



**第74回日本細胞生物学会大会** 2022年6月28日(火)～30日(木)  
The 74th Annual Meeting of the Japan Society for Cell Biology  
会場: タワーホール船堀  
細胞生物若手の会: 6月27日(月) 東京大学本郷キャンパス 理学部4号館 1220教室 + オンライン (ハイブリッド開催)

## 講演情報

シンポジウム

### [English session] Explication of spatiotemporal multicellular dynamics by developing new technology platforms for quantitative analysis.

2022年6月29日(水) 13:45 ~ 16:15 A会場 (瑞雲)

Organizer: Fumiko Toyoshima (Kyoto University)

Recent development of omics analysis, in vivo imaging, bioinformatics, and mathematical science enable us to capture in vivo cell information at the single cell level. However, the technology to capture the spatiotemporal information of individual cells is under development. In this symposium, we will introduce techniques for quantitative analysis of spatiotemporal information and interactions between multiple cells and aim to understand multicellular dynamics.

14:16 ~ 14:44

### [2A-112] Analysis of neural stem cell regulatory mechanisms using optogenetics

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キーワード: Neural Stem Cells, Optogenetics, Transcription Factor, Imaging, Optical Manipulation

The mammalian brain consists of a complex ensemble of neurons and glial cells. Their production during development and remodeling is tightly controlled by various regulatory mechanisms in neural stem cells. Among such regulations, basic helix-loop-helix (bHLH) factors have key functions in the self-renewal, multipotency, and fate determination of neural stem cells. Here, we highlight the importance of the expression dynamics of bHLH factors in these processes. We propose the multipotent state correlates with oscillatory expression of several bHLH factors, whereas the differentiated state correlates with sustained expression of a single bHLH factor. We also developed new optogenetic methods that can manipulate gene expressions in neural stem cells by light. We used this technology to manipulate the growth and

fate-determination of neural stem cells. We are also analyzing dynamic changes in downstream gene expressions and cellular states caused by systematic light-induced manipulation of bHLH transcription factors.

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