

Human Microbiome and Resistome Studies

Mina Rho

Department of Computer Science and Engineering, College of Engineering, Department of Biomedical Informatics, Hanyang University, Seoul, Korea

The human microbiome plays a crucial role in providing metabolic functions and protecting hosts against pathogens. Recent studies have revealed a significant association of the human gut microbiome with the development of obesity, type 2 diabetes, and inflammatory bowel disease [1,2]. Two large-scale international human microbiome projects, Metagenomics of the Human Intestinal Tract (MetaHit) and Human Microbiome Project (HMP), were organized to study the diversity and the functions of microorganisms in the human body. These efforts have also contributed significantly to the development of new computational methods to analyze microbiomes by using high-throughput sequencing data [3,4]. In recent years, the human gut microbiome has received increasing attention as a reservoir of antibiotic resistance genes, which is transferred among and between communities.

In this issue, five groups of experts provide an overview of recent research on the human microbiome and resistome. Two review articles describe the association of human microbiomes with the disease states. Dr. Min-Hye Kim describes how the microbiome impacts the development and pathology of atopic dermatitis [5]. This article also describes the difference in the bacterial composition in the skin and intestinal microbiomes of normal and atopic dermatitis. Drs. Yesul Kim and Dongho Choi describe the composition and functions of the microbiome in hepatobiliary and pancreatic diseases [6]. In particular, they discuss the association of the microbiome in nonalcoholic fatty liver disease, alcoholic liver disease, cirrhosis, hepatocellular carcinoma, and gallbladder cancer. Currently, many compositional changes and dysbiosis in the human microbiome are observed according to the disease status, yet they need to be investigated further to better understand the physiology and causal effect.

Drs. Jae Hong Shin and Mina Rho describe the diversity and exchange of resistome in the human microbiome based on the next-generation sequencing data [7]. Pioneering studies on the human resistome have unveiled the profiles of resistome mainly in the intestinal microbiome. In this article, the authors also discuss state-of-the-art bioinformatics approaches and databases applied in recent resistome studies. For the current status of resistomes in the human microbiome, two articles describe the current status of antibiotics treatment and their resistance in *Enterobacteriaceae* and *Corynebacterium*. Dr. Jieun Kim describes carbapenem-resistant *Enterobacteriaceae*, which currently raises serious resistance issues in the world [8]. Drs. Sae Am Song and Jeong Hwan Shin discuss an emerging pathogen, *Corynebacterium striatum*, which has been known as a member of normal flora in the human microbiome [9]. Recent studies have discovered their association with respiratory infection, bacteremia, and endocarditis, in addition to the resistance to multiple antibiotics.

These five articles provide an excellent overview and future perspectives on the human microbiome and resistome of fundamental importance and significant medicinal implications.

REFERENCES

1. Forslund K, Hildebrand F, Nielsen T, Falony G, Le Chatelier E, Sunagawa S, Prifti E, Vieira-Silva S, Gudmundsdottir V, Krogh Pedersen H, et al: Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. *Nature* 2015, 528:262.
2. David LA, Maurice CE, Carmody RN, Gootenberg DB, Button JE, Wolfe BE, Ling AV, Devlin AS, Varma Y, Fischbach MA, et al: Diet

Corresponding Author: Mina Rho

Department of Computer Science and Engineering, College of Engineering, Hanyang University, Department of Biomedical Informatics, Hanyang University, 222 Wangsimni-ro Seongdong-gu, Seoul 04763, Korea
Tel: +82-2-2220-2379, Fax: +82-2-2220-1886, E-mail: minrho@hanyang.ac.kr

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (<http://creativecommons.org/licenses/by-nc/4.0/>) which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

- rapidly and reproducibly alters the human gut microbiome. *Nature* 2013, 505:559.
3. Consortium HMP: Structure, function and diversity of the healthy human microbiome. *Nature* 2012, 486:207-214.
 4. Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T: A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* 2010, 464:59-65.
 5. Kim MH. Microbiome research in atopic dermatitis. *Hanyang Med Rev* 2018;38:85-92.
 6. Kim Y, Choi D. Microbiome of hepatobiliary diseases. *Hanyang Med Rev* 2018;38:80-84.
 7. Shin JH, Rho M. Human resistome study with metagenomic sequencing data. *Hanyang Med Rev* 2018;38:73-79.
 8. Kim J. Carbapenem-resistant Enterobacteriaceae in Korea. *Hanyang Med Rev* 2018;38:99-102.
 9. Song SA, Shin JH. Microbiological characteristics of *Corynebacterium striatum*, an emerging pathogen. *Hanyang Med Rev* 2018;38:93-98.