Research Paper

Volume : 3 | Issue : 7 | July 2014 • ISSN No 2277 - 8179

Gut Microbiota - A Key to Sustainable Health

Medical Science

KEYWORDS : Autism, Dysbiosis, IBD, Microbiota, Obesity

*** Kutty M.V.H**	Phd scholar, Division of Animal biochemistry, Indian Veterinary Research Institute, Izatnagar-243122, India * Corresponding Author
Remya V	Phd scholar, Division of Surgery, Indian Veterinary Research Institute, zatnagar - 243122, India.
Radhika Syam	Phd scholar, Division of Veterinary Bacteriology and Mycology, Indian Veterinary Research Institute, Izatnagar - 243122, India
Shyma V.H	Assistant Professor, Dept of Epidemiology & Preventive Medicine, College of Veterinary and Animal sciences, Pookode,Wayanad-673576, India

ABSTRACT

Human body is colonized by large number of microorganisms. These microbes are essential for the normal functioning of body. Some disease conditions like obesity, inflammatory bowel disease (IBD), autism are associated with imbalance in microbiota of our body (dysbiosis). Manipulation of gut microbiota can be used to alleviate these disease conditions. Establishment of healthy microbiota should be the target of dietary intervention for sustainable heath.

INTRODUCTION

Gut microbiota became the focus of research now a days due to the converging interests of divergent disciplines of life science. Humans are colonised by about 10^{14} bacterial cells, most of them resides in gut. We can say that humans are outnumbered by their commensals by approximately 10:1 ratio. Gut microbiota can be considered as a "Forgotten organ" (Ballal, 2011). Gut microbiota contributes both to health and disease. The overall dynamics of an individual's health status is influenced by the transient change in the gene expressions of microbial community in him. Changes in composition or lack of diversity in microbiota can leads to reduced ability to resist perturbarations (Virgin and Todd, 2011). This is a brief review on the correlation between dysbiosis of gut and occurance of diseases like obesity, IBD and autism.

Gut Microbiota- General findings

Healthy microbiome is difficult to define. We could explain the context of healthy microbiome only after considering the factors like microbial composition, metabolic activities, host response and environmental factors. Individual differences will also be taken in consideration. It can be defined as a stable microbial community or community at equilibrium. Stability can be the ability to resist changes in environment including the response of microbial community towards change.

Arumugam et al (2011) put forward a concept that all human beings are divide in to three groups based on their enterotypes, and are not country or continent- specific. Recent study suggested that long term exposure to food habits can change enterotypes. Fibre-rich foods like fruit and vegetables, for example, have been shown to increase bacterial diversity, while eating too much red or processed meat might alter the composition of the microbiota, creating a favourable environment for the development of heart disease. The old phrase "We are what we eat" gains more meaning.

A study by Backhead (2012) suggest a view of gut bacterial community structure. Author reports a greater abundance and diversity in populations of Prevotella and Bacteroides against a diverse assemblage of Firmicutes. Community with predominant Firmicutes are characterized by lower levels of Prevotella and Bacteroides, but these two Gram-negative genera are nearly mutually exclusive when either is abundant in communities that are Bacteroidetes predominant.

Dysbiosis

Dysbiosis, also called dysbacteriosis refers to microbial imbalance on or inside the body (Tamboli et al, 2004). Dysbiosis is most commonly reported as a condition in the digestive tract. The intricate relationship between host and microbiome disrupted when the composition of microbial community changes. Changes in composition of gut microbiota can make the host susceptible to many diseases. There are so many reports on this matter such as, alteration of gut microbiota by introducing antibiotic leads to infection by opportunistic pathogen like Clostridium difficile (Backhed, 2012).

Dysbiosis occur in disease conditions like inflammation, or change in diet leading to reduced availability of microbial metabolite essential for normal physiological function. This condition can be reversed by restoration of normal microbial community (Backhed, 2012). Prebiotics, probiotics and antibiotics can modulate the composition of gut microbial community. Faecal transplantation of gut microbiota is another method of replacement of diverse and complex community (Gough et al, 2011). Phage therapy is yet another manipulation technique, by which selective microbes are targeted with bacteriophages and makes a shift towards beneficial microbes.

Diseases associated with dysbiosis

Recently thoughts became stronger that diseases like IBD and obesity are assosciated with reduced diversity of gut microbiota (Turn-baugh et al, 2006; Sartor, 2010). Disruption of the normal equilibrium with microbiota could lead many more diseases like atherosclerosis, autism, insulin disordeds, asthma, cardio vascular diseases etc, though current evidences are insufficient in distinguishing between causes (Backhed, 2012). Research teams have studied the interaction between the microbiota and different disease conditions including cancer and autism, which may help find new ways of fighting these disorders in the future. It is also shown that our behaviour may also be affected by our gut flora, both depression and anxiety possibly related to changes in the composition of our microbiota (Foster et al, 2013).

Obesity

Obesity is massive expansion of fat, accompanied by high risk of diseases like diabetes mellitus, hypertension, respiratory disorders, ischemic heart disease, stroke and cancer (Yanovski, 2002; Whitlock et al, 2009). It can be considered as a transmissible disease as maternal obesity predisposes adulthood obesity (Schwiertz et al, 2010). Gut microbiota composition is altered in people who are obese, and it can respond to changes in body weight (Backhed, 2012). In obesity the gut microbiome profile changes to a low ratio of Bacteroidetes/Firmicutes. Methanobrevibacter smithii is a gut archea found to decrease in obese condition. There is a significant increase of the some specieses observed in connection with obesity, Lactobacillus, Staphylococcus aureus, Escherichia coli, Faecalibacterium prausnitzii. Conversely, Bifidobacterium genus is found to be associated

with lean status. Some of the Lactobacillus and bifidobacterium genus are marketed for the human consumption in probiotics. Wide ingestion of probiotics may increase risk of occurance of obesity especially in those rich in some species of lactobacillus (Million et al, 2012).

Inflammatory Bowel Disease (IBD)

A chronic relapsing inflammatory condition of gastro intestinal tract. IBD includes two main subtypes, ulcerative colitis (UC) and Crohn's disease (CD), which each include distinct microbial perturbations and tissue localizations. The former is confined to the colon, while the latter may affect any part of the digestive tract. IBD is associated with a dysbiosis characterized by changes in Firmicutes and Proteobacteria phyla. Functional investigation of microbiota in IBD showed an increase in the synthesis of cystiene and glutathione points towards the response of microbiome towards the oxidative stress in the inflamed gut of IBD patients (Morgan et al, 2012). Environmental factors also affect the change in microbiome. These must be taken into account during future studies of the microbiota in IBD.

Autism

Autism is developmental disorder, whose onset starts from early childhood itself affecting social, communicative and imaginative development. Autism spectrum disorders(ASD) affected people have an altered gut flora compare to normal people. Parracho et al (2005) employed fluorescent insitu hybridisation (FISH) and 16S rRNA based probes to compare ASD affected children to normal children. The major diffences obtained was on levels of Clostridium histolyticum. Increased levels of Clostridium species were observed in ASD affected childrens. Reducing the number of certain clostridium species and stimulating other favourable microbes may alleviate ASD symptoms.

CONCLUSION

Gut colonizing bacteria of humans are essential for the healthy progression of life. It is difficult to determine the composition and functional properties of stable healthy microbiome. However imbalance or dysbiosis is observed in disease condition, but it is not clear whether it is a cause or consequence of disease. Exploring the healthy microbiota may provide us with new target for manipulation of gut flora and dietary interventions to sustain healthy life. Through increased knowledge of the mechanisms involved in the interactions between the microbiota and its host, we will be in a better position to develop treatments for metabolic disease.

REFERENCE

1. Arumugam, M., Raes, J., Pelletier, E., Le Paslier, D., Yamada, T., Mende, D.R., Fernandes, G.R., Tap, J., Bruls, T., Batto, J.M. et al (2011). Enterotypes of the human gut microbiome. Nature, 473: 174–180. | 2. Backhed, F., Fraser, C.M., Ringel, Y., Sanders M.E., Sartor, B., Sherman P.M., Versalovic J., Young, V. and Finlay B. (2012). Defining a Healthy Human Gut Microbiome: Current Concepts, Future Directions, and Clinical Applications. Cell Host and Microbe, 12: 611-622 | 3. Ballal, S.A., Gallini, C.A. and Segata, N. (2011). Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts. Cellular Microbiology, 13: 508–517 | 4. Foster, J.A. (2013). Gut feelings: bacteria and the brain. Cerebrum, 2013:9 | 5. Gough, E., Shaikh, H. and Manges, A.R. (2011). Systematic review of intestinal microbiota transplantation (fecal bacteriotherapy) for recurrent Clostridium difficile infection. Clinical Infectious Disease, 53: 994–1002. | 6. Million, M., Maraninchi, M ., Henry, M., Armougom, F ., Richet, H., Carrieri, P., Valero , R., Raccah , D., Vialettes, B. and Raoult, D. (2012). Obesity-associated gut microbiota is enriched in Lactobacillus reuteri and depleted in Bifidobacterium animalis and Methanobrevibacter smithii .International Journal of Obesity, 36: 817–825 | 7. Morgan, X.C., Tickle T.L., SokolH., Gevers D., Devaney K.L., Ward D.V., Reyes J.A., Shah S.A., LeLeiko N., Snapper S. B., Bousvaros, A., Korzenik, J., Sands, B E., Xavier R.J. and Huttenhower C.(2012). Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. Genome Biology, 13: 79 | 8. Parracho, H. M. R. T., Bingham M.O. and Gibson, G.R. (2005). Differences between the gut microflora of children with autistic spectrum disorders and that of healthy children. Journal of Medical Microbiology, 54: 987–999 | 9. Sartor, R.B. (2010). Genetics and environmental interactions shape the intestinal microbiome to promote inflammatory bowel disease versus mucosal homeostasis. Gastroenterology, 139: 1816–1819. | 10. Schwiertz, A., Taras, D., Schafer, K., Beijer, S., Bos, N.A., Donus, C. and Hardt, P.D. (2010). Microbiota and SCFA in lean and overweight healthy subjects. Obesity (Silver Spring), 18: 190–195. | 11. Tamboli, C.P., Neut, C., Desreumaux, P. , Colombel, J.F. (2004). Dysbiosis in inflammatory bowel disease. Gut , 53: 1–4. | 12. Turnbaugh, P.J., Ley, R.E., Mahowald, M.A., Magrini, V., Mardis, E.R., and Gordon, J.I. (2006). An obesity-associated gut microbiome with increased capacity for energy harvest. Nature, 444:1027–1031. | 13. Virgin, H.W., and Todd, J.A. (2011). Metagenomics and personalized medicine. Cell,147: 44–56. | 14. Whitlock, G., Lewington, S., Sherliker, P., Clarke, R., Emberson, J., Halsey, J. Qizilbash, N., Collins, R. and Peto, R. (2009). Body-mass index and cause-specific mortality in 900 000 adults: collaborative analyses of 57 prospective studies. Lancet, 373: 1083–1096. | 15. Yanovski, S.Z. and Yanovski, J.A. (2002). Obesity. The New England Journal of Medicine, 346: 591–602. |