

Sabine Hazan, MD, Series Editor

Introduction to a New Series: The Microbiome and Disease



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Simply and elegantly defined by Lynch and Pedersen in their December 2016 article in the *New England Journal of Medicine*, a microbiome is the collection of all genomes of microbes in an ecosystem.³ In the context of human beings and our health, it is the vastly diverse genetic information observable in the microbes colonizing the distal GI tract. Historically, the study of human microbiology has been one of a singular relationship cause and effect, microbe and infection, and our approach to treating the disease states caused by pathogenic bacteria and viruses has been one of nearly indiscriminate eradication. The

problem inherent in this approach is that no microbe is an island. A new, emerging paradigm suggests that the susceptibility, severity, and duration of some diseases, even some previously thought to be independent of microbial involvement, are mediated by a complex interplay of host and microbe genomes. Already, nearly 10 million different microbial genes have been isolated from the human gut.² With the use of contemporary, culture - independent tools for analyzing fecal microbiota, e.g., biomarker sequencing, metagenomics, metatranscriptomics and metabolomics, the genetic diversity will likely continue to expand rapidly.³

Starting at birth and continuing throughout human life, commensal microorganisms function to aid in the development of temporally favorable phenotypes.

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For example, in preadolescents, the gut microbiota is relatively rich with organisms that augment vitamin B₁₂ and folate synthesis, promoting growth.¹ In adulthood, the intestinal microbiota remains comparatively constant in composition.⁴ In addition to biosynthesis, the gut microbiota influences immune maturation, host cell proliferation, vascularization, neurologic signaling, endocrine function, bone density, drug and food metabolism.³ Considering the seemingly global influence on host function, it is but a small leap to infer that the intestinal microbiome has indications for disease, and in turn, that interventions in microbiome makeup could aid in the treatment of disease states identified to correspond to specific dysbiosis. Despite the wealth of research to date, there are obvious limitations to our current understandings of the human microbiome and its implications in human health and disease. There are also limitations to even the most contemporary of research methods and study techniques. For example, patient stool samples are assumed to be accurately representative of intestinal microorganism content and, despite there being robust research evidence connecting changes in the microbiome to disease states, there have been few, if any, studies elucidating the biochemical

mechanisms responsible for the changes in disease states with microbiome intervention.³

Many factors affect the composition of the gut microbiota. Diet, genetics, antibiotics and other medications, environment, and even geography result in differences in individual host microbiome.^{1,3}

In this series, we aim to shed light on some of the most promising research to date that addresses the intestinal microbiome as it relates to common chronic diseases. ■

References

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