Seminar Speaker Series

in the framework of Interreg V-A project CAPSID

presents

Dr. Jeffrey A. Chao

Friedrich Miescher Institute, Basel, CH

Imagining the LIFE and DEATH of mRNAs in single cell

03.12.2020 at **14:00**

Online virtual talk via Zoom

NEW ZOOM ID!

Join this talk here

Organized by:

Dr. Jeffrey A. Chao

FMI
Friedrich Miescher Institute
for Biomedical Research

RESEARCH HIGHLIGHTS

How can the same genome give rise to a diversity of stable cell types? Epigenetics refers to processes that modulate the expression of a genotype into one or multiple distinct phenotypes. Molecularly, such modulation is mainly mediated by transcriptional and post-transcriptional modes of gene regulation.

The Epigenetics research groups at the FMI study basic principles of transcriptional and post-transcriptional gene regulation. We are particularly interested in understanding how such regulatory pathways specify and maintain cell identity, as well as influence cellular differentiation and reprogramming.

Gene expression requires an orchestrated series of events that is regulated temporally and spatially within the cell. After transcription, an mRNA must be spliced, processed, exported, transported and translated before it is eventually degraded. At each step, the factors that control the fate of the mRNA in either the nucleus or cytoplasm must be appropriately assembled, disassembled or remodeled. Not only is the composition of these macromolecular complexes dynamic, but there are also over 2000 proteins in the human genome involved in RNA metabolism, which makes them extremely heterogeneous as well. In order to better understand the molecular underpinnings that regulate these processes and how these complexes function within their cellular context, our research combines biochemical and structural (X-ray crystallography) techniques with single-molecule imaging of mRNAs in living cells.

REFERENCE

Halstead JM, Lionnet T, Wilbertz JH, Wippich F, Ephrussi A, Singer RH, Chao JA (2015) An RNA biosensor for imaging the first round of translation from single cells to living animals. **Science** 347:1367-1370.

Jia, M., Gut, H., Chao, J.A. (2018) Structural basis of IMP3 RRM12 recognition of RNA. **RNA.** 24(12):1659-1666.

Voigt, F.*, Gerbracht, J.V.*, Böhm, V., Horvathova, I., Eglinger, J., Chao, J.A.#, Gehring, N.H.# (2019) Detection and quantification of RNA decay intermediates using XRN1-resistant reporter transcripts. **Nat Protocols.** 14(5):1603-1633.

Organized by: