penyembuhan luka, mencegah fistel, menurunkan inflamasi, mempercepat penyembuhan fungsi usus, menurunkan infeksi, dan lama perawatan.

Pada operasi anastomosis dapat dilakukan pemasangan tube di distal anastomosis atau pemasangan nasojejunostomi sampai ke distal anastomosis dan pemberian makanan dapat dilakukan dalam 24 jam mulai dengan 10-20 ml per jam sampai tercapai target volume dalam 5-7 hari.

S.13 - ABSTRACT METABOLISM AND MICROBIOME ALTERATION IN SURGERY DIGESTIVE PATIENT

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Introduction

The human gastrointestinal (GI) tract represents one of the largest diverse, complex and dynamic populations of microbial communities (microbiomes), which plays a central role in human health and exert a marked influence on the host during homeostasis and disease. The amounts of microorganisms populating in the human GI tract has been estimated up to 100 trillion, which is ~10 times greater than the total number of human cells (Bäckhed, 2005). However, A new study suggest that the ratio of human : bacterial cells is actually closer to 1:1 (Sender, 2016). The constitutional symbiosis between the large number of microbial community and their host it are often referred to as a 'superorganism' (Thursby,2017).

Diet is considered as one of the main drivers in shaping the gut microbiota across the lifetime. In healthy individuals, the microbiome and host have a mutualistic relationship in which both partners sharing benefits. The microbiota provide several benefits to the host, through a range of physiological functions such as strengthening gut integrity or shaping the intestinal epithelium, harvesting energy, protecting against pathogens and regulating host immunity (Thursby,2017). Intestinal bacteria play a crucial role in maintaining immune and metabolic homeostasis and protecting against pathogens. Altered gut bacterial composition known, as dysbiosis has been associated with the pathogenesis of many inflammatory diseases and infections.

...e of the GI microbiota in health

The gut microbiota and its host are living in a mutualistic relationship that is beneficial to both organisms, and it is especially important in the development of the immune system and food digestion of the host. The alterated population of bacteria in GI tract leads to large defects in the development of gut-associated lymph tissues, low levels of secretory IgA antibodies in the intestine, and less and smaller mesenteric lymph nodes. The gut microbiota play an important role in protecting the host against colonization of intestinal pathogens and in maintaining tissue homeostasis (Wang, 2017). In the absence of gut microbiota, the human body was unable digested dietary fibers such as inulin, pectin, xylans, and mannans. The dietary fiber fermented by gut microbiota yields energy, which is important in the growth and maintenance of the

microbial community. Fermentation leads to the formation of metabolic end products that are beneficial to the host (Wang, 2017, Valdes, 2018). The normal gut microbiome produces 50–100 mmol·L−1per day of short-chain fatty acids (SCFAs), such as acetic, propionic and butyric acids and serves as an energy source to the host intestinal epithelium. These SCFAs are very effectively absorbed in the colon and serve many diverse roles in regulating gut motility, inflammation, glucose homeostasis, and energy harvesting, lipogenesis and gluconeogenesis (Flint, 2012). The gut microbiota has been shown to deliver vitamins to the host, such as folates, vitamin K, biotin, riboflavin (B2), cobalamin (B12), and possibly other B vitamins (Kang, 2012, Wang, 2017).

Dysbiosis of gut microbiota in promoting the development of diseases

Multiple factors contribute to the establishment of the human gut microbiota during infancy. Diet is considered as one of the main drivers in shaping the gut microbiota across the lifetime. Intestinal bacteria play a crucial role in maintaining immune and metabolic homeostasis and protecting against pathogens (Thursby,2017, Wang, 2017).

Altered gut bacterial composition (dysbiosis) has been associated with the pathogenesis of many inflammatory diseases and infections. Several studies revealed that colorectal microorganisms is playing a great role in inducing the onset and progression of colorectal cancer (CRC) with different dynamic mechanisms such as acceleration of chronic inflammatory state, the biosynthesis of genotoxins that interfere with cell cycle regulation, the production of toxic metabolites, or heterocyclic amine activation of pro-diet carcinogenic compounds (Zou, 2017). Alterations to the gut microbiota may allow the outgrowth of bacterial populations that induce genomic mutations or exacerbate tumorpromoting inflammation. While cancer is largely considered to be a disease of genetic and environmental factors, increasing evidence has demonstrated a role for the microbiota in shaping inflammatory environments and promoting tumor growth and spread (Zackular, 2016, Brennan, 2016).

Gut Microbiome Alteration After Digestive Surgery

Digestive system surgery or gastrointestinal surgery both upper GI surgery and lower GI surgery caused changes in the structure, diversity, functional genes, and metabolic pathways of the intestinal microbiota. The richness of microbiota taxonomy and abundance from patient stool before and after surgery was changed (Zheng, 2017). At the genus level, Enhydrobacter, Oscillibacter, Anaerotruncus, and Alistipes were significantly higher after surgery, while Eubacterium and Capnocytophaga were significantly decreased after surgery. At the species level, the gut microbiota after surgery was enriched in Bacteroides fragilis, Clostridium bolteae and Lachnospiraceae

bacterium, while gut microbiota before surgery was enriched in Enbacterium rectale, butyrate-producing bacteria, and Bacteroides plebeius, among others. The abundance of various genes in the metagenome differed significantly before and after surgery (Zheng, 2017).

The intestinal flora displayed higher abundance of genes involving generation of spermidine/putrescine transport system permease proteins, flagellar motor switch proteins, and branched-chain amino acid transport system proteins in postoperative patients but displayed a lower abundance of genes involving generation of periplasmic nitrate reductase, cathepsin, nitroreductase, nitrite reductase, tryptophan synthase, and sulfur carrier proteins (Zheng, 2017, Medina, 2017, Lederer, 2017, Hibberd, 2017, Aron-Wisnewsky, 2012).

Modulation the gut microbiota population through diet

Potential therapies aimed at modulation of the gut microbiota are administrated of adequate amounts of live microorganism like strains of the genera Bifidobacterium and Lactobacillus (Prebiotics), administrated selectively fermented ingredient that results in specific changes in the composition and/or activity of the GI microbiota (Probiotics), the introduction of gut bacteria from a healthy donor into a patient (Faecal microbiota transplantation) and selected diet. Diet could re-shape the community structure of gut microbiota and influence its function by modulating the production of metabolites (Yang, 2018, Valdes, 2018, Cani, 2018).

Probiotics can modulate the intestinal immunity and alter the responsiveness of the intestinal epithelia and immune cells to microbes in the intestinal lumen. Probiotics produce antimicrobial agents or metabolic compounds that suppress the growth of other microorganism, or compete for receptors and binding sites with other intestinal microbes on the intestinal mucosa. Probiotic Lactobacillus strains enhance the integrity of the intestinal barrier, which may result in maintenance of immune tolerance, decreased translocation of bacteria across the intestinal mucosa, and disease phenotypes such as gastrointestinal infections (Hemarajata, 2018).

Prebiotics are a subgroup of dietary fibres with resistance to gastric acidity and the digestive enzymes of mammals, and which confer a variety of health benefits. The main characteristic of prebiotics is their selective stimulation of the growth and/or activity of intestinal bacteria associated with health and well-being. The most well-known prebiotics are inulin, fructooligosaccharides (FOS), lactulose and galactooligosaccharides (GOS). Prebiotics have mostly been assessed for the enhancement of strains of Bifidobacterium and Lactobacillus, which produce lactate and acetate and contribute to the health of the host via fermenting prebiotics. However, our increasing understanding of the gut microbiota indicates that the effect

of prebiotics can be broader on the gut community, where competition and cooperation between bacteria are significant (Umu, 2017).

Conclusion

The human microbiome plays an important role in the well-being of the human host, and participates actively in the development of a wide variety of diseases. The gut microbiota potentially influences the host's energy balance through multiple mechanisms, including supplying energy from nondigestible dietary components and influences on gut transit, energy intake and energy expenditure. Digetive surgery caused changes in the structure, diversity, functional genes, and metabolic pathways of the intestinal microbiota. Altered gut bacterial composition (dysbiosis) has been associated with the pathogenesis of many inflammatory diseases and infections. Diet could re-shape the community structure of gut microbiota and influence its function by modulating the production of metabolites. Prebiotics, probiotics and faecal microbiota transplantation are potential therapies to modulate of the gut microbiota population, structure and diversity.

Keywords: Microbiome, gut microbiota, gastrointestinal tract, post operative, colorectal cancer, dysbiosis

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