

Preface

The microorganisms that reside in and on a single human being, the human microbiota, are estimated to number 10–100 trillion cells, similar to or slightly more than the number of cell that make up the human body (37.2 trillion). The microbiota consists of commensal and mutualistic microbes that include bacteria, archaea, fungi protists and their viruses. Numerous microbiome projects have been launched worldwide over the last decade, each aimed at understanding the composition and roles of these microbes in various sites on and within the human body. These studies have not only revealed the extraordinary diversity of microbes that contribute to these communities, but have also begun to show the important roles these commensal communities play in maintaining good health and well-being by excluding pathogens, modulating the immune response and providing essential nutrients. For example, dysbiosis of the normal healthy gut microbiota can lead to serious inflammatory bowel diseases, such as antibiotic-induced ulcerative colitis mediated by *Clostridium difficile* and Crohn's disease.

This volume of *Methods in Microbiology* is therefore dedicated to current and emerging knowledge and technologies used for the metagenomic analysis of the human microbiota. The intended audience includes research scientists and medical professional interested in the relationship between humans and their commensal microbes. I would like to thank the authors of each chapter and the highly professional staff at Elsevier for making my job as editor both straightforward and enjoyable.

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