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REVIEW ARTICLE

Role of microbiota in urban life's well-being

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Abstract
The human beings have evolved together with microbes and are continuously exposed to diverse microbiota. A healthy gut flora promotes health and affords robust immune system, which is often advertised by probiotic supplements. These probiotics promises to build and restore gut flora health. Researches elucidate that gut bacteria are indispensable for our digestive system, and directly influence our moods, our weight, and our perception of the world. We discuss how urbanization possibly disturbs the symbiosis between microbiota and the human beings which leads to a negative impact on health. This review article summarized the previously reported studies and examines the role of microbiota in moods and well-being of urban population, specifically to anxiety and depression. Further, we identify the lacunae in the present research and advise the possible research methods to pursue for further understanding of the role microbiota population has on well-being.

Keywords
Gut Bacteria, Microbiota, Probiotics, Moods, Anxiety, Depression, Migration

We have ambiguous ideas of the importance of our digestive system with common sayings such as "the way to a man's heart is through their stomach," "have the guts to do it," or "listen to your gut feelings." Moreover, we all know the drill- chocolate for bad days, chocolate for a broken-heart, chocolate for motivation, chocolate for everything. This evidently advocates a relationship between our appetite and our moods. Furthermore, urbanization has led to changes in individual's lifestyle diet, alongside stress and anxiety. Could it be that this relationship goes beyond mere sayings? This review article aims to examine the wonderful intersection of microbiota and psychology. The review is presented in the hope of broadening the scope of types of studies of mood and anxiety within the field of psychology, through the investigation of the changes in gut flora and its connection to mental health and individual's well-being.

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The Importance of Gut Bacteria

In human anatomy, the gut (gastrointestinal tract) is the digestive organ consisting of the stomach, small intestine, and large intestine. The ingested food while passing through these systems is converted into molecules that are useful for us such as proteins, vitamins, and hormones. However, our body is incapable of devising mechanisms that are able to digest the large variety of food, as evident by various conditions of allergies, such as lactose intolerance or gluten intolerance. Microbiota are microorganisms inhabiting our gut, and have been proposed as a solution to our digestive problems. Unlike us, a single individual, an army of bacteria made up an incredible genetic diversity, as such, they are able to digest a wide variety of food and even produce beneficial substances from their excrements.

The gut microbiota also plays a crucial role in our immune system (Fung, 2017). Our immune system uses microbiota to train itself to differentiate between our own cells and other organism cells as we grow. This lack of training to our immune system forces it be over-protective and may attack benevolent substances such as peanuts and in the worst case, it attacks our own cells, creating autoimmune diseases (Salzman, 2011). Furthermore, the rise of antibiotics is parallel to the rise of autoimmune diseases, and indicates that they are severely affecting our microbiota.

The microbiota residing in the body consumes our food and appreciates a protected habitat within our gut. They acquire what is necessary for their survival and excrete metabolites that pass through the gut walls and enter our bodies through the bloodstream. The digestive system is indispensable for us (it provides energy for life) and it is crucial for it to communicate with the brain, the manager of our body. The gut establishes it through the Central Nervous System (CNS) by producing various hormones and neural substrates. The gut sends a signal to the brain on consumption of food, to indicate that it requires energy for digestion and creates after-food sleepiness. Similarly, when the brain is stressed, it sends a stop signal to the digestion system to allocate the energy in the brain hence reducing the appetite. However, gut microbiota function independently and may create signals that are not necessarily beneficial for its host.

In summary, the gut bacteria enable us to digest materials we are otherwise unable to digest, trained our immune system, and create metabolites and other substances that we are otherwise unable to create. In return, we became a willing host, providing the bacteria a home in our entire body, and allowing bacteria direct access to our brain through the CNS. Furthermore, the microbiota produces substances essential for neural cells myelination (Stilling et al., 2014). This suggest the possibility for epigenetic regulations by the bacteria in addition to the direct access they already have to communicate with the brain via neural substrates production.

The Gut-Brain Axis

The communication pathways that microbiota use is also known as the gut-brain axis. The gut-brain axis is a bi-directional communication pathway with the CNS (Capuco et al., 2020). The microbiome excretes substances as part of their digestion system that interacts with the brain via neuroimmune, neuroendocrine, and neural pathways (Winter et al., 2018). The primary conduit for this interaction is in the form of the afferent vagus nerve in the nervous system. While the nerve relays signals from the viscera to the brain, it collects sensory information including those from the digestive tract where the microbiome excretes neurotransmitters, for integration and appropriate responses to maintain homeostasis (Berthoud and Neuhuber, 2000). Moreover, this bi-directional communication between the gut microbiota and components of the gut-brain axis may influence normal homeostatic and thus affects moods and contribute to the risk of various diseases. The gut microbiota interacts and affects several important systems, they are the gastrointestinal (GI), the CNS, the Automatic Nervous System, and the immune system. Furthermore, the amendments to any of these systems are directly linked to alterations in fat storage and energy balance, gastrointestinal barrier function, general low-grade inflammation, increased stress reactivity, and increased anxiety and depressive-like behavior (Foster & Neufeld, 2013).

Anxiety and Depression

The goal of this review is to explore the role of gut microbiota on the most prevalent psychological disorders; anxiety and depression. Depression is one of the costliest psychological diseases across countries and socio-economic boundaries. Suicide is the number one cause of mortality in the people aged 20-30s in countries such as South Korea. It stands second to traffic accidents in the United States. Furthermore, in the U.S.A., approximately one-third of the country's health bill ($148 billion) is attributed to anxiety disorders (ADAA). Anxiety disorder includes phobias of all kinds, sleep disturbances, and persistent restlessness. However, these disorders are receiving less attention than depression even though they are equally paralyzing. Anxiety is one of the most dangerous feelings within a society and leads individuals to feel trapped and hopeless and is also the main cause of panic attacks. Additionally, anxiety hovers and lingers without a target unlike anger which is predictable and fear which has directly identified causes. Anxiety creates ripe opportunities for stereotypes to bear fruits and for violence to be masked as self-defense. Anxiety is the cause of unjust discrimination and social unrest. Understanding and mitigating anxiety is thus a pressing concern, especially with the increasing trend of occurrences it has within the urban population.

Furthermore, both anxiety and depression share a biological root- a system under stress. The pharmaceuticals companies have been trying to change the human psychological state through the use of medicine, which contains serotonin for depression and calming substrate for anxiety. However, gut microbiota opens an entirely new frontier, allowing the bodies to produce their own substrates to restore the psychological states. Restoring microbiota compositions to those of healthy or well-functioning individuals is the wholesome approach currently missing in pharmaceuticals. Research has proved the potentials of this approach which are simply tremendous, promising a finite and long-term cure of the most disabling mental conditions. However, most research has been done on animal models. Furthermore, the relationship between gut microbiota and mental disorders requires more exploration as it has captivated the interest of researchers and psychologists. The following sections will delve into scientific inquires on the effect of gut microbiota in behavior and the effect of gut microbiota in a stressed or anxious state and depression.

Microbiota Affects Behavior

Human beings are colonized and inside each of us lives an independent, self-functioning community of 1.5 kg microbiota (in the gut alone) (Parent & Carpenter, 1996). These bacteria have lived with us for as long as we exist. We have co -evolved with them, we went through plagues and prosperity together, and to each, they record a unique history of our parents, diet, stresses, and the troubles of palm-tree holidays (diarrhea). These 100 000 000 000 000 tiny friends are our “second brain,” and our “forgotten organ.” Indeed, there are 10-100 times more bacteria in the gut than eukaryotic cells in the human body (Gill et al., 2006). The sheer diversity of these bacteria is overwhelming, and approximately 400–500 bacterial species make up the gut microbiota (Steinhoff, 2005). The gut microbiome – a term for the collective community of bacteria – amounts to 3.3 million genes diversity dwarfing by far the 23 285 human protein-coding genes (Zhu et al., 2010; ENSEMBL database). They have been referred to as “superorganisms” for their capacity to digest and produce arrays of proteins and amino acids; vitamins and hormones that are impossible to produce otherwise (Hooper et al., 1998; O’hara & Shanahan, 2006). Recent researches have indicated that we have grossly underestimated the influence of the microbiome in our lives (see O’hara & Shanahan, 2006). The microbiome enables us to be omnivores, allowing conquests over belligerent territories and they have a direct access to the CNS, contributing to strong dispositions coming from our unconscious mind.

In an ingenious experiment, a microbiota, Toxoplasma gondii was inserted into a mice gut’s and within three weeks a reduced aversion toward predators (cats) and a liking for the smell of cat’s urine developed in the mice (Webster, et al., 2000). T. gondii is only capable of sexually reproducing in feline (cats), and the altered mice behavior is a perfect adaptation of T. gondii. So, a microbiota is controlling the mind of a mammal? These findings from the study were soon retested and replicated in laboratories all over the world. The urine's boxes were produced and mice were released, and those infected by T. gondii constantly preferred the cat’s urine as compared to non-infected mice who avoided the cat’s urine.

In 2007, Flegr studied the effect of T. gondii infection on human behavior. Consistent and significant differences were observed in infected and non-infected subjects across 9 out of 11 studies conducted. Infected men were more aggressive, while infected women showed more warmth. A computerized simple reaction time test was conducted and infected subjects exhibit lower psychomotor performance. Similar results were obtained in studies performed on 439 blood donors and 623 military servicemen (unpublished studies reported in Felgr, 2007). Furthermore, Yereli et al., 2006, found a higher incidence of T. gondii antibodies among drivers involved in traffic accidents in Turkey. However, more research needs to be done in order to exclude confounding variables and to understand the processes by which T. gondii affects human behavior. Furthermore, T. gondii is estimated to already affect a third of the world's population and is a pressing concern (World Health Organization). In healthy humans, the bacteria remain inactive due to intervention by the immune system. However, in pregnant women, the passed-on infection to an unborn baby is disastrous (see Centers for Disease Control and Prevention).

Additionally, besides affecting aversion, microbiota in the insect fly, Drosophila melanogaster, has been found to affect sexual preference. Two flies' populations were reared on different diets-molasses (sugar) diet, and starch diet. After one generation, when the populations are mixed, "molasses flies" preferred to mate with the other molasses flies, while "starch flies" preferred to mate with the other starch flies. Furthermore, the treatment of antibiotics abolished the mating preference in both the populations. The non-treated antibiotics populations maintained the preferences of mating for at least 37 generations. The findings from the study illustrated that symbiotic bacteria can influence mating preferences (Sharon et al., 2010). A recent study by Noguera-Julian et al. (2016) explored a similar study in the human population. It was reported that European homosexual men as compared to heterosexual men had consistently richer and more diverse microbiota. Homosexual men's microbiome was systematically enriched with bacteria of the genus Prevotella. The strength of such association was unusually high, reaching 95% accuracy in predicting the group from which the fecal sources were collected. These findings are in accordance to the well-established connection between microbiota and the human stress system.

Microbiota Affects Stress and Anxiety Responses

In 2004, a landmark study established a direct link between microbiota and stress correlates, namely the hypothalamic-pituitary-adrenal (HPA) reactivity. The germ-free mice which were born and raised in a germ-free environment, were compared to conventional house-specific pathogen-free mice. The germ-free mice exhibited dysregulation of the HPA axis, which are biological markers of depressive episodes. Furthermore, colonization of Bifidobacterium infantis in germ-free mice fully reversed the dysregulation of the HPA axis and led to exaggerated release of corticoserone and adrenocorticotropic hormone (Sudo et al., 2004). In another study, mice were infected with Trichuris muris, a close relative of the human parasite Trichuris trichiura. The infected mice showed increased anxiety-like behavior as assessed by the light/dark paradigm (Bercik et al., 2011). The light/dark paradigm measures the time spent by the mice in either a dark or a bright test compartment. The more anxious the mice, the more limited exploration of the bright compartment and they preferred to stay in the safe dark environment.

In humans, studies have reported that children with Autism Spectrum Disorders (ASD) as compared with neurologically healthy children have an altered intestinal microbiota composition (de Theije, et al., 2011). Wang et al. in 2012 reported a higher concentration of short-chain fatty acids in the fecal sample of children with ASD (Wang et al., 2012). The fatty acids are products of microbiota metabolism and have been shown to affect neural activity. Furthermore, injecting fatty acids into the stomach of human participants resulted in reduced brain activity to experimentally induced sad emotions (listening to sad music) (Van Oudenhove et al., 2011). Additionally, gut microbiota produced amino acids such as GABA and tryptophan as well as monoamines such as serotonin, histamine and dopamine which play important roles in the brain as neurotransmitters or their precursors.

Furthermore, serotonin is of great interest to pharmaceutical industry for producing antidepressant drugs. Serotonin is an important regulator of mood, appetite, and sleep and synthesized in the CNS. Nearly 10% of total variance in anxiety-related disorder is explained by variation in distribution and frequency of the serotonin transporters (Lesch et al., 1996). In several studies, germ-free mice compared to normal house-mice exhibited increased serotonin in the striatum and hippocampus region, indicating a direct link between gut microbiota and serotonin signaling (Heijtz et al., 2011; Clarke et al., 2013). In another study, it was demonstrated that exposing mice to social stressor significantly changes the microbiota structures in comparison to non-stressed control mice which was confirmed by a deep sequencing method. It was observed that the relative abundance of Bacteroides was decreased while that of the genus Clostridium was increased (Bailey et al., 2011). Furthermore, stressor used in the study was the social disruption (SDR) procedure. In the SDR, an aggressive mouse is placed in the home cage of the target mice. The aggressor will attack and defeat all resident's mice and stayed for up to 2 hours in the cage. The procedure is repeated daily for up to one week.

These studies imply a link between changes in microbiota and changes in the various symptoms of its host. The casual direction is hard to determine and is likely to be interactive in nature. Several studies have tried to change the gut microbiota and examined whether behaviors changed as a result. Health-benefiting microbiota (Probiotics) such as Lactobacillus helveticus and Bifidobacterium Longum, were given to healthy subjects (humans) for 30 days. Examination via questionnaires revealed that the probiotic groups reported less psychological stress as compared to the control group (Messaoudi, et al., 2011). In another study, administration of probiotic, Lactobacillus casei (bacteria in the health drink Yakult) for the duration of three weeks resulted in mood improvements in healthy subjects that were high in depression scale at the beginning of the three weeks (Benton et al., 2007). However, the studies on clinical populations are limited. Apart from probiotic studies, the link between microbiota changes, social stressors, and behaviors have been limited to non-human subjects and requires more exploration.

Microbiota Affects Depression

The link between the gut microbiome and depression is well reported in literature (Winter et al., 2018). Kelly et al., 2016 performed fecal microbiota transplantation from depressed patients into germ-free mice and the mice displayed behavioral changes which correlate with human depression and anxiety, such as less maze exploration and physiological features that are characteristics of depression. Recently, Capuco et al., 2020, have provided a comprehensive review of studies done on mice that shows the relation between microbiome composition to depressive physiology and behavior.

Furthermore, several studies were also conducted on human subjects. An altered gut microbiome composition was found in depressive human subjects in comparison to control subjects (Dinan and Cryan, 2013). Jiang et al. (2015) analyzed fecal and serum samples from subjects with major depressive disorders before and after treatment and showed significant increases in bacterial diversity in subjects that have a 50% reduced Hamilton Depression Rating Scale (HAM-D) scores after treatment. Moreover, studies have also examined the effects of probiotics on human subjects' mental health. Kazemi et. al. (2019) conducted a double-blind, placebo-controlled study to evaluate the effects of probiotics in patients with major depressive disorders. Probiotic supplements used were a combination of Lactobacillus acidophilus, Lactobacillus casei, and Bifidobacterium bifidum. In comparison to the placebo group, in the probiotic group, significantly reduced Beck Depression Inventory scores of patients were observed. Furthermore, Steenbergen et. al. (2015) evaluated the use of probiotics in cognitive reactivity scores of healthy patients in a blinded study. Compared to the placebo, a 4-weeks probiotic food supplement to 20 healthy patients significantly reduced overall cognitive reactivity to sad mood (reduced rumination and aggressive thoughts), which was a known risk factor for depression.

Moreover, a study on the effects of probiotics has also been conducted on postpartum depression. In a study by Slykerman et al. (2017), 423 women were recruited to either receive a placebo or a probiotic capsule containing Lactobacillus rhamnosus daily until after 6 months post-birth. The mothers in the probiotic treatment group reported significantly lower depression scores as compared to those in the placebo group. The treatment group also displayed a lower clinically relevant anxiety score.

Microbiota in Urban Life Context

The stated studies have shown the indispensable effect of microbiota on human health. Hence it is important for human beings to maintain a healthy microbiota composition. However, urbanization and environmental sterilization have reduced microbiota diversity (Hanski, 2012). Furthermore, it has been reported that by 2050, 68% of the world's population would live in urban areas (United Nations, 2018). Hence, it was suggested that urban habitat restoration would provide a human health benefit through microbiome rewilding (Milis et al., 2017).

Urban wild habitat restoration provides several benefits (Spedelwinde et al., 2015; Stein et al., 2016). Urban green space correlates with increased physical activity and lower occurrences of depression and high blood pressure (Shanahan et al., 2016). Rural children who live on farms, or within 5 km of forest or agriculture, have a significantly lower prevalence of asthma and allergic sensitization to harmless environmental particles relative to urban children (Ege et al., 2011). A solution to the restoration of the microbiome community could be a plantation of native plants, in which after eight years of restoration changes in the bacterial community on the ground and belowground were observed (Gellie et al., 2017). Furthermore, an eDNA metabarcoding could be a cost-effective, scalable, and standardizable ecological monitoring tool to measure the microbiome's impact on restored/unrestored sites. Additionally, the competition for space in an urban setting is intense that the World Health Organization suggests the need to create "Urban Green Spaces: A Brief for Action" (WHO, 2017). Through this review, it is hoped that yet another benefit of habitat restoration could be taken into account. Furthermore, it is important for urbanities to understand the benefit of being in nature, or at least to have contact with nature even in the office or urban settings. Studies have concluded that not all bacteria are detrimental. Moreover, human beings could not have survived without them. However, this does not mean we should not take precautions against germs or potential mediums for disease. Nevertheless, we need to be cautious about losing a healthy microbiome composition as they have the potential to affect moods, behavior, and resilience of mental health.

Potential Research Design

Research in the intersection between psychology and microbiota could investigate the differences in microbiota composition between healthy individuals and individuals experiencing stress (anxiety disorder and depressive symptoms). It is recommended to conduct studies using the longitudinal design, as the design allows examination of the influence of social stresses to microbiota compositions as well as the relation between particular microbiota compositions and core psychological constructs. Additionally, the research could aim at discovering empirically derived ethnic-based microbiota signatures.

A correlation between certain microbiota composition and bodily state indeed has been discovered. The comparisons of the gut microbiota of genetically obese mice and their lean littermates revealed that obesity is associated with changes in the relative abundance of the two dominant bacterial Phyla, the Bacteroidetes and the Firmicutes. The Firmicutes have an increased capacity to harvest energy from the diet and were found to be more abundant in obese as compared to lean-mice. The colonialization of germ-free mice with "obese microbiota" as compared to "lean microbiota" resulted in a greater increase in total body fat (food intake was held constant) (Turnbaugh et al., 2006). Similar discovery on the bacteria responsible for anxiety/depression would benefit scientists' understanding of the link between microbiota and behaviors as well as clinicians' repertoire on treatments possibilities for anxiety and depression. Longitudinal observations would further clarify the causal direction between microbiota and anxiety or depressive symptoms.

Correlations with psychological constructs would stimulate psychologists to collaborate and contribute in this challenging and innovative field. The connections between microbial composition and psychological constructs are as yet to be explored and are an untouched territory. The reported studies have been focused mainly on biological measures, such as body fat and increased release of stress hormones. The psychological constructs, such as anxiety or depression, are not referred to as entities (such as anxiety disorder) but rather utilized as categories for behavior (such as anxiety-like or depressive). This discrepancy suggests that treatment recommendation (such as probiotics) relies on the research of microbiota affecting short-term or immediate behavior (anxiety-like), while the target recipients are those with long-term problems (anxiety disorder and depression). Additional studies are required to conclude whether microbiota can affect long-term problems such as anxiety disorder and depression and thus make the project more significant. Furthermore, the immediate reaction to stressors may not necessarily develop into a disorder. However, the immediate negative reaction can be coped depending on individuals' mental and social resilience. Individuals with strength and determination would be able to overcome obstacles and prevail in the face of great danger, effectively nullifying the effect of the stressor and evading the development of disorders such as anxiety and depression. In order to understand the role of microbiota in clinical conditions, psychological factors are indispensable.

Discussion

"Nature vs. Nurture" is the long-standing debate on correlation between biology and psychology and how they influence each other. This term seems to suggest that there are two independent forces- nature and nurture. These two forces both affect behaviors and what is required is to quantify the relative strength of each force. This opinion is gradually being diminished as it is evident that nature and nurture are interdependent and the relationship between biology and psychology is one of the crucial interactions in human beings. What nature provides, nurture will modify, adapt and manage. These in turn will change nature itself (such as epigenetic). In short, instead of being on mere parallel, human's biopsychology is a dynamic system.

Additionally, the scientists are required to go beyond the nature vs. nurture distinction and investigate into these intricacies. There have been fewer studies reported in literature which have attempted to study biopsychology. A notable exception is a research by Chiao and Blizinsky (2010) that connected the prevalence of S and L allele in Western and East Asian populations with their main self-construal, namely collectivism and individualism. S (short) and L (long) alleles refer to different versions of a polymorphic region (5-HTTLPR) in the serotonin transporter gene (SLC64A). In comparison to L allele individuals, S allele individuals produce significantly less 5-HTT mRNA, a protein that is crucial for a mood disorder (serotonin). These individuals experience heightened anxiety, have an attentional bias to negative information, and are vulnerable to environmental risk factors (conflicts, threats, losses). Furthermore, East Asian as compared to the European population has a higher prevalence of individuals with S allele, 70 – 80 % as compared to 40 – 45 %. Despite the higher prevalence, East Asian population reported a lower incidence of depression and mood disorders (the trend is increasing in increasingly individualistic cities such as Tokyo and Seoul). Controlling for reporting bias, socioeconomic status, and other relevant factors, Chiao and Blizinksy showed that collectivism mediates the effect of low uncertainty tolerance and manifested depressive symptoms. Furthermore, collectivism self-construal shelters individuals from the negative impact of situational threats by relying on interdependency and strengthening inter-individuals' relationships. They further argued that collectivism does not merely mediate this effect, but collectivism evolves in order to mediate this effect. This concept has been termed "culture-gene coevolution." Could values and personality also develop as reactions to innate tendencies driven by genes and microbiota?

Conclusions

The understanding of microbiota patterns in depressed patients are incomplete. However, utilizing current knowledge of the microbiota-gut-brain axis and functional catalogs of various bacteria, the process involved in depression by microbiota can be clarified. Equipped with a battery of psychological information on the individuals, fine classification could be made on which composition is associated with which facets of depression. A refined classification will allow for better-targeted probiotics and diet alteration treatments. In addition, the microbiota and the psychological information combined would allow for a quantification of effect. Furthermore, it would allow us to answer questions such as to what extent does the microbiota composition is associated with depressive symptoms? Do the more depressed individuals have a higher degree of alteration in comparison to less depressed individuals? Are these relations moderated by specific psychological constructs such as resilience, optimism, and conservatism?

Moreover, the causal direction of microbiota and behavior is unclear. Researches have illustrated that the implementation of microbiota causes the associated effect. Implementing "fat-mice microbiota" to lean-mice caused the lean-mice to be fat. However, the development of microbiota in the gut (e.g. of the fat-mice) is affected by the host's diet (e.g. individuals on fiber diet are more likely to harbor Prevotella bacteria). Similarly, physical and psychological stresses are known to disturb the gut microbiome (Foster & Neufeld, 2013). In order to expand and test the causality link between microbiota and behavior, a longitudinal study would be appropriate. Furthermore, ecological validity would be crucial in an applied context. Scientists often have to rely on opportunities which could be provided by migration. Migration could be in the form of incoming migration from the villages to the big-cities (urbanization), or immigration at the national level, such as expats that lives in Indonesia (e.g. Bali has such a population).

Finally, there are evidences that microbial population could be categorized based on geographical location. Human gut microbiome classification, known as entereotype is thus far divided into three groups. Each of the three entereotypes consists of particular compositions of bacteria. Some bacteria are in symbiosis or competitive relationships with each other and thus their co-occurrences in the human gut follow particular patterns. To simplify, Entereotype 1 is characterized by high levels of bacteria in the genus Bacteroides, Entereotype 2 has few Bacteroides but a higher number of bacteria in the genus Prevotella, and Entereotype 3 has high levels of bacteria in the genus Ruminococcus. In 2011, Arumugam and colleagues found that type 1 is predominant in their Japanese sample. Bacteria in the gut gain energy through the food that we (the host) eat, in turns, we benefit from the metabolites that are produced by the bacteria. Due to their reliance, our long-term diet is strongly associated with the gut microbiome composition. Long-term diet, in turn, is one defining characteristic of ethnicity. Individuals who consume plenty of protein and animal fats have predominantly Bacteroides, while those consuming more carbohydrates, especially fiber, have predominantly Prevotella. Furthermore, children in Burkina Faso, have a gut composition made up of 53% Prevotella (De Filippo et al., 2010), while age-matched European children, did not have any Prevotella in their gut. Mason and colleagues (2013) tried to predict ethnicity from compositions of bacteria, in this case from oral and not fecal bacteria samples. Their machine classifier was able to predict that compositions come from African American individuals with 100% accuracy and from Latinos American individuals with 67% accuracy. These lead to the concept of microbial signatures belonging to certain ethnicities. It is interesting to note that African Americans have a highly similar diet to Caucasian Americans. Nevertheless, differences in microbiota compositions were found. Lastly, it must be mentioned that Arumugam and colleagues (2011) above did not find nationality to be a significant factor determining the classification of entereotypes.

Contributing to this field (geographical-based microbial signature) will allow scientists and clinicians to dig deeper and understand better the functionality of various classes of microbiota. The variations across cultures can be beneficial in explaining why certain attributes are more pronounced in some ethnicities more than others. For instance, the Japanese fishermen's village of Ogimi in Okinawa has the highest average age compared to anywhere else in the world. Furthermore, Hongkongers or Taiwanese ate considerably plenty and rarely exercise, yet the average body weights in these regions are lower than in countries explicitly addressing obesity. Lastly, it is a common assumption that individuals of African origins have better endurance and physical build (the exact prevalence and causes up for debate). Isn't it intriguing to ponder whether adopting a diet pattern from these cultures would allow benefit transfer of the same attributes? If it is too late to switch diets within one generation, could probiotics made of these signatures allow us to instantly embrace the centuries-old benefit? The microbiota field offers such fascinating possibilities; we should all be part of it.

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