DIET INFLUENCES THE GUT MICROBIOTA: A MINIREVIEW

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ABSTRACT

The human gut ecosystem is dynamic in nature which harbors trillions of microorganisms. These microorganisms constituting the gut microbiota are highly diverse and abundant having multiple implications on wellbeing and health of a person. There is a complex interaction between diet and microorganisms which can lead to beneficial or detrimental outcomes to host health. Each individual harbors specific and diverse microbiota depending upon his diet intake, genetic makeup, medication, metabolic regulations, external environment and his way of living the life. Among all these factors, diet plays a major role in deciding and influencing the microbiota of any person. The effects of diet on the gut microbiota are mostly temporary in nature. The microbiota of a person can be modulated by consumption of dietary fibres and prebiotics. This review focuses on the role of diet in influencing the gut microbiota of varied populations in different regions of the world.

Keywords: Microbiota, Microbiome, Microorganisms, Prebiotics, Probiotic

GUT MICROBIOTA

The collective genomes of the micro-organisms in a particular environment are referred to as Microbiome (Valdes *et al.*, 2018). Trillions of microbial cells colonize human large intestine which are responsible for variations in host physiology and behavior (Whitman *et al.*, 1998; Xu & Knight, 2015). These gut microbiota plays a major role in assisting nutrient digestion, regulating host metabolism, providing resistance to pathogens and boosting immunity as illustrated in Figure 1. (Guarner & Malagelada, 2003; Turnbaugh *et al.*, 2006; Kelly *et al.*, 2007; Neish, 2009; Qin *et al.*, 2010). The microbiota is

highly diverse which includes viruses, bacteria, fungi and protozoa in commensal with the gut (Lozupone *et al.*, 2012; Gill *et al.*, 2006; Eckburg *et al.*, 2005). Firmicutes (gram positive bacteria) and Bacteroides (gram negative) are the predominant species in the human gut microbiota which act as an indicator of the gut microbiota composition (Flint *et al.*, 2007; Walker *et al.*, 2011; Hou *et al.*, 2020). The mechanisms by which microbiome produces different byproducts and secondary metabolites in still poorly understood and is infancy stage of research. Some common species of microbiota harboring gut are listed in Table. 1.

Table 1 Gut Microbiota and their basic features

Species Name	Characteristics Features	References
<i>Bifidobacterium</i> spp	Gram positive obligate anaerobe branched; nonmotile	Pinzone <i>et al.</i> , 2012; Schwiertz <i>et al.</i> , 2010
<i>Lactobacillus</i> spp.	Gram positive facultative anaerobe rod-shaped	Chen <i>et al.</i> , 2009; Venturi <i>et al.</i> , 1999, Hou <i>et al.</i> , 2020
<i>Bacteroides</i> spp.	Gram negative obligate anaerobe rod-shaped; variable motility	Raisch <i>et al.</i> , 2016; Lucke, 2006; Wexler, 2007; Prindiville, 2000
<i>Bilophila</i> spp.	Gram negative obligate anaerobe urease-positive, bile resistant, catalase-positive	Baron, 1997; Kamada <i>et al.</i> , 2013
<i>Clostridium</i> spp.	Gram positive obligate anaerobe rod-shaped; spore-forming	Baron, 1996; Gaboriau <i>et al.</i> , 2009, Hou <i>et al.</i> , 2020
<i>Eubacterium</i> spp.	Gram positive obligate anaerobe rod-shaped	Barcenilla <i>et al.</i> , 2000; Schneider <i>et al.</i> , 2000, Hou <i>et al.</i> , 2020
<i>Enterococcus</i> spp.	Gram positive facultative anaerobe cocci	Fisher & Phillips, 2009
<i>Escherichia coli</i>	Gram negative facultative anaerobe rod-shaped	Rallabhandi <i>et al.</i> , 2008; Todar, 2007; Darfeuille <i>et al.</i> , 2004
<i>Helicobacter pylori</i>	Gram negative microaerophilic helix-shaped; motile	Kusters <i>et al.</i> , 2006; Chang & Parsonnet, 2010
<i>Streptococcus</i> spp.	Gram positive facultative anaerobe cocci	Patterson, 1996
<i>Faecalibacterium prausnitzii</i>	anaerobic, gram-negative, non-spore-producing butyrate-producing bacterium	Hou <i>et al.</i> , 2020; Lopez-Siles <i>et al.</i> , 2012; Heinken <i>et al.</i> , 2014; Miquel <i>et al.</i> , 2013; Machiels <i>et al.</i> , 2014
<i>Anaerostipes caccae</i> & <i>Anaerostipes hadrus</i>	Butyrate producers, lactate and acetate utilizers	Duncan <i>et al.</i> , 2004; Allen-Vercoe <i>et al.</i> , 2012

The microbiota of human gut is influenced by many factors like host genotype (Ley *et al.*, 2005; Khachatryan *et al.*, 2008; Benson *et al.*, 2010), disease (Turnbaugh *et al.*, 2006; Qin *et al.*, 2010), diet (Harmsen *et al.*, 2000; De Filippo *et al.*, 2010) and external disturbances (De La Cochetiere *et al.*, 2005; Dethlefsen & Relman, 2010; van Vliet *et al.*, 2009).

Figure 1 Role of the gut microbiota in health and disease (Valdes Ana *et al.*, 2018)

INFLUENCE OF DIET ON THE GUT MICROBIOTA OF A PERSON

Diet of a person modulates the gut microbiota (genes are known as microbiome) influencing the well being and health of the person (Johnson *et al.*, 2020). Human health is influenced by the interaction of the microbiota and the type of diet intake (Figure 2). The immune system is activated by the gut microbiota, they protect against the opportunistic pathogens, nutrient and energy is harvested from the diet by them (Chow *et al.*, 2010; Fukuda *et al.*, 2011; Sonnenburg *et al.*, 2005). Any deviation in normal gut microbiota can cause obesity, diabetes and other plethora of reactions (Turnbaugh *et al.*, 2006; Kallus & Brandt 2012; Qin *et al.*, 2012). Apart from diet, gut microbiota is also influenced by genetic and environmental factors (Xu & Knight 2015).

Different studies have been undertaken to show the response of microbiota species to the different dietary components. Protein, fats, probiotics and carbohydrates induces different effects on gut microbiota (Singh *et al.* 2017). Diet components- diet composition, diet uptake habits or changes in diet have impact on the gut microbiota. Switching from a high-fat/ low-fiber to a low-fat/high-fiber diet affects the relative abundances of several microbial taxa in humans within 24 hrs (Wu *et al.*, 2011; David *et al.*, 2011). These diet-related changes may increase energy extraction from food and consequently alter host metabolic pathways (Sommer *et al.*, 2016; Turnbaugh *et al.*, 2008; Springer *et al.*, 2017). A study done on the western population by Wu *et al.*, (2011) has shown that the structure and composition of the human gut microbiota is influenced by the long-term dietary habits. They observed that the microbiota was enriched with *Prevotella* spp. in people with fiber and carbohydrate rich diets and whereas *Bacteroides* was major spp in the microbiota of people with diet rich in protein and fat. In another study, it has been reported that people on a fat-restricted or a carbohydrate-restricted low-energy diet have increased ratio of Bacteroidetes:Firmicutes in their gut microbiota (Ley *et al.*, 2006). In a similar way, studies on Asian population have also been conducted to evaluate their gut microbiota. Hou *et al.*, (2020) observed that in all participants of Asian populations harbors *Faecalibacterium prausnitzii* in their gut. This species is used as a potential probiotic and alleviates diabetic symptoms and have

immunomodulatory effect; hence maintains health of Asian population. Mediterranean diet constituting eggs, chicken, sea food and fruits which are a rich source of Vitamin A and Vitamin B₅ promotes and favors the growth of *Prevotella* spp. in the gut microbiota (David *et al.*, 2014; De Filippis *et al.*, 2016). In another study, Brassica consumption was associated with decrease in sulphate-producing bacteria (Kellingray *et al.*, 2017). Microbiota composition is also determined by the fiber content in the diet of a person (Chassaing *et al.*, 2017). In a study, dietary fibre- fructans and galactooligosaccharides resulted in an increase in *Bifidobacterium* and *Lactobacillus* species in faecal matter of the subjects (So *et al.*, 2018). Fruits and grain fibre also influences gut microbiota (Johnson *et al.*, 2019).

Figure 2 Interaction of Gut Microbiota and Diet Influences Human Health (Johnson *et al.*, 2020)

PROBIOTICS AND GUT MICROBIOTA

Certain live microorganisms conferring health benefits when administered in adequate quantity are popularly known as Probiotics. These probiotics colonize and proliferate in the GI tract and alter the gut microbiota. The potential benefits of probiotics are in the treatment of infectious- and antibiotic-associated diarrhoea, insulin resistance in diabetes, and remission and maintenance of inflammatory bowel disease (Li *et al.*, 2019; Hungin *et al.*, 2018; Derwa *et al.*, 2017; Krumbek *et al.*, 2018). The variability is very high in establishing probiotics as a part of gut microbial community as they have to compete against the host microbes for substrates for their survival (Shepherd *et al.*, 2018).

PREBIOTICS AND GUT MICROBIOTA

Fibre content of certain food compounds like fruit, vegetables, legumes, grains and nuts is very high and has beneficial effects on the health. The term prebiotics is defined as “a substrate that is selectively used by host microorganisms conferring a health benefit” (Ferrarese *et al.*, 2018; Gibson *et al.*, 2017). Inulin, FOS and GOS are the common examples of prebiotics present in dietary fibres. They favor the health promoting microorganism in gut microbiota. These prebiotic compounds are resistant to gastric acid and hydrolytic activity of the digestive enzymes and therefore are metabolized in the colon by the microbiota. The metabolism of these prebiotics results in the production of short-chain fatty acids (SCFAs), including acetate, propionate and butyrate (Holscher, 2017). Different studies have shown the growth promoting effect of prebiotics on *Bifidobacterium* and *Lactobacillus* and Lactic acid bacteria (Gibson & Roberfroid, 1995; Macfarlane *et al.*, 2006; Gibson *et al.*, 2017; Dewulf *et al.*, 2013). *Faecalibacterium prausnitzii* (a butyrate- producing bacteria) and *Akkermansia muciniphila* (a mucin degrading bacterium) have beneficial health effects- reduces inflammation and improves gut barrier function (Thomas *et al.*, 2015). The dietary fibre or prebiotics impacts the human GI microbiota both functionally and in composition which has been briefly illustrated in Table. 2 (Holscher, 2017) and Figure 3.

Table 2 Impact of Dietary Fibre or Prebiotic on GI Microbiota

Dietary Fibre or Prebiotic	Changes in Microbiota	References
Arabinoxylan-oligosaccharides	Increased Lactobacilli, Bacteroides, Bifidobacterium	Walton <i>et al.</i> , 2012; Francois <i>et al.</i> , 2012, Francois <i>et al.</i> , 2014
Whole grains	No significant changes	Ampatzoglou <i>et al.</i> , 2015
Galactooligosaccharides	Increase Bifidobacterium spp, Bacteroides spp,	Vulevic <i>et al.</i> , 2015
Inulin + oligofructose	Increased Bifidobacterium longum, Bifidobacterium pseudocatenulatum and Bifidobacterium adolescentis	Salazar <i>et al.</i> , 2014
Xylooligosaccharide	Increased Bifidobacterium, Bacteroides fragilis	Finegold <i>et al.</i> , 2014
Polydextrose	decreased C. histolyticum, lactobacilli/enterococci	Costabile <i>et al.</i> , 2012
Butyrylated high-amylose maize starch,	Increased Clostridium coccoides, Clostridium leptum, Lactobacillus spp, Parabacteroides distasonis and Ruminococcus bromii	Le Leu <i>et al.</i> , 2015
Resistant starch	Decreased Ruminococcus torques and Ruminococcus gnavus, Ruminococcus torques and Escherichia coli	Salonen <i>et al.</i> , 2014
Non-starch polysaccharides	Increased Oscillospira guillermoidii, R. bromii, Sporobacter termitis, Clostridium leptum, C. cellulosi, Alistipes spp, E. rectal, Decreased Papillibacter cinnamivorans, Increased Eggerthella, Collinsella, Corynebacterium, Bacteroides vulgatus and Prevotella oralis	Salonen <i>et al.</i> , 2014
	Decreased: C. leptum, C. cellulosi, Oscillospira spp and Sporobacter spp

Figure 3 Beneficial impacts of prebiotic on the gut microbiota (Cathy *et al.*, 2020)

CONCLUSIONS

The interaction between host and gut microbiota is multi-faceted and highly complex; a balance of benefit and harm depends on many dietary and microbial factors. Diet can significantly influence and alter the gut microbiota of a person. The major dietary components affecting the gut microbiota are fibre, fruits, vegetables, carbohydrates, protein and other plant foods. More elaborative studies on the mechanisms involved in interaction of gut microbiota and diet need to be carried out to answer plethora of questions like role of diet induced microbiota in obesity, diabetes and other disorders. Therapeutic dietetic strategies on the

microbiota further requires understanding of the relation between diet and gut microbiota. The dietary modulation of the gut microbiota for health can be clinically recommended after extensive and elaborative research in this direction.

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