Department of Biomedical Sciences

presents the seminar

香港城市大學
City University of Hong Kong

Profiling the dynamics of protein complexes at scale and in situ with thermal proximity co-aggregation

Dr Chris Soon Heng TAN
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Date : 13 June 2023 (Tuesday)
Time : 11:00 - 12:00
Venue : Leung Ko Yuk Tak Lecture Theatre (LT-14), 4/F Yeung Kin Man Academic Building

Abstract

The interaction of proteins with metabolites and other proteins underlies most if not all cellular activities, and many bioactive xenobiotics perturb cellular processes through direct physical interactions with proteins. Mapping these biomolecular interactions can help unravel the complex protein machines and molecular pathways underlying various cellular processes to systematically unveil wiring of the cells that are dysregulated in diseases and perturbed by chemicals. Nevertheless, there are currently limited time- and cost-effective techniques for profiling intracellular protein-protein and protein-chemical interactions at scale and *in situ*. My laboratory integrates methods in computational sciences, analytical chemistry and molecular biology with new cellular protein biophysics techniques for large-scale profiling of protein-protein and protein-chemical interactions. We previously contributed to the development of CETSA (Cellular Thermal Shift Assay) with protein mass spectrometry (MS) for label-free identification of endogenous proteins interacting with drugs and metabolites (Huber et al., Nature 2015), which we subsequently extended into an unorthodox approach for elucidating the temporal modulation of protein complexes en masse. This biophysics-based method, termed Thermal Proximity Co-aggregation (TPCA) profiling (Tan et al. Science 2018), arguably is the only method applicable presently for the system-wide study of protein complex dynamics in primary cell and tissues without antibodies and protein tagging. I will present our recent work advancing the technique further with higher throughputs and increased sensitivity which was deployed to elucidate mechanism-of-actions of autophagy-inducing drugs and bioactive compounds revealing novel protein complexes implicated in the process.

About the Speaker

Graduated with a B.Sc. in Molecular Biology but inspired by his computer science colleagues at the Institute of Infocomm Research (I2R, A*STAR, Singapore), Chris completed a M.Sc. in Computer Science at National University of Singapore before heading off to Canada for his PhD training with the late Tony Pawson at the University of Toronto, Canada. There, he made seminal contribution to our understanding of signaling network evolution in human diseases and organismal Complexity (Tan et al. Science 2009; Tan et al. Science Signaling 2009, Tan et al. Nature Method 2012). He completed his postdoctoral training at the Center of Molecular Medicine in Vienna, Austria where he was exposed to mass spectrometry, chemical proteomics, and academic drug discovery. Prior joining the Southern University of Science & Technology at Shenzhen, China as an Associate Professor, Chris led a research group as a joint independent fellow (group leader) in IMCB and Bioinformatics Institute (BII, A*STAR, Singapore). Armed with unique tools and knowledge in chemical and network biology for elucidating mode-of-action of drugs and toxic chemicals, he is an advocate of phenotypic drug discovery for uncovering novel therapeutic approaches and new biology.

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All are welcome!