

Preface

Gut microbiota, gut microbiome, or gut flora are the microorganisms, including bacteria, archaea, fungi, and viruses, that live in the digestive tracts of animals. The gastrointestinal metagenome is the aggregate of all the genomes of the gut microbiota. The gut is the main location of the human microbiome. The gut microbiota has broad impacts, including effects on colonization, resistance to pathogens, maintaining the intestinal epithelium, metabolizing dietary and pharmaceutical compounds, controlling immune function, and even behavior through the gut–brain axis.

The microbial composition of the gut microbiota varies across regions of the digestive tract. The colon contains the highest microbial density of any human-associated microbial community studied so far, representing between 300 and 1000 different species. Bacteria are the largest and to date, best studied component and 99% of gut bacteria come from about 30 or 40 species. Up to 60% of the dry mass of feces is bacteria. Over 99% of the bacteria in the gut are anaerobes, but in the cecum, aerobic bacteria reach high densities. It is estimated that the human gut microbiota have around a hundred times as many genes as there are in the human genome.

In the present book, twelve typical literatures about gut microbiome published on international authoritative journals were selected to introduce the worldwide newest progress, which contains reviews or original researches on gut microbiome. We hope this book can demonstrate advances in gut microbiome as well as give references to the researchers, students and other related people.

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