Theoretical Biology Seminar

Large-Scale Transcriptome Profiling of Signaling Responses During Human Cell Differentiation

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Room 501, 5th floor, Bldg. #3
Institute for Life and Medical Sciences,
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Understanding how signaling pathways regulate human cell differentiation requires systematic comparisons of gene expression responses over time and across lineages. To enable such comparisons, we developed a high-throughput culture and transcriptome profiling system using human iPS cells under standardized experimental conditions. Our initial dataset comprised 21,888 samples collected at seven time points over 96 hours following treatment with 340 compounds that modulate signaling pathways, including experiments under endoderm differentiation conditions. Collaborative analysis of this dataset has identified candidate genes that may regulate differentiation, and experimental validation is ongoing. We have since expanded the dataset with approximately 80,000 additional samples covering differentiation toward all three germ layers. In this presentation, I will discuss findings from the initial analysis and ongoing validation, introduce the experimental design and scope of the expanded dataset, and outline how these data can help elucidate shared and lineage-specific transcriptional responses and the temporal regulation of cell fate.

Language: Japanese

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