香港中文大學醫學院
Faculty of Medicine
The Chinese University of Hong Kong

35th Anniversary 三十五週年

Co-organized by:
Department of Chemical Pathology
Li Ka Shing Institute of Health Sciences

Seminar: Reversible DNA and RNA methylation in gene expression regulation

Date: *20 December 2016 (Tuesday)*

Time: *3:00 pm – 4:00 pm*

Venue: *Room 301, 3/F, Li Ka Shing Medical Sciences Building,*
Prince of Wales Hospital, Shatin, New Territories

Speaker: *Professor Chuan HE*

John T. Wilson Distinguished Service Professor
Department of Chemistry, Department of Biochemistry and Molecular Biology,
and Institute for Biophysical Dynamics,
Howard Hughes Medical Institute, The University of Chicago

Abstract:

Cytosine methylation (5mC) is a well-established epigenetic mechanism essential for genomic imprinting, X chromosome inactivation, silencing of retrotransposons, and lineage-specific expression of many developmental regulatory genes. This epigenetic mark is installed and maintained by DNA methyltransfeases (DNMTs), and has been recently shown to be oxidized to 5-hydroxymethylcytosine (5hmC), 5-formylcytosine (5fC) and 5-carboxylcytosine (5caC) by the Ten-eleven- translocation (TET) family of protein dioxygenases. Prof He and his team have developed several methods that allow selective detection and sequencing of 5hmC, 5fC, and 5caC with limited genomic materials. They show that sensitive detection of 5hmC offers the best means to interrogate and monitor cell transformation and gene expression changes in future disease diagnosis and prognosis.

Prior to their work, no example of reversible chemical modifications on RNA that could affect gene expression had been shown. They have discovered the first two RNA demethylases: FTO, a protein associated with human fat mass obesity and development, and ALKBH5, a protein that affects spermatogenesis in a mouse model. These two proteins catalyze oxidative demethylation of the most prevalent internal modifications of mammalian messenger RNA (mRNA) and other nuclear RNA, N^6-methyladenosine (m^6A). These results indicate that reversible RNA modification could impact biological regulation analogous to the well-known reversible DNA and histone chemical modifications. The Team has also identified and characterized proteins that can selectively recognize m^6A-modified mRNA and affect the translation status, lifetime, nuclear export, and localization of the target mRNA, as well as molecular machines that deposit the m^6A methylation on nuclear RNA. This mRNA methylation appears to be a mark for fast track of target mRNA. Their discoveries indicate the presence of a new mode of post-transcriptional gene regulation that depends on dynamic/reversible RNA modifications.

All are welcome. For enquiries, please contact Ms Begonia Yuen at 2632 2960 or Mr. Jonathan Lee at 3763 6005.