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Jockey Club College of Veterinary
Medicine and Life Sciences

香港城市大學
City University of Hong Kong
in collaboration with Cornell University



JCC Research Seminar



TOPIC

Cell fate determination: from transcription factors to epigenetics

Dr. Yimeng Yin

Professor of Medical Systems Biology
School of Medicine, Tongji University

HONG KONG TIME

15 Nov 2022 (TUE) **Online via ZOOM**
10:00am-11:00am

Abstract:

Transcription factors (TFs) are believed to play a key role in the cell lineage specification process during development, but the molecular mechanisms underlying are still not fully resolved. To determine the molecular basis of biological specificity of transcription factor action, we developed a high throughput method, consecutive-affinity purification SELEX (CAP-SELEX), to screen the cooperativity between TFs. We identified >2500 novel interactions, including >2000 spacing preferences and ~400 composite motifs. We found that TFs that define embryonic axes bind to distinct composite motifs, explaining how TFs with similar specificity can define distinct cell types. TFs are believed to contribute to establishment of cell identity through shaping the epigenetic landscapes. To investigate how the epigenetic landscape was shaped during development, we developed a nanopore-sequencing-based-method, termed nanoHiMe-seq, to profile two or multiple epigenetic marks on the same DNA molecules in a single assay. We uncovered the intrinsic connectivity between epigenetic marks along multikilobase segments of the genome during the early stage of neurogenesis.

Speaker's Biography:

Dr. Yimeng Yin is Professor of Medical Systems Biology in Tongji University School of Medicine. Dr. Yin received his PhD in Molecular Biology from University of Science and Technology of China in 2012 and conducted his postdoc research at Karolinska Institute from 2013 to 2018. Dr. Yin worked as a research associate at Department of Biochemistry, University of Cambridge before he joined Tongji University. The mission of Dr. Yin's group is to develop and apply combined experimental and computational techniques to understand the precisely orchestrated transcriptional programmes in complex organisms and to decipher the underlying mechanisms by which cell identities are specified during the processes of cellular differentiation and development.