Impact of sanitary living environment on gut microbiota

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The human gut microbiota contributes to human health by aiding functions such as digestion, protection against pathogens, host immunity activation, and central nervous system regulation. Its composition is influenced by many effectors such as diet, genetics, and delivery mode. The hygiene hypothesis suggests that an overly clean living environment increases the incidence of asthma, inflammation, and autism. To test if good hygiene is linked to the composition of the gut microbiota, we raised mice with the same diet in living environments with different levels of hygiene and found that each group had special gut microbiota. Hygiene levels of the living environment influenced early establishment of the human gut microbiota. It is also suspected that a sanitary environment alters the composition of gut microbiota through activating development of the immune system and inoculating the gut with microbial components when some microorganism were killed by oral antibiotics or died due to lack of related nutrition.

Keywords: Gut microbiota; hygiene hypothesis; microflora hypothesis; western lifestyle

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The growing reports on the human gut microbiota have implicated it in functions such as digestion, protection against pathogens, host immunity activation [1], and central nervous system regulation [2]. The fact that it could act as both an indicator of and a contributor to human health suggests that the gut microbiota could play important roles in the diagnosis, treatment, and ultimately, prevention of human disease. There is growing concern that the high-fat/high-sugar western diets have altered the composition of the gut microbiota [3]. Such diet-induced changes to gut-associated microbial communities are now even suspected of contributing to growing epidemics of chronic illnesses in the developed world [3].

Recently, the hygiene hypothesis was proved by providing step by step evidence through epidemic disease investigation [4, 5]. More reports suggest that an overly clean living environment in westernized countries, as compared to developing countries, plays an important role in the increased incidence of epidemic diseases such as asthma, inflammation, and autism in western countries [5, 6]. For example, the incidence of atopic sensitization was 37% in the former West Germany as compared to 18% in the former East Germany [7, 8]. Low levels of asthma and allergies were observed among people who had early exposure to pets [9], farm environment [10] or a wide range of microbes [4, 5]. Children who grow up in a larger family size or has lower in the birth order, are also protected from childhood asthma and atopy [11-13].
Is good hygiene linked to the composition of the gut microbiota? Recently, studies comparing unindustrialized rural communities from Africa and South America with industrialized western communities from Europe and North America have revealed that there is higher biodiversity and enrichment of Bacteroidetes and Actinobacteria in rural communities, and conversely, an overall reduction in microbial diversity and stability in the western population [14–16]. The authors thought the main cause for this is the difference in the diet of the populations. People in undeveloped countries or in rural villages have more fiber in their diets compared to people from western countries. In addition, the cleanliness levels of the living environment are different between the two areas. This raises the question, “Is the main cause diet or sanitary living environment?”

To answer the above question, we raised BALB/c mice under three distinct environmental conditions: a specific pathogen free animal room, a general animal room, and a farm house [17]. All other variables like diet, age, genetic background, physiological status, and original gut microbiota were controlled. The results show that mice from a sanitary environment had more diverse microbiota and a higher ratio of Bacteroidetes to Firmicutes [17], which has previously been shown to be good for human health.

The impact of environmental effectors on the composition of gut microbiota is a long-term and sustained process. The early establishment of human gut microbiota can be influenced by an overly hygienic environment [8]. For example, the enterobacterial colonization of infants occurs later in modern Sweden than in developing countries. 25% of the infants (who were born during the early 1980s) did not acquire any enterobacterial species during their first week of life [18]. As a rule, infants are colonized by day 3 with Escherichia coli and related enterobacterial species in developing countries [18–20]. Therefore, it was postulated that it was difficult for enterobacteria to reach high numbers in the infant gut since it was already colonized by anaerobes, which provided stiff competition to the enterobacteria before they could finally colonize the gut in Swedish infants [8, 21, 22].

The immune system plays an important role in host control over microbiota composition [23]. For example, RegIIIy is an antibacterial lectin that limits bacterial penetration of the mucus layer of the small intestinal [23]. IgAs bind to bacteria to prevent microbial translocation across the epithelial barrier [23]. However, the development of the immune system is impacted by many effectors in the human living environment. Transient bacteria, which are mainly acquired from the living environment, can activate human immune cells and conditioned pathogens have a big effect on their development. Fungi, helminths, viruses, and pollen all have an impact on immune system development.

In addition, the microbes in sanitary environment inoculate the gut with microbial components when some microorganism are killed by oral antibiotics or die due to lack of related nutrition. People from western countries, who live in an overly hygienic environment and often use antibiotics, tend to break the balance of intestinal microecology due to a lack of replenishment of the necessary microbes and contribute to growing epidemics of chronic illnesses in the developed world.

We are just beginning to understand the impact of living environmental effectors on the composition of the human gut microbiota. In our study, each group of mice displayed a special microbial community only because they had specialized living environments. These results will help us elucidate the effect of environment in control of the microbiota.

Conflicting interests

The author has declared that no conflict of interests exist.

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Abbreviations

IgA: immunoglobulin A.

Author contributions

Dongrui Zhou wrote the manuscript and reviewed the manuscript. The author read and approved the final manuscript.

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