

School of Life Sciences Seminar Series

Thursday
4:00 PM

26 November

This seminar will be held in the manner of online and offline both.

Offline: Jukhyun Bio Auditorium (RM.121)

Online: Zoom ID 315 451 8934 (Password: 101320)


Big Data, Big Challenges - future of human microbiome



 **연사** Sunjae Lee, Ph.D.

 **소속** GIST

 **Host** 생명과학부장

 언어: English

학력

- 2015** Ph.D., Dept. of Bio and Brain Engineering, KAIST,
(Supervisor: Doheon Lee)
- 2008** M.S., Dept. of Bio and Brain Engineering, KAIST,
- 2006** B.S., Dept. of BioSystems, KAIST

경력

- 2020 - 현재** Assistant professor, School of Life Sciences, GIST
- 2018 - 2020** Senior Research Associate, Centre for Host-Microbiome Interactions, King's College London, UK
- 2015 - 2018** Post-doctoral researcher, Science for Life Laboratory, KTH – Royal institute of technology, Sweden
- 2014 - 2015** Post-doctoral/visiting researcher, Chalmers university of technology, Sweden

Abstract

Human microbiome, our “second genome”, was recently known to harbour more than 100 trillion cells, which is ten times larger than human cells, and 10 million microbial genes, which is hundred times larger than human genes. Such genetic diversity provides extensive biochemical repertoire that may benefit or harm host humans. Recently, mounting evidence has suggested that the dysbiosis of human microbiome could lead to the disease pathogenesis, including neurological diseases. On the other hand, human microbiome could be used as therapeutics of many diseases. For example, faecal microbiota transplant has proven its therapeutic potentials in obesity, diarrhoea and inflammatory bowel diseases, and even the efficacy of immunotherapy. To facilitate the understanding of human microbiome in health and disease, international consortiums have been initiated to generate massive amounts of human microbiome data, including Human Microbiome Project (HMP) consortium investing 170 million USD for the sequencing of 13,000 metagenomics samples. Recently, millions of human microbiome project (MMHP) has been initiated, producing metagenomic data at tremendous scale. Now human microbiome addressed the challenges of big data, but due to the lack of quantitative approaches and less developed bioinformatics tools, its mystery is poorly understood and biased on small number of observational studies. In this seminar, the speaker will address the recent efforts of establishing reference of human microbiome and big data approaches for the identification of global microbiome signatures in health and disease. In addition, based on state-of-art technique of metagenomics assembly, called metagenomic species pan-genomes (MSP), many unculturable species were identified from metagenomics species, together with their functional capacities. Lastly, the speaker would discuss the future of human microbiome for the advancement of healthcare sector, such as systems medicine.