CURRICULUM VITAE

이선재

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[학력]

2006	KAIST 바이오시스템학과 학사
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2015-2018	스웨덴 KTH 왕립공과대학 박사후연구원
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[관심분야]

Bioinformatics, Metabolism, Microbiome, Systems Biology

[논문]

1. Vishal Patel*, Sunjae Lee* et al., “Rifaximin reduces gut-derived inflammation and mucin degradation in cirrhosis and encephalopathy: RIFSYS Randomised-Controlled Trial”, J Hepatology (2022)
2. Byong-Sop Song et al., "Mitoribosomal defects aggravate liver cancer via aberrant glycolytic flux and T cell exhaustion", BMJ Journal for Immunotherapy of Cancer (2022)
3. Chang-Hyun Kim*, Sang-Moo Park*, Sunjae Lee* et al., “NSrp70 is a lymphocyte-essential splicing factor that controls thymocyte development”, Nucleic Acids Research (2021)
4. Sara Omenetti et al., “The intestine harbours functionally distinct homeostatic tissue-resident and inflammatory Th17 cells”, Immunity (2019)
5. Sunjae Lee et al., “Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance”, Cell Metabolism (2016)

Systems biology of human metabolism - multi-omics and modeling approach

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In public health sector, chronic diseases, including cardiovascular disease, obesity, diabetes, and liver disease, are the most life-threatening diseases, projected to account for 85% of all deaths. Unlike infectious disease, it is not curable by vaccines or medication, and even worse, people of chronic diseases are likely to have multiple chronic conditions, impeding proper therapeutic developments.

Since the recent advance in high throughput technology, molecular profiling of chronic disease patients has been provided - transcriptome, epigenome, proteome, metabolome, and metagenome (Sunjae Lee et al., 2016, Cell Metabolism; Mardinoglu at al., 2017, Cell Metabolism; Brian D. Piening et al., 2018, Cell Systems; Nathan Price et al., 2017, Nature Biotechnology) - guiding us to understand its pathophysiology based on extensive scale of molecular evidence.

For instance, in insulin resistant patients, decreased uptake of mannose in liver tissue and thereby increased blood mannose was identified from multi-omics clues, such as transcriptome, epigenome and metabolome (Sunjae Lee et al., 2016, Cell Metabolism). In addition, metabolic dysfunctions of cardiovascular diseases and liver diseases were identified by multi-omics and modeling approaches, providing metabolic map that helps the design of therapeutic interventions (Stephen Doran et al., Briefings in Bioinformatics, 2021).

In this talk, the speaker will present recent systems biology-based approaches to understand health and disease, especially focusing on understanding human metabolism of chronic diseases. Such paradigm shift in future medicine will make a new promise of proactive medicine based on data-driven approaches.