

Gut Microbiome: The New Organ?

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The prevalence of metabolic syndrome (mainly type 2 diabetes, obesity and cardiovascular disease) is increasing rapidly in developing countries more than developed countries in recent times. Recent WHO statistics indicates that number of people with type 2 diabetes around the world was about 382 Million in 2013 and is projected to be about 592 Million by 2035. The prevalence of type 2 diabetes mellitus is almost similar in population of high and upper middle income countries, but the age group which are affected in the population is lower in population of lower middle income countries, impacting the economy of the these countries. In addition to the genetic variations known in GWAS, intrauterine growth restriction in the process of development of the fetus and influence of external environment (mainly those that are obesogenic during the growth phase induce insulin resistance, reduce β cell mass and organ dysfunction) contribute to the development of type 2 diabetes. Majority of the children in these countries are under nourished during childhood days but as they grow, increased accumulation of increased body fat occurs, which leads to obesity.

The nutrient processing in the gut is affected by various factors that also include the gut microbiome. They influence the use of energy from the diet and their metabolites also affect the modulation of signaling molecules. Evidences shows that gut microbes can influence whole body metabolism by affecting different area like the energy balance, gut permeability, endotoxemia, and inflammation (both systemic or gut) that influences several metabolic disorders. Trillions of microbes have evolved with and keep on living within human body. A range of environmental factors can affect intestinal microbial imbalance, which has a very close relationship with human health and disease in recent understanding. The human microbiota, especially those in the gut, has even been considered to be an “important organ”, consists of approximately 150 times more genes than are found in the entire human genome. The composition of this microbial community is dependent on host, changes throughout an individual’s lifetime and susceptible to both exogenous and endogenous modifications. Recently there is renewed interest in the composition of this “organ” has illuminated its central position in health and disease. The microbiotas are intimately involved in numerous aspects of human physiology, from nutritional status to behavior and even stress response. Additionally, they can be a central or a contributing cause of many diseases. The studies demonstrated that the extent of diversity within the samples or between subjects varied based on their habitat and environment. Oral and fecal samples showed higher bacterial diversity whereas vaginal samples were least diverse in nature. The majority of the gut microbiota is composed of strict anaerobes, they dominate the facultative anaerobes and aerobes by two to three orders of magnitude. Although there have been over 50 bacterial phyla described to date, the human gut microbiota is dominated by only 2 of them: the *Bacteroidetes* and the *Firmicutes*, whereas *Proteobacteria*, *Verrucomicrobia*, *Actinobacteria*, *Fusobacteria*, and *Cyanobacteria* are also present in minor proportions. The number of bacteria present in gut shows a continuum that goes from 10^1 to 10^3 bacteria per gram of contents in the stomach and duodenum, progressing to 10^4 to 10^7 bacteria per gram in the jejunum and ileum and culminating in 10^{11} to 10^{12} cells per gram in the colon.

First human metagenome-wide association studies shown highly significant correlations of certain intestinal bacteria, important metabolic pathways with T2D. Importantly, important butyrate-producing bacteria such as *Roseburia intestinalis* and *Faecalibacterium*

prausnitzii presence were lower in T2D subjects. This evidence, that butyrate and other short-chain fatty acids exert profound immunometabolic effects. Gut-derived endotoxaemia has also seen in patients with metabolic syndrome and T2D and has important role in metabolic inflammation.

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