A molecular altas of subcellular RNA localization and interaction using proximity labeling

Shuo Han*

Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, Shanghai 200031,People's Republic of China
E-mail: shuohan@sibcb.ac.cn

The spatial distribution of RNA in cells profoundly affects various processes such as RNA production, modification, translation, and degradation. Dysregulated RNA localization leads to many RNA-related diseases such as neurodegeneration. Therefore, profiling the dynamic spatial distribution of RNA in different cell types at the transcriptome level is key to in-depth understanding of how RNA regulates cell fate and function. Using chemical biology methods such as protein evolution and probe design, our research group focuses on developing RNA proximity labeling and enrichment technologies based on genetically-encoded enzymatic tools[1-4]. We aim to apply our proximity labeling toolkit to comprehensively map RNA composition and RNA-protein interactions in different subcellular regions in diverse cell types, such as neurons and cancer cells. These novel resources and tools will help to mechanistically dissect cell-type specific RNA localization and interaction patterns, and provide a new roadmap for diagnosing RNA-related diseases at the molecular level.
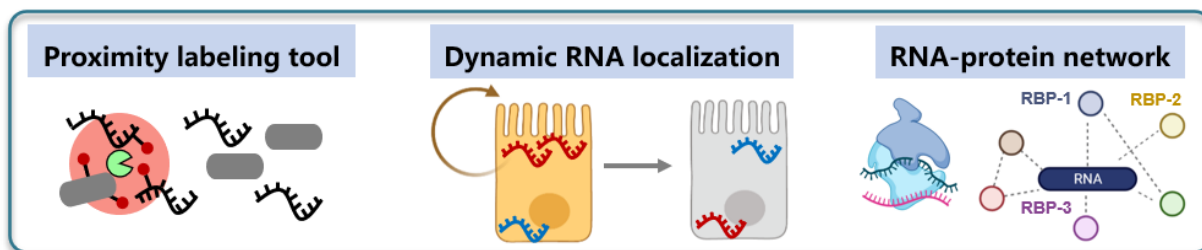
References

[1] Han S., Zhao B.S., Myers S.A., Carr S.A., He C., Ting A.Y., *PNAS*, **2020**, 117: 22068-22079.
[2] Li J*., Han S.*, et al, Ting A.Y., Luo L., *Cell*, **2020**, 180: 373-386. (*co-first author)
[3] Fazal F., Han S.*, et al, Chang H.Y., Ting A.Y., *Cell*, **2019**, 178: 473-490. (*co-first author)
[4] Han S.*, Udeshi N. D., et al, Ting A.Y., *Cell Chem. Biol.*, **2017**, 24: 404-414.

Shuo Han. Tsinghua University (BS, 2014), Stanford University (Ph.D., 2020, Alice Ting), Stanford University (Postdoc, 2020-2022, Philip Beachy), Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences (Principal Investigator, 2023-present).

[Field of Research] Protein engineering, proteomics, transcriptomics, proximity lableing, stem cell biology.