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Editorial

Gut Dysbiosis; An Altered Gut Microbial Ecology Major Risk Factor for Human Diseases

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Human gastrointestinal tract habitats trillions of microbes play a central role in physiology. These microbes evolved to establish a host-microbe interaction for beneficial outputs; however, a few also reported to cause harmful events [1]. It has been well established that gut Microbiota has a central role in infectious diseases, inflammation, neurological disorders, obesity, and associated metabolic syndromes. Extensive research over a period brought an understanding of how these microbes modulate the energy balance (energy harvest and storage) and the onset of obesity. Further, a few microbes profiled were associated with the initiation of low-level inflammation (induce Lipopolysaccharide (LPS) based inflammation) and various metabolic syndromes (T2D, CVD and obesity) [2]. These microbes were also indulged in the remodeling of Endocannabinoid (e-CB) system; however, the exact mechanism for Endocannabinoid (e-CB) signaling under the influence of gut microbes is not explored yet. Additionally, a few studies have suggested LPS-eCB is involved in altered energy balance and leads to obesity. The key problem in this context remains intact as how these microbes reprogram the gut barrier and result in metabolic endotoxemia [3]. Further, aberrant gut Microbiota and their metabolites mimic several other receptors such lipopolysaccharides (LPS), Toll-Like Receptor (TLR), nucleotide-binding oligomerization domain-like receptors (NOD) and NOD-like receptors (NLRs) over natural ligand and alter the fate of native signaling cascade [4].

Classically, the gut dysbiosis is defined as an aberration in Gut Microbiota affecting microbial diversity and population [5]. The Gut Microbiota has a commensal relationship with the host composed of trillions of microbes from more than thousands of different species [6]. In the given gut Microbiota population, both useful (non-pathogenic) and harmful (pathogenic) microbes reside in synchronization with crosstalk to not offer any harm to host [7]. Gut dysbiosis is multifactorial and remains a highly versatile process. However, gut dysbiosis seems to be essential in a particular aspect, which depends on microbial diversity and population. Since the time of birth up to the completion of human life, gut Microbiota keeps on changing [8]. Such changes in gut Microbiota largely depends on daily habits, food pattern, food content, pathophysiology, use of probiotics and antibiotics, geographical condition, drugs, infections, and toxins, etc. However, these changes are minor, stating their significant gut population remains constant [9]. Among these food content and food, the habit remains a crucial factor affecting gut Microbiota. Countries like India, where food remains changing from city to city (state to state), and hence the Indian population remains a significant source of the diverse gut population [10]. Similarly, such a community is much prone to diseases associated with the alteration of Gut Microbiota.

Considering extensive research findings carried out in the last few decades and a preponderance of research data the gut dysbiosis is a major trigger for human diseases and disorders both including extraintestinal and extraintestinal [11]. There is the growing list of diseases and disorders associated with aberrant gut Microbiota include inflammatory bowel disease, irritable bowel syndrome (IBS), and coeliac disease as intra-intestinal diseases and disorders [12]. Further, extra-intestinal disorders list is rapidly growing based on newly profiled aberrant gut Microbiota include allergy, asthma, metabolic syndrome, cardiovascular disease, and obesity [13]. There is a preponderance of the evidence demonstrate an imbalance/diversity in Gut Microbiota associated with various diseases

and metabolic disorders in animal models and human beings [14]. Further, altered gut Microbiota, along with associated metabolome, seems linked and a fundamental cause of onset and progression of metabolic disorders. Recent studies have demonstrated a change in gut Microbiota leads to various metabolic diseases such as diabetes (both type I and II), obesity, RA and cardiovascular disease, pulmonary hypertension, sleep apnea, and some cancers [15]. Though research findings towards altered gut Microbiota and their link to metabolic disorders have gained substantial progress, the connection to metabolome remains fussy and unconquered [16]. The diseases and complications associated with aberrant gut Microbiota can be classified as- (a) Infectious diseases, (b) Inflammatory diseases (c) Neurological disorders, (d) Obesity and metabolic disorders.

Bibliography

1. Brennan CA and Garrett WS. "Gut microbiota, inflammation, and colorectal cancer". *Annual Review of Microbiology* 70 (2016): 395-411.

2. Henke MT., *et al.* "Ruminococcus gnavus, a member of the human gut microbiome associated with Crohn's disease, produces an inflammatory polysaccharide". *Proceedings of the National Academy of Sciences of the United States of America* 116 (2019): 12672-12677.

3. Gentile CL and Weir TL. "The gut microbiota at the intersection of diet and human health". *Science* 362 (2018): 776-780.

4. Hills RD., *et al.* "Gut Microbiome: Profound Implications for Diet and Disease". *Nutrients* 11.7 (2019): 1613.

5. Arianna K DeGruttola., *et al.* "Current understanding of dysbiosis in disease in human and animal models". *Inflammatory Bowel Disease* 22.5 (2016): 1137-1150.

6. Simon Carding., *et al.* "Dysbiosis of the gut microbiota in disease". *Microbial Ecology in Health and Disease* 26 (2015): 10.

7. Mudd JC and Brenchley JM. "Gut Mucosal Barrier Dysfunction, Microbial Dysbiosis, and Their Role in HIV-1 Disease Progression". *The Journal of Infectious Diseases* 214.2 (2016): S58-S66.

8. Ringel Y and Ringel-Kulka T. "The Intestinal Microbiota and Irritable Bowel Syndrome". *Journal of Clinical Gastroenterology* 49.1 (2015): S56-S59.

9. Chung H., *et al.* "Gut immune maturation depends on colonization with a host-specific microbiota". *Cell* 149 (2012): 1578-1593.

10. Fonseca DM., *et al.* "Microbiota-dependent sequelae of acute infection compromise tissue-specific immunity". *Cell* 163 (2015): 354-366.

11. Kim YG., *et al.* "Gut dysbiosis promotes M2 macrophage polarization and allergic airway inflammation via fungi-induced PGE2". *Cell Host and Microbe* 15 (2014): 95-102.

12. Hill DA., *et al.* "Commensal bacteria-derived signals regulates basophil hematopoiesis and allergic inflammation". *Nature Medicine* 18 (2012): 538-546.

13. Elinav E., *et al.* "NLRP6 inflammasome regulates colonic microbial ecology and risk for colitis". *Cell* 145 (2016): 745-757.

14. Sartor RB. "Microbial influences in inflammatory bowel diseases". *Gastroenterology* 134 (2008): 577-594.

15. Turnbaugh PJ., *et al.* "Acore gut microbiome in obese and lean twins". *Nature* 457 (2009): 480-484.

16. Li N., *et al.* "Butyrate and type 1 diabetes mellitus: can we fix the intestinal leak?" *Journal of Pediatric Gastroenterology and Nutrition* 51 (2010): 414-417.