Gut dysbiosis and food microbiology: scientific advances and open opportunity to publish articles.

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Editorial

We are facing an exponential growing wave of remarkable discoveries related with the reciprocal benefits between the gut microbiota and the function of systemic organs. Gut microbiota means the composition and an activity of a community of trillions of microorganisms hosted by the intestines and represents the major percentage of microbes in the human body. The type of microbes and the respective beneficial contribution to the health of the individual differs accordingly with the segment of the gut. For instance, in healthy conditions and in terms of vertical location, the small intestine hosts several genera, including the anaerobe Lactobacillus, while in the large intestine is common the Bifidobacterium. The normal microbiota also differs horizontally according with the distance from the intestinal walls; the epithelial surface is less colonized and the lumen is where there is a major variability of microorganism. In the mucus layer, predominates Clostridium, Lactobacillus and Enterococcus, while in the gut lumen the predominance is of other microbes, such as Bifidobacterium. However, the identification of microbes occupying the human gut microbiota has not been an easy task due to the diversity in the composition, relative proportion and activity of microbes in the microbiota even among healthy individuals. However, it is expected that ongoing translational research will help to completely elucidate the characterization of the structure and function of the normal gut microbiota in the healthy population. This issue has been reviewed in the last 5 years by several researchers [1-4].

Although the mechanism by which the microbiota protects the intestinal tract still remains to be clarified, it is well known that the gut microbiota plays an important role, protecting the host against invasion of malefic microorganisms. Such disturbance is very common in persons under treatment with current generation of antibiotics of broad spectrum, which affect the host innate gut microbiota. The natural healthy gut microbiota can be influenced by several factors, including the aging process, diet, environment, personal hygiene, and other factors. The interpersonal variability in the gut microbiota is greater in older than younger people [2-4].

Several research groups worldwide are using animal models to design experiments aiming the understanding of mechanisms of the bidirectional interaction between gut microbiota and the function/dysfunction of the different organs [5]. Some of these groups are designing translational studies focused on the use of nutritional products, including prebiotics, probiotics, bioactive products and microencapsulation of living cells, to preserve or re-establish the natural gut microbiote. In this regard, there are recent studies showing that the use of the probiotic kefir resulted in remarkable repair of structural and functional disturbances observed in experimental models of metabolic and cardiovascular diseases. Our group has recently shown that chronic treatment with kefir was able to decrease the lipid deposition and ameliorating the circulating cytokine profiles of LDL knockout mice [6], indicating new beneficial effects of this probiotic and providing new perspectives for its use as an adjuvant in the prevention of atherosclerosis. The beneficial effects of kefir were also demonstrated in spontaneously hypertensive rat model, in which kefir improved the cardiac autonomic control of the heart and the dysfunction and the baroreflex control of arterial pressure [7]. In the same model, it was demonstrated beneficial effects of kefir on the excessive production of oxidative stress and endothelial dysfunction that characterizes this hypertension model [8]. Currently, probiotics are widely used in the production of food and contain the bacteria belonging to the genera Lactobacillus and Bifidobacterium, which have been demonstrated that have beneficial effects on the gut dysbiosis has been implicated several disturbances, including diabetes, obesity and inflammatory diseases. It is expected that soon, probiotic bacteria, apart from dairy products, will be incorporated into other food products apart from dairy products; an example of delivery of probiotics is the growing sector of probiotic juices.

Despite the advances up to date [1,9,10], the scientists are being challenged to develop new treatment strategies for several diseases by means of manipulation of the gut microbiota. As recently reviewed [11,12], new insights led the faecal microbiota transplantation approach, as an entirely new perspective to treat gut dysbiosis This is an innovative and reliable strategy because of its efficacy, low risk, minimal adverse effects and low cost, which can be used to correct abnormal gut microbiota and to prevent intestinal and systemic further diseases. It is a promise alternative to threat the systemic metabolic abnormalities and inflammation that is a hallmark of obesity and subsequent insulin resistance. Based on case reports, case series, original translational articles, controlled trials, and cohort studies, faecal microbiota transplantation is a promise alternative strategy to prevent/treat several microbiota-related abnormalities, including gastrointestinal, hematologic, neurologic, metabolic, infectious, and autoimmune disorders.

Therefore, we are living a moment in which It is expected that the research in this field results in new insights capable to translate into diagnostic, therapeutic and preventive measures to improve the life style of population. We are very proud to announce that a new vehicle was launched to serve the researchers that need rapidly to publish their discoveries in this field. Therefore, the aim of this editorial is to give the good scientific news saying that the Journal of Food Microbiology encourages and welcomes the researchers to use this new scientific channel to contribute with their conclusive/relevant experimental or clinical studies related with microbiota and/or related with other topics about food and microbiology.

References

1. Pereira TM, Pimenta FS, Porto ML, et al. Coadjuvants in the diabetic complications: Nutraceuticals and drugs with pleiotropic effects. Int J Mol Sci. 2016;17(8):1273.
2. Sonnenburg JL, Bäckhed F. Diet-microbiota interactions as moderators of human metabolism. Nature. 2016;535(7610):56-64.
3. Blum HE. The human microbiome. Adv Med Sci. 2017;62(2):414-20.
4. Gupta VK, Paul S, Dutta C. Geography, ethnicity or subsistence-specific variations in human microbiome composition and diversity. Front Microbiol. 2017;8:1162.
5. Harmsen HJ, de Goffau MC. The human gut microbiota. Adv Exp Med Biol. 2016;902:95-108.
6. Santanna AF, Filete PF, Lima EM, et al. Chronic administration of the soluble, nonbacterial fraction of kefir attenuates lipid deposition in LDLr-/- mice. Nutrition. 2017;35:100-5.
7. Klippel BF, Duemke LB, Leal MA, et al. Effects of kefir on the cardiac autonomic tones and baroreflex sensitivity in spontaneously hypertensive rats. Front Physiol. 2016;7:211.
8. Friques AG, Arpini CM, Kalil IC, et al. Chronic administration of the probiotic kefir improves the endothelial function in spontaneously hypertensive rats. J Transl Med. 2015;13:390.
9. Marco ML, Heeney D, Binda S, et al. Health benefits of fermented foods: microbiota and beyond. Curr Opin Biotechnol. 2017;44:94-102.
10. Li D, Wang P, Wang P, et al. The gut microbiota: A treasure for human health. Biotechnol Adv. 2016;34(7):1210-24.
11. Udayappan SD, Hartstra AV, Dallinga-Thie GM, et al. Intestinal microbiota and faecal transplantation as treatment modality for insulin resistance and type 2 diabetes mellitus. Clin Exp Immunol. 2014;177(1):24-9.
12. Cohen NA, Maharshak N. Novel indications for fecal microbial transplantation: Update and Review of the Literature. Dig Dis Sci. 2017;62(5):1131-45.

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