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Review Article: Gut Microbiota as Biological Regulators for Human Health

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ABSTRACT

Gut microbiota, formerly called gut flora, is the name given today to the microbial population living in human intestine. It has the largest number of species in comparison to other body parts. In humans, the gut flora was established at childhood through one to two years after birth. The relationship between some gut flora and humans is not only commensal, but also a mutualistic relationship, in a way that intestine support the growth of healthy gut flora that provides a barrier to pathogenic organisms. Some beneficial human gut microorganisms ferment dietary fiber into short-chain fatty acids (SCFAs), such as acetic and butyric acid. In additional, play a role in synthesizing vitamin B and vitamin K as well as metabolizing bile acids and sterols. There are several factors affecting the change on human gut flora varieties over time such as, the diet type and composition, the bacterial infections, the human lifestyle, physical activity and antibiotic or surgical treatment. The key factor between them is the diet types and its composition. It was suggested the frequency of bacteria present in the intestine significantly associated with the dietary patterns. Thus, this article describes current indication regarding the links between gut microbiota varieties and dietary patterns throughout life. In addition, the importance of microbiota-diet interactions extensively studied by modern new bioinformatics tools and molecular based techniques to demonstrate the potential microbiota-diet interactions which could change future approaches to nutrition in healthy and diseased human bodies.

Keywords: Gut microbiota, gut flora, the benefit of gut flora, and the factors affecting gut flora.

INTRODUCTION

Gut microbiota refers to more trillions of microbes commensally inhabitant the human gut. It was reported previously that gut microbiota performs more important vital functions particularly as a barrier inhibiting the proliferation of pathogenic organisms. Thus, a great number of gut microbiota inhabited and reside in the large bowel and significantly considered as an essential agent for both human health and survival (Linares *et al*., 2016).

Most studied showed that gut microbiota can protect human bodies by contributing in the main physiological process such as nutrition, immunity and protection against harmful microbes (O'Hara and Shanahan 2006). Thus, the activity and occurrence of the gut microbiota as an essential health indicator significantly shaped by a number of factors including diet, environmental elements and the host's genetic background. Most notably, diet and dietary factors are major determinants of gut microbiota composition and activity (David *et al*., 2009).

Although, various factors influence upon the frequency and importance of the human gut microbiota, diet being a very important one which signify the number, type as well as the benefits of such microbial community as in (Fig. 1) (Daniela *et al*., 2015).

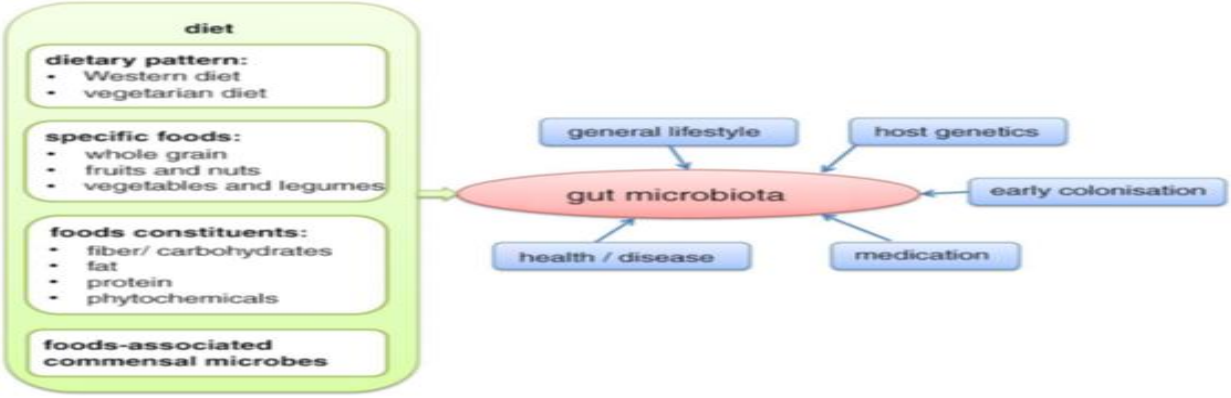

Fig. 1. Factors, which influence the composition of the human gut microbiota, with special focus on diet (Daniela *et al*., 2015).

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During microbial metabolism. intestinal microbes use indigestible food components like fibers which are hardly to utilize by human enzymes. Whereas bacteria are efficient and specific in fermentation processes especially for complex diets. Thus, for specific phylotypes, complex diets could be used as measuring factor for both promoting and inhibiting growth of bacteria. In addition, a useful end product produced during the growth of bacteria such as short-chain fatty acids (SCFA) and vitamins. These compounds are such important for human health (Bindels *et al*., 2015).

Moreover, gut microbiota contributes in additional vital processes such as help in the digestion of food, the breakdown of toxins, and drugs (Linares *et al*., 2016), regulates lipid and glucose metabolism (Ejtahed *et al*., 2016), plays a fundamental role in the induction, training, and function of the host immune system (Belkaid and Hand 2014), modulates gene expression (Takahashi, 2014), and reduces inflammation (Van de Wiele *et al*., 2016). In addition, 20-40% of the small molecules in the peripheral blood are microbial metabolites, many of which have profound effects on the development and function of the central nervous system (CNS) (Belkaid and Hand, 2014 and Takahashi, 2014). The diversity and dynamics of gut microbial communities has recently of tremendous interest in designing dietary approaches based upon understanding of the underlying mechanisms by which dietary components influence on gut microbiota (Bindels *et al*., 2015), and to assist in the establishment and maintenance of a beneficial gut microbiota in human health.

In this regard, the aim of this review is to explore the effect of dietary patterns on variability, occurrence, and beneficial of human gut microbiota. Thus, the study includes nutrients, specific foods, dietary patterns (e.g. Western diet).

1. Gut microbiota:

Microbiota refers to a group of microorganisms genetically known as microbiome. They are living on and inside human body and responsible for certain vital biological processes within human bodies. In the adult bowel, approximately 10-100 trillion microorganisms are present. The composition of gut microbiota was affected by several demographic factors such as age, sex, geo-graphical area, ethnicity, family, and diet. In addition, prebiotics, probiotics, and antibiotics received by human bodies could have a modulated effect on the community of gut microbiota (Ley *et al*., 2006). It was reported that gut microbes are able to use human nutrients and the luminal environment, particularly pH in producing a vast range of biological products which are beneficial to human bodies (Duncan *et al*., 2009). While, several types of a microbiota such as *Lactobacillus*, *Prevotella* and *Sneathia spp* coming from the maternal vaginal tract were significantly reported in infants vaginally born. However, *Staphylococcus*, *Corynebacterium*, and *Propionibacterium spp* were demonstrated predominantly in newborns delivered by caesarean section (Power *et al*., 2014).

Moreover, physical exercise as active life style is able to modulate gut microbiota. It was suggested previously that the abundance of beneficial microbial species could be increased by increasing human physical activity (Prakash *et al*., 2011). To date, significant interactions were reported among different types of gut microbiota and with the human host. These interactions constitute a dynamic entity to human body and showed to be modified by the type of diet, lifestyle, antibiotics, and genetic background (Rodriguez-Valera *et al*., 2009 and Dominguez-Bello *et al*., 2010).

Human ecology significantly showed to affect upon the biodiversity of microbiota. In developed countries, significant loss was reported in certain species of microbiota that colonized human bowel which in turn effects on the biodiversity of human microbiota (Emerson and Wilson 2009).

In European and African children, the present microbiota has completely different compositions. Bacteroidetes and Gram-positive organisms were present in higher ratios in the bowels of African children, while a Western lifestyle appears to promote an increase in Firmicutes and Gram-negative organisms (De Fillipo *et al*., 2010).

It was reported that, gut microbiota involved in the activation of a variety of metabolic functions especially, fermentation and absorption of undigested carbohydrates, absorption of electrolytes and minerals as well as modulation of bowel motility, and synthesis of some micronutrients (Gill *et al*., 2006). In addition, the gut microbiota helps the host in such a way to eliminate calories from indigestible complex carbohydrates and plant polysaccharides via enzymes that are not encoded within the human genome (Zhang *et al*., 2014). Recently, colonic microbes showed to ferment non-digestible, leading to the production of short-chain fatty acids (SCFAs) such as butyrate, which has trophic effects on intestinal epithelium (Kotzampassi *et al*., 2014). Bacteria produce essential numerous lipids such as lipopolysaccharide, a component of the cell wall of gram negative bacteria that can cause tissue inflammation (Trent *et al*., 2006).

Also, many enteropathogenic bacteria can cause diarrhea or produce toxins under the exact conditions (Kamada *et al*., 2012). Bacteria such as Bifidobacterium can also help prevent pathogenic infection through production of acetate (Fukuda *et al*., 2011). In addition to its metabolic functions, microbiota is involved in interaction with the immune system, providing signals to promote maturity of immune cells and normal performance of their functions, as well as toxin and carcinogen destruction, preventing colonization by pathogenic bacteria (Gill *et al*., 2006).

2. Nutrients in a diet affecting gut microbiota:

Previous studies showed that the comprises and composition of healthy microbiota significantly controlled by varies factors such as the diet, lifestyle, and many other factors (Backhed *et al*., 2012). Thus, the major features of the healthy microflora should be identified in healthy people. However, the same type and quantity of microbiota were identified in people who live in the same geographical community. This may be due to contact in such away to each other (Palmer *et al*.,2007 and Yatsunenko *et al*.,2012). The type of food consumed significantly determine also the type and number of proposed microbiota. In this regard, three predominance enterotypes were identified based upon the type of food consumed. Previous studies determined Bacteroides enterotype which commonly present in people who received a Western diet enriched with both protein and fat, however Prevotella enterotype was identified in people

who consumed diets with higher fiber content (Arumugam *et al*., 2011). Similarly, people like the US population who eat more fat and protein, their gut enriched with bacteria which capable of degrading both protein and fats. Also, the guts of Malawi (East Africa) residents showed to have microorganisms capable of degrading more polysaccharide (Yatsunenko *et al*., 2012).

Gut microbiota and carbohydrates

Colonic microbes have an immense capacity to hydrolyze and use carbohydrates, especially complex polysaccharides present in nutrients. In this regard, resistant starches (RS), non-starch polysaccharides, and oligosaccharides these components that reach the gut are the most important sources of both carbon and energy for microbes (Verdu and Riddle, 2012). The composition and variety of intestinal microbiota can be abnormally shifted according to short-term changes in carbohydrate consumption (Russell *et al*., 2011 and Walker *et al*., 2011). Whoever, it was reported that the composition of microbiota is similar in Europeans (Qin *et al*., 2011). A profound alteration in microbiota composition might be associated with consummation food for a long-term (Wu *et al*., 2011).

The colonic microbiota is capable to ferment fibers present in diet and release many active metabolites that are very benefits to human health. For example, carbohydrates fermented to organic acids and the produced energy is essential for the bowel epithelium, peripheral tissues, and for other inhabitant bacteria (Windey *et al*., 2012).

Polysaccharides are the present components present in diets enriched with fibers, chemically polysaccharides formed of ten units of monosaccharide that hardly to digest by human enzymes. Based up on recommendations of the American Dietetic Association, the consumption rates varied according to gender, whereas only 38 g were recommended for men, whereas14 g or 25 g dietary fibers are sufficient to adult women. Whoever, the World Health Organization (WHO) recommended a quantity of 25 - 35 g/d of dietary fibers for both genders. whereas, a dose of 40 - 45 g (maximum dose sixty g/ day) of dietary fibers were prescribed as the therapeutic dose (Slavin, 2008).

For proper digestion, essential dietary fibers such as resistant starch and non-starch polysaccharides (Fig.2) (Daria *et al*., 2016) are required. The data showed that there are 4 types of indigestible Resistant Starch (Flint *et al*., 2012), Which significantly metabolized in different ways by intestinal microbiota (Martinez *et al*., 2013).

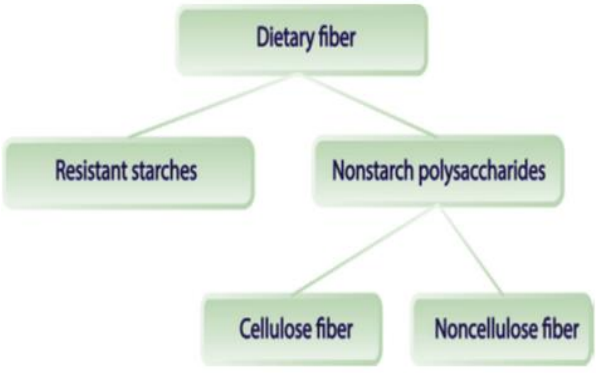

Fig. 2. Dietary fiber types (Daria *et al*., 2016).

The fermentation of starch by microbiota to use it as a source of carbon and energy depend mainly up on its chemical constituents whereas amylose (20-25%) and amylopectin (75- 80%) are the main components of starch. (Ramsay *et al*., 2006 and Ze *et al*., 2012). Starch is the commonly carbohydrates provided to human via wheat, rice, root vegetables, beans, fruits, and the like.

A significant increase in the microbiota; *Ruminococcus bromii* abundance (Clostridia class) was reported in 46 healthy adults following dietary intervention containing a diet rich in RS (Abell *et al*., 2008). Similarly, obese men received a food with high starch content for10 weeks showed significantly higher levels of gut microbiota especially, *Ruminococcus bromii* and *Eubacterium rectale* (Firmicutes phylum). In this study, *Ruminococcus bromii* was identified in lower levels whereas more than 69 % of the starch food not fermented by microbiota (Walker *et al*., 2011).

Recently, intake of maltodextrin; a dietary resistant non-viscous fiber lead to significant increase in the cummunity of the Ruminococcus, Eubacterium, Lachnospiraceae, Bacteroides, Holdemania, and Faecalibacterium (Baer *et al*., 2014).

Diets containing non-starch polysaccharides showed to increase beneficial bacteria in the gut of human. (Duncan *et al*., 2007). Cellulose is the most common non-starch polysaccharide provided to human via diets in vegetables and fruits, whole grain and bran products, as well as it used as a substrate for the production of short-chain fatty acid (SCFA). In other study, the growth of Bifidobacterium was significantly promoted in healthy preadolescent children following administration of diet containing the wheat bran extract riches with arabinoxylan-oligosaccharides (Francois *et al*., 2014).

Gut microbiota and proteins

It was reported that approximately 10% of dietary protein which reaches the colon considers as a vital substrate sources for proteolytic bacteria and nitrogenous source for saccharolytic species. Protein degradation was the most energy and diets sources for different categories of proteolytic bacteria which lives mostly in the distal colon where carbohydrate sources are too small. (Walker *et al*., 2005 and Hamer *et al*., 2012). Gut health differentially affected by the type dietary proteins which might be beneficial or harmful (Chao *et al*., 2005 and WCR F. *et al*., 2011).

Microorganisms in the colon degrade amino acids by deamination process and use it in vital human process. Clostridium, *Enterobacterium spp*, and some Bacteroides are involved in the deamination process. Lactobacillus and Bifidobacterium bacteria are involved in the lactic fermentation. Also, bacteria ferment L-carnitine present in proteins to trimethylamine N-oxide (TMAO) which supposed to induce atherosclerosis (Koeth *et al*., 2013).

In human and animal studies, the consumption of dietary proteins is positively associated with the levels of byproducts released form protein fermentation such as sulphide. This, bio feedback of the effect of higher dietary protein intake on DNA damage in colonic mucosa holds true evidences for humans (Russell *et al*., 2011 and Humphreys *et al*., 2014).

In most cases, higher protein intake not necessary to produce higher amounts for protein fermentation products in human feces (Brinkworth *et al*., 2009). This actually has more

benefits for renal health. On the other hand, L-carnitine present in red meat utilized by microbial metabolism to produce Trimethylamine-N-oxide that significantly initiates and might increase the risk of atherosclerosis (Koeth *et al*., 2013).

Gut microbiota and Fat

The combinatory effects of all biological macronutrients significantly influence on cellular biological processes. Whereas, overall all energy intake showed to be affected by the percentage of each macronutrient whereas one proportion rate of nutrient causes or inherently affects the segment of other macronutrients. For example, the deficiency of high-fat diets (HFD) in the quantity of complex carbohydrates and only contains low carbohydrates contributes to such extent with the precise effects caused by a high-fat intake (Daniela *et al.* 2015). It was reported that the quality and quantity of fat may affect intestinal Microbiota composition. Previously, it was suggested that modulation in the composition of intestinal microbiota proceed according to the consumption rates of dietary fat which indirectly modulates the community of microbiota via influencing up on both the secretion of bile acid and its composition.

High fat intakes showed to stimulate the secretion of bile acids and increase fecal concentrations of secondary bile acids, such as deoxycholic acid (DCA) (Rafter *et al*., 1987). In addition, SCFA and Bifidobacterium concentrations were significantly reduced following high-fat diets interventions (Brinkworth *et al*., 2009).

Actually, various ways reported studying the effect of unsaturated and saturated fats on gut microbiota. It found out that the negative effects of a high fat diet can be overrode by consumption of meat and dairy products which contain conjugated linoleic acids. These acids can exert a prebiotic action on *Akkermansia muciniphila* and *Bacteroidetes*/*Prevotella* levels in mice (Chaplin *et al*., 2015).

Dietary polyphenols are also another example which shown to promote *Akkermansia muciniphila* growth, and decrease the ratio of Firmicutes to Bacteroidetes in mice following receiving minimum quantities of high-fat diet (Roopchand *et al*., 2015), while the ratio of Firmicutes to Bacteroidetes was significantly increased following high cholesterol diet (Lee *et al*., 2015).

Specific foods:

Whole grain products

These products with a high amount of dietary fiber which hardly to digest by any enzymes of the human body. It was reported that microbiota is capable of metabolizing whole grain fibers such as WG breakfast cereals as soon as it reaches the colon, which in turn effects on the growth and community numbers of different inhabitant bacterial groups (Carvalho-Wells *et al*., 2010 and Martinez *et al*., 2013). Also, it was reported in a controlled study that higher levels of Bifidobacteria were identified in individuals consumed a cereal breakfast containing maize-based WG for three weeks (Carvalho-Wells *et al*., 2010). Similarly, significant increase in the ratio of Lactobacillus/Enterococcus group was reported in subjects received either WG rich cereals or placebo cereals. A breakfast cereal diet containing a wheat or bran showed to increase in the community levels of Lactobacillus/Enterococcus compared to food breakfast containing a WG wheat (Costabile *et al*., 2008). However, administration of the WG wheat break-fast significantly increase the levels of *Bifidobacterium spp.* and the Enterococcus/Lactobacillus group. The results significantly compared with lower ratios of bacteria for those who received wheat-bran-based breakfast cereal. However, neither study detected effects on SCFA concentrations (Carvalho-Wells *et al*., 2010 and Costabile *et al*., 2008).

Similarly, the effect of types of grain products such as whole grain brown rice flakes, whole grain barley flakes, or a mixture of both on the growth, composition, and community numbers of microbiota were studied (Martinez *et al*.,2013). The results of this study showed an increase in microbial diversity with increasing in the levels of Firmicutes and a reduction of the Bacteroidetes phylum following diet interventions containing WG. During the WG barley intervention, the changes occurred at phylum level significantly associated with the presence of Blautia and Roseburia in higher quantity and Bacteroides with lower amounts. Also, the WG barley intervention significantly increased the community levels of Bifidobacteria with sufficient statistical significance (Carvalho-Wells *et al*., 2010; Costabile *et al*., 2008).

Other studies reported the influence of consuming WG rye and refined wheat bread on the microbiota composition (Lappi *et al*, 2013). The results showed significant increase in composition of microbiota in the group consumed white wheat bread for 12 weeks. In the same time, the WG rye bread group showed no significant differences for any bacterial taxa.

Fruits and nuts

The influence of the consumption of both nut and fruit on the community levels of the gut microbiota was investigated in many studies (Vendrame *et al*., 2011). In this study, in the faces of the subjects were enriched with higher communities of *Bifidobacterium spp*. and *Lactobacillus acidophilus* following consumption of blueberry drink. Whereas, no change observed in the ratios of other communities present such as *Clostridium coccoides*, *Prevotella spp*., *Bacteroides spp*., and *Enterococcus spp*.. Furthermore, human gut microbiota composition significantly influenced following administration of both almonds and pistachios (Ukhanova *et al*., 2014). In this study, the participants received 0, 1.5, and 3 servings of nuts per day, with each intervention period lasting for 18 days. a stronger effect was reported on the composition of microbiota following the consumption of pistachios than for almonds.

Vegetables and legumes

The influence of chickpeas on the composition of gut microbiota was significantly evaluated in human subjects (Fernando *et al*., 2010). In this study, lower ratios of Clostridium cluster XI (30 %) and Clostridium cluster I / II (40%) were identified in all the subjects consumed chickpea for three weeks compared to other subjects received the control diet either alone or in combination with raffinose. However, no change in both the Shannon diversity index and the SCFA concentrations was reported when performed by unweight pair group method with arithmetic mean (UPGMA).

Similarly, the influence of conventional soymilk on gut microbiota investigated in relation to the effect of both low glycinin, soymilk, and bovine milk (Fernandez-Raudales *et al*., 2012). A decrease in the ratio of Firmicutes to Bacteroidetes was identified following administration of diets

containing both low glycinin and soymilk in relation to standard values, which showed no differences in the group received the bovine milk. Finally, it is hardly to conclude the pivotal effect of fruits, nuts, vegetables and legumes on the composition of the gut microbiota. This might be due to the lake of limitation in the available published data (Daniela *et al*., 2015).

Diet and Dietary Change:

There was a significant variability or frequency in the gene complement between the inhabitant microbial gene and the targeted host (human). The data previously reported that the microbial gene set is 150 times larger than the complemented gene of the host (Qin *et al.* 2010). However, 99% of biomass present in human body comprises only for about fifty microbial species, fitting to just 5 or 6 genera and two phyla. Of the genera *Eubacterium*, *Bifidobacterium* and *Bacteroides* are numerically the most important microbial genera which may account for more than 60 % of cultivable bacteria present in human stool. Followed by least amounts of *Clostridium*, *Enterobacteriaceae* and *Streptococcus* respectively. In addition, acute dietary change (daily variation) is significantly responsive to variability in the structure of the population, whereas a quick and substantial increases in populations particularly in the genus and species level significantly affects upon gut microbiota (Wu *et al*., 2011).

Dietary patterns:

Vegetarian diets

The data showed that Clostridium bunch XIVa which are butyrate producing bacteria significantly increased as the microbiota of omnivores (Kabeerdoss *et al*., 2012 and Matijasic *et al*., 2014).

In addition, subjects who depend mainly up on the omnivore mode of food showed an increase in the gene level of butyryl – CoA - transferase which significantly enhance the production capacity of butyrate and promotes more beneficial effects to human health. The geographical parameters play significant role in the effect of the dietary habits on the community of microbiota.

Thus, in previous studies, the proportions of microbiota; *Clostridium clostridioforme*, *Bacteroides thetaiotaomicron*, Bacteroides/Prevotella group, and *Faecalibacterium prausnitzii* were significantly increased in vegetarian's subjects (Matijasic *et al*., 2014). Whereas, the microbiota composition of omnivores and vegetarians has no significant differences (Liszt *et al*., 2009). Even so, Bacteroides are identified in a higher amount along with lower ratios of Clostridium cluster IV in vegetarians (Kabeerdoss *et al.* 2012).

Western diet

It was reported that these diets are highly refined diets with poor nutritional quality. The influence of these diets on the gut microbiota are extensively studied among US Americans or Europeans in comparison with those of Africans or South Americans (De Filippo *et al*., 2010; Grzeskowiak *et al*., 2012; and Ou *et al*., 2013). The composition of gut microbiota significantly changed in amounts in 6 month old infants from Malawi in comparison to age matched finish infants (Grzeskowiak *et al*., 2012). Older subjects aged 0-70 years old from Venezuela, Malawi, and the United States showed significant change the composition of microbiota following administration of western omnivorous diets (Yatsunenko *et al.* (2012).

In this study, the composition of microbiota showed to be controlled by age and the type of country. A least microbial diversity was observed in adult Americans whereas similar levels were reported in both Malawian and Venezuelan samples (Yatsunenko *et al*., 2012). Besides, the genus Prevotella was diminished in Americans which may be related to discriminatory taxon. Similarly, De Filippo *et al*. (2010) observed an increase the amounts of Prevotella in African children compared with European children. In addition, several studies reported enrichment in Prevotellain Africans compared with African Americans (Ou *et al*. ,2013), and similar observations relating to Prevotellain were reported in the Hadza hunter-gatherers (from Tanzania) compared with Italian people (Schnorr *et al*., 2014). In addition, the ratios of Succinivibrio and Treponeman are increased in several African populations. These bacteria are capable for degrading a high-fiber with complex carbohydrates. For the rural African populations, Succinivibrio and Treponeman diets are significantly important as the typical diet (De Filippo *et al*., 2010; Ou *et al*., 2013; and Schnorr *et al*., 2014).

Ketogenic diet

It is a type of diets characterized by a lower carbohydrate consumption which to enhance ketone production. The variability of gut microbiota showed to be sensitive to a ketogenic diet. It was reported that the sensitivity of gut microbiota to a ketogenic diet appears to play a role in the efficacy of these diet interventions as refractory treatment for childhood epilepsy (Zhang *et al*., 2018). In addition, modulation of specific gut bacteria by ketogenic diet significantly regulates the neuroprotective effects via enhancing hippocampal g-aminobutyric acid/glutamate levels (Olson *et al*., 2018). Recently, weight loss, longevity and a reduction in the disease onset showed to be modulated by ketogenic diets which effects on certain gut microbiota (Roberts *et al*., 2017). In contrast, some human studies reported that intervention based ketogenic diets showed negative impacts on microbial ecology and gut health (Swidsinski *et al*., 2017and Tagliabue *et al*., 2017). These contradictory reports may be related to small cohorts used with specific metabolic conditions (Swidsinski *et al*., 2017 and Tagliabue *et al*., 2017), restricting generality to larger populations. Thus, in common the effects and long-term safety of ketogenic diets on the gut microbiota and intestinal environment should be extensively studied in larger population.

Mediterranean diet

A variety of food items (unsaturated fats, vegetables, fruits, legumes and limited red meat intake) were included in the Mediterranean diet. In the Mediterranean region, people have no particular or specialized food groups, they consume foods without confinement to specific macronutrient ratios (Salas-Salvadó *et al*.,2014; Sofi *et al*., 2010). In addition, Mediterranean diet showed to produces metabolite production and favorable microbiota profiles, with microbial diversity paralleling levels of dietary adherence (De Filippis *et al*., 2016; Pastori *et al*., 2017; Garcia-Mantrana *et al*., 2018).

Perspectives and future directions

The data collected in this review significantly recognized the gut microbiota as a vital factor in human

health and disease. It has a confirmative defining variation depending on the dietary pattern response in healthy and diseased human bodies. It was reported that, the variability and existence of gut microbiota are significantly associated with the dietary patterns. Whereas, short- and long- term dietary interventions alter the ratios of the gut microbiota in human bodies. Thus, in microbiota directed interventions, the degree of microbiota and its potential for response depend mainly up on dietary patterns (Griffin *et al*., 2016 and Zmora *et al*., 2018).

The importance of microbiota-diet interactions showed be realized and extensively studied by modern new bioinformatics tools and molecular based techniques (Vrieze *et al*., 2012; iHMP, 2014; West and Powrie, 2015 and Thaiss *et al*.,2016), to demonstrate the potential microbiota diet interactions which could change future approaches to nutrition in healthy and diseased human bodies.

CONCLUSIONS

It is clear that diet types and its composition has a vital influence on the human gut microbiota varieties, which is in particularly important for people in all ages. This influence reflects the factors within the diet that support the gut flora growth. For that, it is mandatory to control the diet composition with the purpose of detect their short term effects on the gut flora growth and use this knowledge to produce the desired shifts in microbial populations, health outcomes and products. To understand the effect of foods and food constituents, more studies based up on the consumption of food products especially fruits, and vegetables were recommended. In addition, the influence of phytochemicals and drug on the gut flora which might inhabit human intestine should also study briefly in future studies.

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الميكروبات المعوية كمنظمات بيولوجية لصحة الانسان

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الملخص

يطلق علي الميكروبات التي تعيش في امعاء الانسان مصطلح الميكروبات المعوية و التي تشمل اكبر عدد من الكائنات الحية مقارنة بمناطق الجسم الاخري. وتتكون هذه الكائنات الحية المعوية خلال عام الي عامين من الميلاد. والعلاقة بين بعض الكائنات الحية المعوية و الانسان ليست علاقه تكافلية فقط و لكن علاقة تبادل منفعه عن طريق دعم الامعاء لنمو الميكروبات المعوية الصحية و التي تعد حاجزا امام الكائنات الممرضة. تقوم بعض الميكروبات المعوية المفيدة بعملية تخمير للالياف الغذائية الي احماض دهنية قصيرة السلسله مثل حمض الاستيك و البيوتريك , هذا بالاضافة الي انها تلعب دورا هاما في تخليق فيتامين ب و ك , و كذلك تمثيل الصفراء و الاستيرولات. هناك العديد من العوامل التي تؤثر علي نوعية الميكروبات المعوية بمرور الزمن مثل نوع و تركيب الوجبة , العدوى الميكروبية , نمط المعيشة, النشاط البدني, المضادات الحيوية و العمليات الجراحية, و يعتبر نوع و تركيب الغذاء اهم هذه العوامل.و قد ظهر ارتباط كبير بين النمط الغذائي و انواع البكتيريا الموجوده بالامعاء , لهذا فإن هذه الدراسة المرجعية تصف الدليل و الارتباط بين انواع الميكروبات المعوية و النمط الغذائي خلال مراحل الحياة. بالاضافة الي دراسة اهمية التداخل بين الميكروبات المعوية و الوجبة الغذائية باستخدام ادوات المعلوماتيه الحيوية الجديدة و التقنيات الجزيئية بمحاوله اقرار التداخلات الممكنة بين الميكروبات المعوية و الغذاء كي نستطيع تغيير الاتجاهات المستقبلية لتغذية الاصحاء و المرضي.