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Letter to Editor

The Symbiosis or Dysbiosis of Gut Microbiota: Friend or Foe?

Seyed Davar Siadat* and Sara Ahmadi Badi

Microbiota Lab, Microbiology Research Center, Pasteur Institute of Iran

***Corresponding Author:** Seyed Davar Siadat, Microbiota Lab, Microbiology Research Center, Pasteur Institute of Iran, Iran

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Abbreviations

Gastrointestinal tract: GIT; pattern recognition receptor: PRR; G-protein coupled receptors: GPRs; Lipopolysaccharide: LPS; microbial associated molecular patterns: MAMPs; toll-like receptors: TLRs; nod like receptors: NLRs; Short chain fatty acids: SCFAs; extracellular vesicles: EVs; glucagon-like peptide-1: GLP-1

The human body contains 40 trillion eukaryotic cells and about 22,000 human genes, but as many as 100 trillion microbial cells (the microbiota) and 10 million microbial genes (the metagenome). The human microbiota consists of a wide variety of bacteria, archaea, viruses, fungi, and other eukarya that inhabit different parts of human body. The microbiome is the name given to all of the collective genomes of the microbial cells that reside in a specific environmental niche such as the human gastrointestinal tract (GIT) [1,2].

The internal surface area of GIT has long been considered to be between 180 and 300 square meters (m^2). the total weight of gut microbiota which colonizes GIT is about 1–2 kg (1,5 kg), similar to the weight of the human brain (1.3 kg). The gut microbiota harbours more than 1,000 bacterial species, however, 99% of the bacteria come from about 30 or 40 species. Firmicutes and Bacteroidetes are the predominant phyla in this microbial community. Other phyla including Actinobacteria, Fusobacteria, Proteobacteria, Verrucomicrobia are constitutive 10% or less of gut microbiota. As a consequence of their abundance in the intestine, bacteria also make up to 60% of the dry mass of feces. The gut microbiota composition could be highly influenced by internal and external factors such as genetic background and life style (diet, drug consumtion, physical activity and exposure to environmental microbes) [3,4]. However, learning how to reproducibly manipulate the composition of gut microbiota despite differences between individuals remains a major challenge.

The microbiome and host emerged during evolution as a synergistic unit from epigenetics and genetic characteristics, sometimes collectively referred to as a holobiont [5].

The gut microbiota continuously interacts with host and has critical role to the normal development of the host physiological pathway and metabolic homeostasis such as the immune, endocrine and neural systems [6].

Gut microbiota affects these putative pathways due to have various immunologic components and metabolites which are sensed by several types host receptors including pattern recognition receptor (PRR) and G-protein coupled receptors (GPRs). To regulation of immunity by gut Microbiota, Lipopolysaccharide (LPS) and peptidoglycan which are the best known microbial associated molecular patterns (MAMPs) stimulate toll-like receptors (TLRs) and nod like receptors (NLRs). Short chain fatty acids (SCFAs) are considered as substantial gut microbiota derived metabolites due to the presence of metabolism, immune system and epigenetic regulating potentials [7,8]. Also, the gut microbiota derived extracellular vesicles (EVs) are key players in gut microbiota-host interaction [9].

It is now well established that gut microbiota can influence metabolism and mental health and are associated with a wide range of metabolic disorder and mental illness. Alteration of gut microbiota pattern which is referred as dysbiosis has been associated with the pathogenesis of many inflammatory diseases and infections. In other words, gut microbes can make chemicals that speak the brain's language. In addition to the role played by gut microbiota in regulation of metabolism and mental health, these microbes have recently been shown to have numerous immunomodulation effect and anti-inflammatory properties in normal status. It is both well known connection between the microbiota and the immune regulation and the malleability of the microbiota that makes it a prime target for regulating inflammation that is considered a turning point of the many diseases and disorders [10,11].

Several researches revealed that the microbiota employs several information carriers from the gut to the brain including microbiota-derived signaling molecules, immune mediators, gut hormones as well as vagal and spinal afferent neurons. Gut peptides and neuropeptides play a critical role in many of these communication pathways. This is true for peptides produced by enteroendocrine L-cells which respond to metabolites generated with the help of the microbiota. These cells are stimulated by particular nutrients and gut microbiota derived component/metabolites, which leads to the release of various peptides such as PYY, glucagon-like peptide-1 (GLP-1) and GLP-2. Following their release from L cells, PYY and GLP-1 not only inhibit gastric motility and improve glucose homeostasis but also induce satiety and behavioral changes [12,13].

In conclusion the gut microbiota has determinative roles in health and diseases. Therefore, understanding of gut microbiota-host interaction and determination of healthy gut microbiota composition could be a promising approach in prevention, control and treatment of metabolic, immune and mental disorders.

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