

Editorial

Gut Microbiota and Health.

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Microbiota also known as ‘the Hidden organ’ a vast number of microorganisms, including bacteria, yeasts and viruses; coexist in various sites of the human body (gut, skin, lung, oral cavity).¹ In the gut, bacterial components of microbiota are *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, *Proteobacteria*, *Fusobacteria*, and *Verrucomicrobia*, among which *Firmicutes* and *Bacteroidetes* are the major types where as *Candida*, *Saccharomyces*, *Malassezia*, and *Cladosporium* are the fungal organisms and viruses like phages and archaea, mainly *M. smithii* are abundant.² The microbiota contribute over 150 times more genetic information than that of the entire human genome.³

To maintain healthy condition of human as whole, gut microbiota is considered the most significant role that exhibits stability, resilience and symbiotic interaction with the host.⁴ They (Microbiota) may affect human biological processes via several mechanisms by energy and nutrient extraction from food and plays crucial roles due to the versatile metabolic genes which provide independent unique enzymes and biochemical pathways.⁵ Moreover, the biosynthesis of bioactive molecules such as vitamins, amino acids and lipids are also highly dependent on the gut microbiota.⁶ The human microbiota also protects the host from external pathogens by producing antimicrobial substances and serves as a significant component in the development of intestinal mucosa and immune system.⁷

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Gut microbiota may vary due to age and environmental factors (like medication usage) and also varies in different anatomical parts of the GI tract.⁸ In the small intestine the transit time is short and bile concentration is high, while in the colon, which has slower flow rates and milder pH, as well as larger microbial communities, especially anaerobic types are commonly observed.⁸ The diversity of microbiota occurs according to age variation. At about age 3, children’s gut microbiota becomes comparable to that of adults and subsequently at older age the composition of the human gut microbiota changes potentially due to dietary habit and immune system activities.⁹ The decrease in the anaerobic bacteria *Bifidobacterium* is considered relevant to deteriorated inflammatory status due to its role in stimulating the immune system.^{8,9}

Since the microbiota plays an important role in human well-being thus the substitution/ alteration of the normal gut flora (Dysbiosis) lead to a dysfunctional array of organisms that can promote disease states.¹⁰ Changes in gut microbiota seem to influence the outcome of multiple inflammatory pathways in older adults and may contribute to systemic chronic inflammation.^{9,10} Additionally, dysbiosis has been positively correlated with increased fat mass, proinflammatory biomarkers and insulin resistance.¹¹ Extrapolating out, obesity has been linked to changes in the gut biome, which is associated with increased intestinal permeability and endotoxemia.¹¹ Zonulin is a protein that regulates intestinal permeability.¹² Elevated levels of zonulin seem to predict inflammation and physical frailty and are found in increased levels in obese children and adults as well as in patients with type 2 diabetes, fatty liver disease, coronary heart

disease, polycystic ovary syndrome, autoimmune diseases and cancer.¹²

Organisms in the gut biome exist in a delicate ecosystem, which has immense influence over proper system-wide physiologic function.¹³ Medications, especially antibiotics, will directly affect the gut microbiota.¹⁴ Besides antibiotics, non-antibiotic drugs like osmotic laxatives, hormones, benzodiazepines, antidepressants, antihistamines and inflammatory bowel disease drugs were found to be highly relevant to the variation of gut microbiota composition as well as neurophysiology and behavior.¹⁴ Proton pump inhibitors, metformin, statins and psychotropic medications like serotonin antagonists such as sertraline, paroxetine, and fluoxetine, which have antimicrobial activity may change the normal composition of gut microbiota.^{14,15}

As the intestinal microbiota making up the human microbiome can have a profound influence on energy and immune homeostasis which result in significant metabolic and immunologic effects on the host and ultimately leading to many local and systemic diseases.¹⁶ So, attention to paid for maintaining perfect (normal) and healthy microbiota within gut. Good attention to be paid on daily dietary habits. As diet contains components that provide energy to the host as well as microbiota can play a significant role in the maintenance of the complex microbiome. Such as diet containing high-fat, high sugar and that are low in fermentable fiber lead to dysbiosis; while diets of low in fat and sugar and high in fermentable fibers, particularly prebiotic fiber can significantly promote proper energy homeostasis and immune response and to reduce disease risk as well as promote overall health. Dietary modification as well as treatment with pro- and prebiotic use can help maintain proper microbiota balance and promote proper energy and immune homeostasis lead to healthy well being to all.

REFERENCES:

1. Shreiner, A. B., Kao, J. Y. & Young, V. B. The gut microbiome in health and in disease. *Curr. Opin. Gastroenterol* 2015; 31: 69–75
2. Ursell, L. K. et al. The intestinal metabolome: an intersection between microbiota and host. *Gastroenterology* 2014; 146: 1470–1476.
3. Berg, G. et al. Microbiome definition revisited: old concepts and new challenges. *Microbiome* 2020; 8: 103
4. Grice, E. A. & Segre, J. A. The human microbiome: our second genome. *Annu. Rev. Genom. Hum. Genet* 2012; 13: 151–170.
5. Fan, Y. & Pedersen, O. Gut microbiota in human metabolic health and disease. *Nat. Rev. Microbiol* 2021; 19: 55–71.
6. Flint, H. J., Scott, K. P., Louis, P. & Duncan, S. H. The role of the gut microbiota in nutrition and health. *Nat. Rev. Gastroenterol. Hepatol* 2012; 9: 577–589 .
7. Laterza, L. et al. The gut microbiota and immune system relationship in human graft-versus-host disease. *Mediterranean J. Hematol. Infect. Dis.* 2016; 16-25.
8. Milani, C. et al. The first microbial colonizers of the human gut: composition, activities, and health implications of the infant gut microbiota. *Microbiol. Mol. Biol. Rev.* 2017; 81: e00036–00017.
9. Rinninella, E. et al. What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms* 2019; 7: 14
10. Amabebe, E., Robert, F. O., Agbalalah, T. & Orubu, E. S. F. Microbial dysbiosis-induced obesity: role of gut microbiota in homeostasis of energy metabolism. *Br. J. Nutr* 2020; 123 : 1127–1137.
11. Lozupone, C. A. et al. Diversity, stability and resilience of the human gut microbiota. *Nature* 2012; 489: 220–230.
12. Tong, X. et al. Structural alteration of gut microbiota during the amelioration of human type 2 diabetes with hyperlipidemia by metformin and a traditional Chinese herbal formula: a multicenter, randomized, open label clinical trial. *mBio*.2018; 9: e02392–17 .
13. 14. Ley, R. E., Turnbaugh, P. J., Klein, S. & Gordon, J. I. Human gut microbes associated with obesity. *Nature* 2006; 444: 1022–1023.

14. Bohnhoff, M., Drake, B. L. & Miller, C. P. The effect of an antibiotic on the susceptibility of the mouse's intestinal tract to Salmonella infection. *Antibiotics Annu.*1955; 3: 453–455 .
15. Ducarmon, Q. R. et al. Gut Microbiota and colonization resistance against bacterial enteric infection. *Microbiol. Mol. Biol. Rev.*2019; 83: e00007–19.
16. Freter, R. et al. Mechanisms that control bacterial populations in continuous-flow culture models of mouse large intestinal flora. *Infect. Immun.*1983; 39: 676–685.