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***Revised**

THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY
Division of Life Science

LIFS Seminar Series

"Combination of RNA-Seq and high-throughput genetic screening identify novel cell fate determining genes in both Drosophila and mouse"

delivered by

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Abstract

How different cell types are specified from common progenitors is a fundamental question in developmental biology. It is also of importance in terms of how to regenerate one cell type after damage. Through combination of compound genetics and manual cell picking, we obtained different cell types with high purity and performed thorough RNA-Seq analysis afterwards. Candidate genes were quickly screened by RNAi library and we identified *Imp* and *Syp* which show opposite gradient in development and play counteracting roles in Drosophila neural stem cell fate specification. Similarly, using cochlea organ as an example, we have found that Crispr/Cas9-mediated base editing (Crispr-stop) can be used to screen mouse developmental genes in a high-throughput manner. It means that single or triple gene homozygous knockout mice (F0) can be generated within 6 weeks for functional validation *in vivo*. Taken together, RNA-Seq and high-throughput genetic screening will allow us to quickly identify and prove functions of novel genes.

Date : 1 June 2018 (Friday)

Time : 4:00 p.m.

Venue : *Lee Wing Tat Lecture Theatre (LT-D)
HKUST, Clear Water Bay, Kowloon

(Host faculty: Prof. Pingbo Huang)

All are Welcome!