Institute of Medical Biology
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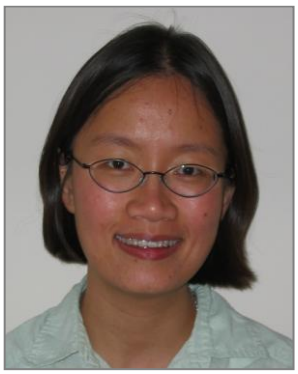
Seminar Announcement

- All Are Welcome -



Speaker : **Siu Sylvia Lee, Ph.D**
Associate Professor, Department of Molecular Biology & Genetics, Cornell University, Ithaca, NY

Title : ***"Transcriptional and global chromatin regulation key to longevity of C. elegans"***

Date : **16 July 2014 (Wednesday)**

Time : **11:00am – 12:00pm**

Venue : **Aspiration Theatrette, Matrix Level 2M, Biopolis**

Host : **Dr Colin Stewart**
(Tel: 64070156; e-mail: colin.stewart@imb.a-star.edu.sg)

Abstract:

We use *C. elegans* as a model system to dissect the evolutionarily conserved molecular pathways important for longevity. I will discuss the regulation of the key longevity determinant DAF-16/FOXO by the transcriptional co-regulator HCF-1, and the role of histone H3 lysine 36 trimethylation (H3K36me3) in age-dependent gene regulation.

The highly conserved transcriptional co-regulator HCF-1 is capable of coordinating many transcription and chromatin factor complexes and participates in a wide variety of biological processes. We previously identified the *C. elegans hcf-1* null mutant to be long-lived and stress resistant. Our investigations revealed that HCF-1 modulates longevity and stress response by acting with the protein deacetylase SIR-2.1/SIRT1 to regulate the activity of DAF-16/FOXO. Our data suggest HCF-1 is an integral component of the transcriptional network key to longevity determination and stress regulation.

Whereas functional data point to specific histone modification enzymes to be critical for longevity in *C. elegans*, how major histone modification marks change with aging is not known. We explored the global profile of H3K36me3 in the somatic cells of young and old *C. elegans* and found that the H3K36me3 mark is inversely correlated to mRNA expression variation during aging. Genes with dramatic expression change during aging are marked with low or even undetectable levels of H3K36me3 in their gene-bodies, irrespective of their corresponding mRNA abundance. Importantly, RNAi knockdown of the methytransferase *met-1* resulted in a decrease in global H3K36me3 marking and an increase in mRNA expression variation with age. Our findings revealed a new role for H3K36me3 in restraining gene expression fluctuation with important consequence on longevity.

About the Speaker:

Siu Sylvia Lee is an Associate Professor at the Department of Molecular Biology and Genetics at Cornell University. She received a B.A. in Biochemistry from Rice University in 1995 and a Ph.D. from Baylor College of Medicine in 1999. She received her postdoctoral training in Gary Ruvkun's laboratory at the Department of Molecular Biology at Massachusetts General Hospital & the Department of Genetics at Harvard Medical School. She joined the faculty at Cornell in 2003 and was promoted to Associate Professor in 2010. The overall research goal of her laboratory is to elucidate the molecular basis of longevity determination. She largely uses *C. elegans* as a model system for her research, but she has also extended some of the investigations into mammalian systems. Her current research focuses on several major areas, including dissecting the transcriptional regulation of the master regulator FOXO, probing how the chromatin landscape changes with age, and elucidating the molecular mechanisms whereby mitochondrial electron transport chain dysfunction impact longevity.