

# We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

5,500

Open access books available

135,000

International authors and editors

165M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index  
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?  
Contact [book.department@intechopen.com](mailto:book.department@intechopen.com)

Numbers displayed above are based on latest data collected.  
For more information visit [www.intechopen.com](http://www.intechopen.com)



# Introductory Chapter: Human and Microbes in Health and Diseases

*Nar Singh Chauhan*

## 1. Introduction

Microbes are ubiquitous in nature and humans are no exception. Microbes have coevolved with humans and reside in and on human body to develop a host associated structure, called “Human Microbiome” or “Human Microbiota.” These microbial counterparts account toward 10% of human body weight and outnumber human cells by approximately by tenfold and considered as commensals. Human microbiome is defined as the total genomes of microbes (constitute bacteria, bacteriophage, fungi, protozoa and viruses) that live inside or on the human body [1]. There are trillions of microbes living in/on human body plays a fundamental role in normal functioning of metabolic, physiological and immune system. Microbiota is a complex ecosystem consisting of bacteria, protozoa, viruses and fungi; all varies in number even in body parts of same individual. Human body has 10 times more bacteria than the number of human cells in our body [2]. Most of these bacteria are present in gastrointestinal tract [3] which account for approximate 70% of the total microbial load in or on human body (particular in large intestine) [4]. Humans are born sterile and start acquiring human companion to shape resilient microbiome structure. Establishment of microbiome starts with birth and matures with age. Microbial introduction and the establishment of microbiome is a random process influenced by many factor like mode of delivery, diet, sex, age, genetics, geographical location have a strong impact in shaping human microbiome structure [5–10]. These microbes are in symbiotic relationship, beside gut they are also found in mouth, respiratory tract, vagina and skin.

## 2. Human and microbes

The study of human microbiome diversity started with Antonie Van Leeuwenhoek, when he had a comparison of his oral and fecal microbiota in 1680s. He found that different microbes are present in different habitats and also different microbes are present in healthy and diseased person [11, 12]. There is a growing evidence that any change in microbiota composition leads to several metabolic diseases including obesity, diabetes and cardiovascular. Different parts of intestinal tract have different composition of microbes and it varies according to age, weight, site and diet. Composition of microbiota in gut alters by nutrition, drugs, diet and genetic background and lifestyle. Microbiota regulates metabolic and physiological mechanisms by producing metabolites. It has been found out that different species of microbiota in gut works under same metabolic pathway [9]. Qualitative and quantitative alteration in gut microbiota leads to dysbiosis by consuming antibiotics, physical and psychological stress [13]. Recent studies shows evidence regarding change in composition by urban and rural environment, affects skin (allergic symptoms) of

particular organisms. Age alter the environmental effects on individual such as alter microbiota variations in skin between children and teenager cause skin allergies [14]. Microbiome structure varies in respect of host anatomical and physiological sites. Normally, flora found in/on the body surface in stable condition to compete with pathogenic microbes in environment or those microbes entered in specific body parts [15]. As in addition to these permanent residents, a number of microbes known as causative agent for various infectious diseases. Likewise commensals, these infectious agents have evolved an efficient machinery to evade host protective gears for their successful proliferation in various anatomical locations. Normal bacteria defend host against the invasion of pathogenic microorganisms by inducing barrier against them [16]. It was observed that host commensals plays a critical role in balancing the abundance of pathogenic and nonpathogenic microbial strains and protects the host from the onset of any infectious diseases. However a number of factors like change in diet, variable host immune response, fluctuating environmental conditions like pH, oxygen saturation, ionic strength, etc., could induce microbial dysbiosis and induce microbial community dynamics. These microbial community dynamics could induce favorable conditions for growth of earlier dormant pathogenic microbes and result in onset of infectious diseases [16].

### **3. Conclusion**

Microbes have been identified to play a vital role in human health and diseases. Physiological characterization of these microbes and defining their functional molecular machinery could enable us to develop potential therapeutic and diagnostic targets. Additionally, holistic overview of human microbiome structure, human microbe interactions and role of microbes in human health and diseases are the key areas of current research focus. In-depth information about host microbial interaction in human health and diseases could enable to identify causative factors for development of host physiological/metabolic disorders. Current book comprises of various chapters defining a relation among human and microbes in health and diseases.


#### **Author details**

**Nar Singh Chauhan**

Department of Biochemistry, Maharshi Dayanand University, Rohtak, Haryana, India

\*Address all correspondence to: [nschauhanmdu@gmail.com](mailto:nschauhanmdu@gmail.com)

#### **IntechOpen**

© 2019 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/3.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. 

## References

- [1] Xu J. Invited review: Microbial ecology in the age of genomics and metagenomics: Concepts, tools, and recent advances. *Molecular Ecology*. 2006;**15**(7):1713-1731
- [2] Sender R, Fuchs S, Milo R. Revised estimates for the number of human and bacteria cells in the body. *PLoS Biology*. 2016;**14**(8):e1002533
- [3] Zoetendal EG, von Wright A, Vilpponen-Salmela T, Ben-Amor K, Akkermans AD, de Vos WM. Mucosa-associated bacteria in the human gastrointestinal tract are uniformly distributed along the colon and differ from the community recovered from feces. *Applied and Environmental Microbiology*. 2002;**68**(7):3401-3407
- [4] Turnbaugh PJ, Hamady M, Yatsunenkov T, Cantarel BL, Duncan A, Ley RE, et al. A core gut microbiome in obese and lean twins. *Nature*. 2009; **457**(7228):480
- [5] David LA, Maurice CF, Carmody RN, Gootenberg DB, Button JE, Wolfe BE, et al. Diet rapidly and reproducibly alters the human gut microbiome. *Nature*. 2014;**505**(7484):559-563. DOI: 10.1038/nature12820
- [6] Chu DM, Ma J, Prince AL, Antony KM, Seferovic MD, Aagaard KM. Maturation of the infant microbiome community structure and function across multiple body sites and in relation to mode of delivery. *Nature Medicine*. 2017;**23**:314-326. DOI: 10.1038/nm.4272
- [7] Dominianni C, Sinha R, Goedert JJ, Pei Z, Yang L, Hayes RB, et al. Sex, body mass index, and dietary fiber intake influence the human gut microbiome. *PLoS One*. 2015;**10**(4):e0124599. DOI: 10.1371/journal.pone.0124599. eCollection 2015
- [8] Jakobsson HE, Abrahamsson TR, Jenmalm MC, Harris K, Quince C, Jernberg C, et al. Decreased gut microbiota diversity, delayed bacteroidetes colonisation and reduced Th1 responses in infants delivered by caesarean section. *Gut*. 2013; **63**(4):559-566. DOI: 10.1136/gutjnl-2012-303249
- [9] Joice R, Yasuda K, Shafquat A, Morgan XC, Huttenhower C. Determining microbial products and identifying molecular targets in the human microbiome. *Cell Metabolism*. 2014;**20**(5):731-741. DOI: 10.1016/j.cmet.2014.10.003
- [10] Milan AM, Cameron-Smith D. Digestion and postprandial metabolism in the elderly. *Advances in Food and Nutrition Research*. 2015;**76**:79-124
- [11] Dobell C. The discovery of the intestinal protozoa of man. *Proceedings of the Royal Society of Medicine*. 1920; **13**(Sect\_Hist\_Med):1-15
- [12] Van Leeuwenhoek A. An abstract of a letter from Antonie van Leeuwenhoek. About animals in the scurf of the teeth. *Philosophical Transactions of the Royal Society of London*. 1683;**14**:568-574
- [13] Ley RE, Peterson DA, Gordon JI. Ecological and evolutionary forces shaping microbial diversity in the human intestine. *Cell*. 2006;**124**:837-848
- [14] Ley RE, Bäckhed F, Turnbaugh P, Lozupone CA, Knight RD, Gordon JI. Obesity alters gut microbial ecology. *Proceedings of the National Academy of Sciences*. 2005;**102**(31):11070-11075
- [15] Faust K, Sathirapongsasuti JF, Izard J, Segata N, Gevers D, Raes J, et al. Microbial co-occurrence relationships in the human microbiome. *PLoS Computational Biology*. 2012;**8**(7):

e1002606. DOI: 10.1371/journal.  
pcbi.1002606

[16] Littman DR, Pamer EG. Role of the commensal microbiota in normal and pathogenic host immune responses. *Cell Host & Microbe*. 2011;**10**(4):311-323. DOI: 10.1016/j.chom.2011.10.004

IntechOpen

IntechOpen