

# The New Perspectives on the Microbiome and Probiotics

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The human body is a cocktail of human and bacteria cells. Recent studies have revealed that being healthy is not about the absence of bacteria in the body, but rather a balance in the ratios of 'good' and 'bad' bacteria in the gut. In fact, not even the placenta of a mother is sterile since bacteria have been isolated from umbilical cordblood and amniotic fluids of healthy mothers [1]. Therefore, it is possible to suggest that humans probably require certain bacteria for proper development during gestation. This is evident in the meconium microbiome of full term and preterm babies. The relatively higher abundance of Lactobacillus genus in the meconium of preterm babies than their full term counterparts have been suggested to be involved in events that trigger preterm labor [2]. The human microbiome acts to enhance homeostasis [3] by communicating with each other through quorum sensing and with the host cells through hormonal response and immune regulation. However, factors such as diet, drug usage, the immune system, and emotions (stress, chronic anxiety, etc) may alter the composition of bacteria in the gut resulting in dysbiosis. Recent advances in metagenomics and metabolomics have made it possible to identify changes in the microbiome and in metabolic profiles during dysbiosis, thus helping to identify biomarkers of diseases. For instance, in obesity, the levels of Firmicutes increase but Bacteriodetes decrease (Lecomte) relative to lean controls. These alterations result in significant increase in the urine 2-hydroxyisobutyrate levels (indicating improper digestion of dietary proteins) and decreased levels of urinary xanthine levels (indicating high serum uric acid levels) in obese people [4]. Also, the microbiota profiles of children with celiac disease (CD) differ significantly from healthy controls. CD childrens have higher levels of Bacteroides particularly B. vulgatus and B. fragilis which have proinflammatory effects [5]. Using metabolomics, Tjellström., et al. [6] observed higher levels of acetic, iso-butyric, and iso-valeric acids in the feces of CD children compared to healthy controls, indicating a change in gut metabolic activity during the disease. Other diseases associated with dysbiosis include autism spectrum disorder, type 2 diabetes (T2D), inflammatory bowel disease (IBD), Clostridium difficile infection (CDI), etc [7]. The therapies available for treating these diseases include abstinence from foods that trigger the disease (as in CD and T2D), the use of anti-inflammatory drugs or surgery (as in IBD) or antibiotic treatment (as seen in CDI) which do not completely treat the disease. However, a number of studies have shown the possibility of restoring the gut microbiota through the consumption of probiotics and symbiotics (probiotics plus prebiotics) and also by fecal microbiota transplantation [8]. These strategies promise cheaper therapies with no adverse effects. Simrén., et al. [9] have extensively reviewed studies showing the effects of probiotics such as *Bifidobacterium bifidum* MIMBb75 in treating functional bowel disorders. Other probiotics (*Bifidobacterium animalis* subsp lactis, Streptococcus thermophiles, Lactobacillus bulgaricus, and Lactococcus lactis subsp lactis) have psychoactive effect as they alter emotions and cognitive functions in humans when consumed [10]. They do this probably by producing neuroactive substances; GABA (gammaaminobutyric acid) that affects the brain [11]. GABA has mostly been produced in lactic acid bacteria by L-glutamate decarboxylase when L-glutamate is added to the culture medium. GABA also has other application as a major building block for the synthesis of 2-pyrrolidone and biodegradable polyamide nylon 4, which opens its application area in the industrial biotechnology. Therefore, many recombinant Corynebacterium glutamicum (the major L-glutamate producing microorganism), have been successfully used to achieve direct fermentative production of GABA from glucose [12]. Fecal microbiota transplant has also been applied successfully to treat Clostridium difficile infection, Chron's disease and many others [13]. However, its low acceptability and the tendency of pathogen transfer through stool

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administration; new stool substitute transplants are being developed. This synthetic stool approach proved promising as it treated two patients with *C. difficile* following 2-3 days of administration and they remained symptom free even after 6 months [14]. The University of Guelph researchers in Canada have developed a more sanitary way of synthetic poop, named Re POO Pulate by careful examination of bacterial colonies grown from the stool of healthy volunteers, and 33 different bacteria were grown in a robotic intestine simulator affectionately called Robo-gut to create a 'super-probiotic' stool substitute. Since Open Biome, Boston (USA) based first human stool bank in pill form was opened, several companies are under development for other diseases. Indeed, probiotic bacteria ingested into the body may not remain in the gut forever to produce their health effects, but they may stimulate the growth of indigenous bacteria to recolonize the gut and perform their natural functions to ensure homeostasis.

### **Biblioigraphy**

- 1. Di Giulio DB., *et al.* "Microbial prevalence, diversity and abundance in amniotic fluid during preterm labor: a molecular and culturebased investigation". *PLoS ONE* 3.8 (2008): e3056.
- 2. Ardissone AN., *et al.* "Meconium microbiome analysis identifies bacteria correlated with premature birth". *PLoS ONE* 9.3 (2014): e90784.
- 3. D'Argenio V and Salvatore F. "The role of the gut microbiome in the healthy adult status". *Clinica Chimica Acta* 451.A (2015): 97-102.
- 4. Calvani R., *et al.* "Gut microbiome-derived metabolites characterize a peculiar obese urinary metabotype". *International Journal of Obesity* 34.6 (2010): 1095-1098.
- 5. de Sousa ML., et al. "Intestinal microbiota and probiotics in celiac disease". Clinical Microbiology Review 27.3 (2014): 482-489.
- 6. Tjellström B., *et al.* "Gut microflora associated characteristics in children with celiac disease". *American Journal of Gastroenterology* 100.12 (2005): 2784-2788.
- 7. Carding S., et al. "Dysbiosis of the gut microbiota in disease". Microbial Ecology in Health and Disease 26. (2015): 26191.
- Trubiano JA., *et al.* "A different kind of "allogeneic transplant": successful fecal microbiota transplant for recurrent and refractory Clostridium Difficile infection in a patient with relapsed aggressive B-Cell Lymphoma". *Leukemia and Lymphoma* 56.2 (2015): 512-514.
- 9. Simrén M., et al. "Intestinal microbiota in functional bowel disorders: a Rome foundation report". Gut 62.1 (2013): 159-176.
- 10. Tillisch K., *et al.* "Consumption of fermented milk product with probiotics modulates brain activity". *Gastroenterology* 144.7 (2013): 1394-1401.
- 11. Bravo JA., *et al.* "Ingestion of Lactobacillus strain regulates emotional behavior and central GABA receptor expression in a mouse via the vagus nerve". *Proceedings of the National Academy of Sciences USA* 108.38 (2011): 16050-16055.
- 12. Choi JW., *et al.* "Enhanced production of gamma-aminobutyrate (GABA) in recombinant Corynebacterium glutamicum by expressing glutamate decarboxylase active in expanded pH range". *Microbial Cell Factories* 14 (2015): 21.
- 13. Suskind DL., *et al.* "Fecal microbial transplant effect on clinical outcomes and fecal microbiome in active Crohn's disease". *Inflammatory Bowel Diseases* 21.3 (2015): 556-563.
- 14. Petrof EO., *et al.* "Stool substitute transplant therapy for the eradication of Clostridium difficile infection: 'Repoopulating' the gut". *Microbiome* 1.1 (2013): 3.

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