SINGAPORE RNA SEMINAR SERIES

FUNCTIONS AND MECHANISMS OF SEQUENTIAL POLYADENYLATION

Monday 25 November 2024
10.30am (SGT, GMT+8)

Via Zoom

About the speaker

Dr. Yu Zhou, Professor of Wuhan University. In 2003, he graduated with a biology bachelor from Wuhan University; in 2008, he completed joint doctor training at Paris-Sud University in France and Wuhan University in computer, biochemistry & molecular biology. In 2009, he went to UC San Diego for postdoctoral research; in 2015, he returned to the College of Life Sciences of Wuhan University as an independent PI. He has focused primarily on the regulatory mechanisms and functions of RNA processing and established a research paradigm of building multi-strategic high-resolution RNA maps to decode regulatory mechanisms. In recent five years, he has published 20 original research articles as a (co-)corresponding author (Mol Cell 3, NSMB 2, Cell, EMBO J, EMBO Rep, Genome Biol, Nat Commun, etc.). His lab is developing new RNA technologies, studying new functional mechanisms of RNA regulation, and analyzing the pathogenic mechanisms of RNA dysregulation in multiple diseases.

Dr. Yu ZHOU
Professor
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About the seminar

RNA biogenesis and processing are highly regulated at multiple layers, such as transcription, splicing, 3′-end cleavage and polyadenylation, and RNA modification. Both alternative polyadenylation (APA) and N6-methyladenosine (m6A) are broadly engaged in the regulation of critical cellular functions. Recently, through a series of genome-wide experiments, including fractionation-seq and Cleave-seq, we uncovered a novel mode of APA: sequential polyadenylation (SPA), by which polyadenylated mRNAs at distal polyA sites can be further processed at the proximal PASs before nuclear export. Furthermore, we have developed two new high-throughput techniques to quantify the m6A level of newly synthesized RNA and steady-state RNA in parallel, and one measures the m6A level at single-nucleotide resolution, which also enables dissecting the relationship between m6A modification and APA. Unexpectedly, our results reveal the pervasiveness of post-transcriptional m6A modification, especially for genes with high m6A levels. We further demonstrate that sequential polyadenylation coupled with nuclear retention dictates the preferential m6A modification on shorter 3′UTR isoform. These findings elucidate functional interplays between sequential polyadenylation and m6A modification at post-transcriptional levels to establish and dynamically regulate the epi-transcriptomics in mammalian cells.

Co-organised by: Agency for Science, Technology and Research SINGAPORE; NUS National University of Singapore; NANYANG TECHNOLOGICAL UNIVERSITY SINGAPORE

Supported by: RNA Society