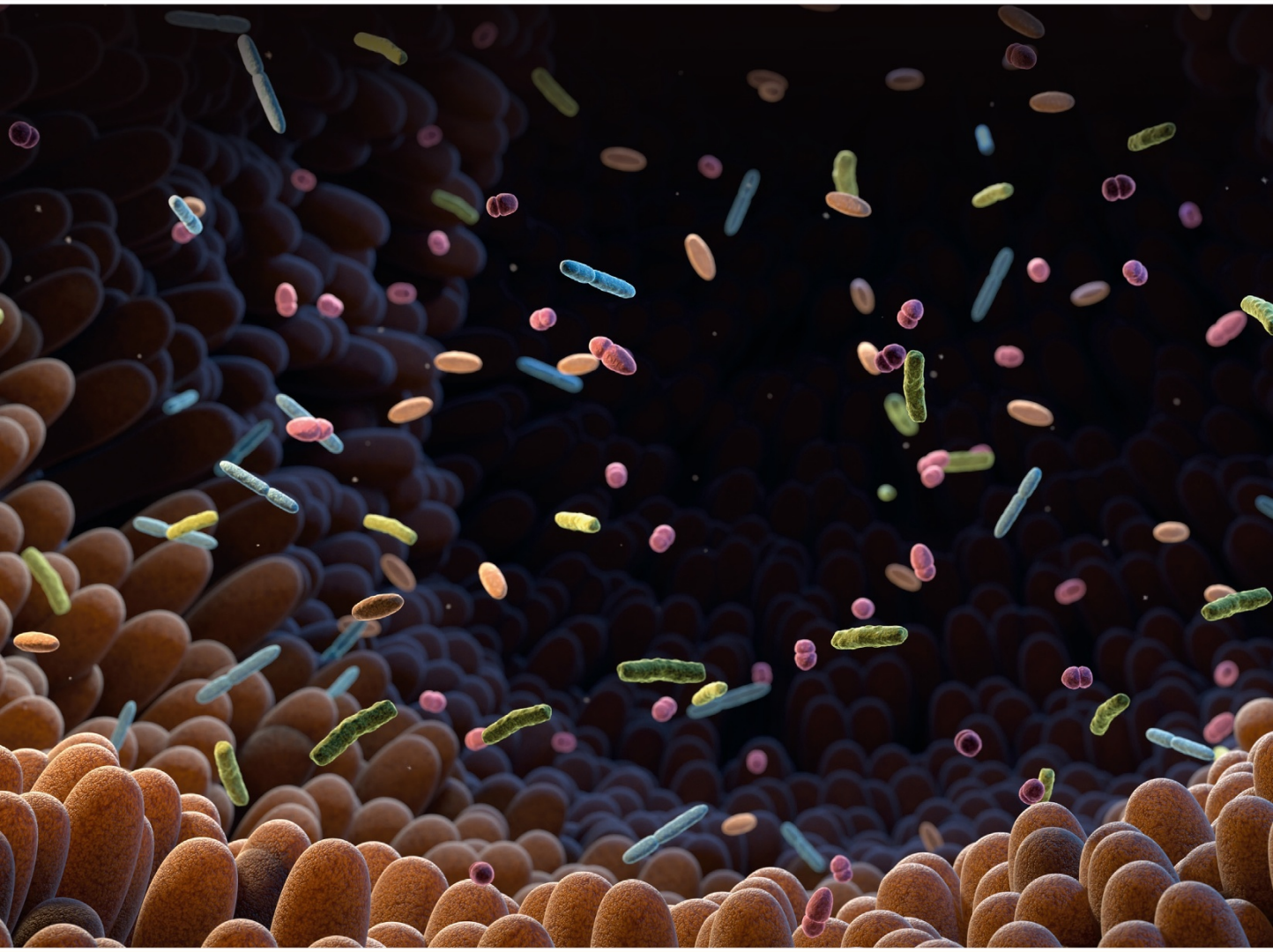
Human Microbiome and their Implications for Oncological Diagnosis and Treatment

A Handbook for Clinicians and Researchers



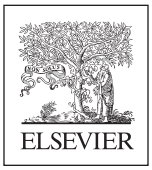
Edited by
Mohammad Akram

HUMAN MICROBIOME AND THEIR IMPLICATIONS FOR ONCOLOGICAL DIAGNOSIS AND TREATMENT

A HANDBOOK FOR CLINICIANS AND RESEARCHERS

Edited by

MOHAMMAD AKRAM
Department of Radiation Oncology
Jawaharlal Nehru Medical College & Hospital
Aligarh Muslim University
Aligarh, Uttar Pradesh, India



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Data analysis using high-throughput sequencing technologies and bioinformatics tools

Mohd Aamir Qureshi[a,b], Umamah Siddiqui[c], and Shahper Nazeer Khan[a]
[a]Department of Biosciences, Integral University, Lucknow, UP, India
[b]Department of Radiation Oncology, Jawaharlal Nehru Medical College & Hospital, Aligarh Muslim University, Aligarh, Uttar Pradesh, India
[c]Department of Biosciences and Bioengineering, Indian Institute of Technology, Roorkee, Uttarakhand, India

1 Introduction

The relationship between the microbiome and cancer has gained significant attention, with accumulating evidence suggesting that microbial communities influence cancer initiation, progression, and treatment response (Garrett, 2015; Zitvogel et al., 2017). High-throughput sequencing technologies (HTS) have been instrumental in characterizing these relationships across different cancer types and anatomical sites (Marchesi et al., 2016). Cancer-associated microbiome alterations, termed oncobiosis, involve shifts in microbial composition, diversity, and function. These changes can occur locally at tumor sites or systemically, affecting distant microbial communities (Gopalakrishnan et al., 2018). Understanding these alterations requires robust analytical approaches capable of detecting subtle but biologically significant changes in microbial communities. The human microbiome, which is made up of trillions of bacteria that live in different parts of the body, has become an important element in human health and disease (Turnbaugh et al., 2007; Gilbert et al., 2018). The introduction of HTS technology has changed the way we study these complicated microbial communities. We can now learn a lot more about their diversity, function, and dynamics than we could with culture-dependent methods (Lloyd-Price et al., 2016). Next-generation sequencing (NGS), also known as HTS, is a group of technologies and methods that allow for the quick and cost-effective sequencing of millions of DNA fragments at once (Shendure et al., 2017). These tools have made microbiome research more accessible to everyone, enabling scientists to study microbial communities in ways that were never possible before, across a wide range of environments and clinical settings.

Frederick Sanger, often referred to as the "Father of Genomics," revolutionized modern biology by developing a technique for sequencing the human genome. This breakthrough laid the foundation for first-generation sequencing, which subsequently

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