infants, as ethnicity rarely changes. Hence, a better diet can healthily modify an infant's microflora [22].

Seasonal effect

Zhang., *et al*.[35] has defined the impact of tradition and ethnicity on the gut's microbial composition in Canadian Inuit with seasonal food variations. The change of food staples in different parts of Canada has a significant role in the modification of gut microflora. The stool sample from Inuit and Montreal were examined, and information showed much variability. In Inuit, diet showed 17%, gender showed 3-4%, and population distribution showed 3-5% variability in microbial culture. Even the microbial composition was variable among genders. No seasonal shift in gut microflora was examined in the Montreal group, as even the remote Canadian population no longer relies on traditional food products. This showed that the same food could be available all around the year. A little variability was observed in the Inuit group. It was also observed that the microflora of elders was different from others as they were less reliant on westernized food. The type of food consumed more specifically changes the gut microbiota and also the pattern of eating. Like Nunavut (Inuit), people used to eat more eggs and meat than in Montreal; those consume more milk items and alcoholic products. Montreal consumed more fruits and vegetables than Nunavut. Traditional foods like meat storage in summers and consumption practiced in Alaska near Nunavut also impact seasonal microbiota composition [7].

Conclusion

Microbes perform a very significant role in the bodies of animals by performing and regulating specific functions, which include the process of digestion, metabolism of endogenous and exogenous compounds, regulation of the body's immune system, and many more. The gastrointestinal tract of humans is known to be one of the largest interfaces through which about 60 tons of food passes in the average life span of a human. The combination of different types of archaea and eukarya bacteria that make up the microbial flora of the gastrointestinal tract is known as the "gut microbiota." The metagenome, also known as the collection of genomes of microorganisms inhabiting the gut, can even be regarded to be a whole organ. A particular type of equilibrium is maintained inside the body because of the specific type of symbiotic interaction between the body of the host and the gut microbiota. Some important factors that influence the density and composition of host gut microbiota are certain environmental conditions, availability of substrate, volume, and composition of the diet, ethnicity, amount of antibiotics taken during medication, temperature, and geography.

Similarly, dietary products and the connected eating habits, as well as the geographical provenance of various individuals, affect the diversity of gut microbiota. The amounts of various biomolecules that make up the diet of individuals include carbohydrates, proteins, lipids, minerals, and vitamins. Most studies comparing eating habits have revealed that there is significantly greater bacterial diversity in omnivorous groups because of the greater spectra of dietary products consumed. The geographical provenance indicates that people inhabiting the non-Western countries, especially Africans, possessed a higher range of microbiota diversity than people living in other areas. However, the composition of the diet can be different because of variations in the cultural, agricultural variations, and different ethnicities present worldwide. For example, China is known to have 56 ethnic groups, and each group possesses a different lifestyle. So, the ethnicity study of various Chinese groups can compare different groups of microbiota present in respective groups. But the people inhabiting the same geographic area have shown to possess similar microbiota. Microbiota composition varies for different groups because of variations in the diet in different regions of the world. Hence, the composition of the diet and different ethnic groups are interconnected; both factors combine and influence the gut microbiota.

Conflict of Interest

The author declare no conflict of interest.

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