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Intestinal Microbiota: A Big World of Evolving Knowledge

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Editorial

In the human digestive system reside more than 100 trillion of microbes, 10 fold the number of eukaryotic cells of the human body, subdivided into about 1000 different types of bacteria, 100-fold more genes than the human genome [1]. This enormous quantity of bacteria gradually increases from the esophagus to the colon and composes our intestinal microbiota which helps keep the intestines healthy and assists in digesting food. Moreover it can also enhance the immune system [2,3]. We are being colonized immediately after birth and obviously the microbiota of born by spontaneous delivery is different from neonate born by caesarean one. The first microrganisms that colonize the digestive system are facultative anaerobic bacteria including *Enterococci* and *Lactobacilli*. Then anaerobes such as Bifidobacteria, Bacteoides, and Clostridium gradually increase, causing a progressive decrease of the facultative anaerobes. These gradual changes are completed around the age of three when the intestinal microbiota remains more or less stable throughout adulthood. Considering the intra- and inter-individual variations, Actinobacteria mainly *Bifidobacterium*, Proteobacteria such as *Enterobacteriacee*, *Firmicutes* such as *Faecalibacterium*, *Clostridiacee*, *Lactobacillus*, and *Bacteroidetes* such as *Bacteroides* are prevalent in infancy, whereas Bacteroidetes and *Firmicutes* usually dominate the adult intestine. Instead, during elderly new changes develop and in this age *Bacteroidetes* are the more prevalent bacteria followed by *Actinobacteria* and *Proteobacteria* [4].

Changes in gut microbiota have been linked to several health and pathological conditions including obesity, gastrointestinal infections, inflammatory bowel diseases (IBD) and functional gastrointestinal disorders (FGD) like irritable bowel syndrome [5].

Intestinal microbiota composition is influenced by a realtionship between host genetic, age, geographic locations of people, immune and environmental factors. This relationship has been developed throughout the entire course of human kind. In babies the type of milk (breast- or formula fed) greatly affects the microbiota composition as well as the age at birth. The industrialization has also led to changes in the human diet and microbiota. In fact microbiota of african rural children whose diet is rich in polysaccharide is different from that of european city children whose diet is rich in fats and proteins [6]. Some host factors such as diet, age, use of antibiotics, and intestinal transit could determine changes in the microbiota with subsequent risk to develop some diseases like functional gastrointestinal disorders [3,5].

The intestinal microbiota is essential for fermentation of non-digestible dietary nutrients in the colon producing short chain fatty acids which in turn interact with the microbiota and host cells.

Intestinal microbiota has many actions in the human body. It may act as a barrier against foodborne pathogens, or regulate several physiological functions such as glucose homeostasis and satiety. Furthermore intestinal microbiota interacts with intestinal immune system and intestinal neurological system thus contributing to the overall homeostasis of the organism over a lifetime [7].

For these reasons you think that the intestinal microbiota has an essential role in maintaining health and it misbalance can cause several gastrointestinal and extra-gastrointestinal diseases. Among gastrointestinal pathologies associated to alteration of intestinal microbiota, dysbiosis, IBD, colorectal cancer and FGD are the most studied.

In recent years, in fact, intestinal microbiota is the target for numerous scientific research not only in gastroenterology.

The more frequent misbalance of intestinal microbiota (dysbiosis) is due to gastrointestinal infections or inflammations or secondary to antibiotic therapy [8].

Clostridium difficile infection is, so far, the only disease in which the dysbiosis clearly plays a crucial role in the onset and perpetuation of the pathological process [3]. In fact, in these patients the fecal microbiota transplantation is proved to completely restore the normal healthy gut flora [9].

Recently, several authors have been hypothesized that an imbalance of intestinal microbiota can have an important role in the onset of IBD. Some studies showed that in IBD there is a decreased complexity of the composition in intestinal microbiota with a reduction of normal anaerobic bacteria [10].

Considering the high amount of bacteria in the colon, they could have a role in the pathogenesis of colorectal cancer. Some studies in fact described several changes in intestinal microbiota of these patients, but it is not clear if these bacterial modifications are the cause or the expression of altered mucosal environment secondary to cancer [11].

Although some studies support that intestinal microbiota is altered in patients with FGD, we do not still know the exact related mechanisms [7].

In the previous issue of this Journal, Hong and Poroyko reported an interaction between Hirschsprung-associated enterocolitis (HAEC) and alterations in intestinal microbiota [12].

Hirschsprung disease (HD) is a developmental disorder characterized by absence of ganglia in the distal colon, resulting in a functional obstruction. It affects around 1:5000 live births [13]. Hirschsprung-associated enterocolitis is the most common

complication in HD patients and it represents the greatest cause of morbidity and mortality in children with HD. Despite many proposed etiologies, the exact mechanisms underlying HAEC are still poorly understood [14]. Several studies have shown that not only the increase of Clostridium difficile and Rotavirus, but also a reduction in Bifidobacteria and Lactobacillus may play a role in the pathogenesis of HAEC [15]. Other authors suggested that the replacement of these commensal strains may restore microbiota equilibria and gives a preventive role against HAEC. The most studied probiotic strains in this regard are Lactobacillus, Bifidobacterium, Saccharomyces, and Streptococcus sp [16,17].

Hong and Poroyko found a significant difference in the intestinal microbiota between HAEC and HD patients although their study relates to a small number of patients and they hypothesize that the colonization by specific type of intestinal microbiota might be responsible for the development of HAEC [12]. They noted highest proportion of Bacteroides (Bacteroidetes followed by *Proteobacteria*) followed by *Enterobacteriacae* among intestinal flora in HD patients, whereas *Enterobacteriacee* were the more prevalent bacterial genus founded in patients with HAEC [12].

In the recent years the study of intestinal microbiota has been become one of the most important research fields not only in medicine, but in human sciences in general and therefore the use of probiotics have been extensively studied in the promoting health as well as in treating several diseases. By now alterations in intestinal microbiota were put in relation to many diseases not only belonging to gastrointestinal system [5]. Therefore the use of probiotics not only can improve or heal gastrointestinal disorders but they can even have positive effects in extra digestive pathologies such as immune, allergic, cardiovascular, skin, and endocrinological diseases. Furthermore probiotics can be used in the prevention of these diseases by helping to strengthen the intestinal microbiota and fight the bad strains by the healthy ones.

In conclusion intestinal microbiota is a developing world of knowledge both regarding to the different subtypes of bacteria forming it and for the actions that these bacteria may have in the prevention or in causing several diseases. The better comprehension of the intestinal microbiota composition and its role in the pathogenesis of diseases, will probably allow new and more targeted therapeutic approaches.

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