Preface

The evolving role of the gut microbiome in human disease

We are delighted to introduce this Special Issue, which summarizes the current understanding of the complex relationship between the gut microbiome and the host.

Animals and humans have evolved a digestive system that allows them to walk, swim or fly free of the constraints of terra firma. The gut is a remarkably complex organ involved in both homeostasis and susceptibility to disease.

The importance of commensal microbial populations in human health and disease was first suggested by Joshua Lederberg (Science 288 (5464): 291, 2000). Lederberg introduced the term microbiome to describe the community of all microorganisms residing in the human body, and their collective genome. Later, Lora Hooper and Jeff Gordon proposed that the microbiome should be viewed as part of the total human genome (Science 292 (5519): 1115–1118, 2001).

The adult human intestine harbors a population of up to 100 trillion bacteria cells. This number is over ten-fold the total number of human somatic and germ cells. Impressively, the gut microbiome weighs nearly 2.5 kg dry weight. The collective genome of the gut microbiome exceeds by over 300 times the size of the human genome, and provides additional functional features that mammals have not evolved.

The symbiotic relationship that has evolved between the gut microbiome and the host shapes immune and digestive functions of the host, and allows the organism to adjust to environmental cues. Thus, the gut microbiome has multiple physiological functions. Among others, it is involved in defense against pathogen colonization; fortification of the intestinal epithelial barrier; digestion of nutrients and dietary fibers; and maturation and functionality of the intestinal immune system. Notably, there is a binary interaction between the host and commensal microorganisms that dwell within each of us. Not only does the gut microbiome contribute important functions to the host, but also the host immune system is conditioned from birth on to tolerate the vast array of microorganisms that compose the microbiome.

As discussed by several articles in this Special Issue, a wide variety of factors — both endogenous (such as host and microorganism genetics, developmental stage, hormone signaling and immune cell populations) and exogenous (such as dietary habits, medical treatment, exposure to antibiotics, vitamin insufficiency, environmental pollutants and vaccination) — can influence the composition of the gut microbiome. All these factors are implicated in dysbiosis that is the loss of microbiome homeostasis.

Dysbiosis may influence susceptibility to disease. Several articles in this Special Issue examine how changes in the gut microbiome composition might be associated with diseases, including obesity, type I diabetes, autoimmunity, affective disorders, neural degeneration, and cardiovascular disease. The impact of dysbiosis on susceptibility to disease is just beginning to be appreciated and will be reflected in time with significant changes in approaches to develop disease treatments.

Overall, it can be proposed that understanding the gut microbiome may lead to the realization that changes in its composition may represent the greatest environmental risk factor to our health. So, we hope that you will enjoy reading the articles of this Special Issue, which collectively illustrate an emerging new “treasure trove” for understanding and treating human disease.

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