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Human microbiome: an academic update on human body site specific surveillance and its possible role

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Abstract

Human body is inhabited by vast number of microorganisms which form a complex ecological community and influence the human physiology, in the aspect of both health and diseases. These microbes show a relationship with the human immune system based on coevolution and, therefore, have a tremendous potential to contribute to the metabolic function, protection against the pathogen and in providing nutrients and energy. However, of these microbes, many carry out some functions that play a crucial role in the host physiology and may even cause diseases. The introduction of new molecular technologies such as transcriptomics, metagenomics and metabolomics has contributed to the upliftment on the findings of the microbiome linked to the humans in the recent past. These rapidly developing technologies are boosting our capacity to understand about the human body-associated microbiome and its association with the human health. The highlights of this review are inclusion of how to derive microbiome data and the interaction between human and associated microbiome to provide an insight on the role played by the microbiome in biological processes of the human body as well as the development of major human diseases.

Keywords Human microbiome · Microbiota · Metagenomics · Metabolomics

Introduction

The human microbiome is a complex aggregate of the microbes residing at various sites in the human body (Shreiner et al. 2015) and consisting of communities of a variety of microorganisms including Eukaryotes, Archaea, Bacteria, and the virus that reside in the different body habitat including the skin, the oral cavity, respiratory tract, gastrointestinal tract, urinary tract, reproductive tract etc. (Sender et al. 2016; Shreiner et al. 2015). A microbiota is described as a community of microorganisms that resides in a distinct environment and the collection of entire genomic

elements of a distinct microbiota is the microbiome. Earlier the microbiome was estimated to encode approximately 100-fold more gene than the entire human genome but later it was studied to account for tenfolds (Sender et al. 2016). The Nobel laureate Joshua Lederberg used the term microbiome to define the complex ecological communities of the symbiotic, commensal and pathogenic microorganisms residing the human body (Kilian et al. 2016). The development of various new technologies namely meta-transcriptomics, metagenomics, metabolomics and some other bioinformatics tools have aided in the understanding of contribution of the different human microbiome and their importance in human health and diseases (Aguiar-pulido et al. 2016). The Human-Microbiome Project (HMP) and the Metagenomics of the Human Intestinal Tract (MetaHIT) project, financed by the National Institutes of Health, USA and the European Commission respectively, have initiated immense programs aimed at surveying the reserve of microbial genes and genomes collectively termed as the microbiome (Elloe-Fadrosh and Rasko 2013; Peterson et al. 2009). The human microbiota, along with the gastrointestinal tract, consists of more than 100 trillion microbial cells harbored in every individual (Ursell et al. 2012). Of the total human cell,

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