Hiroshima University
Graduate School of Integrated Sciences for Life

Invitation Seminar

統合生命科学研究科セミナー/プログラム共同セミナー

Functional elements in the non-coding genome: from populations to single cells

Speaker: **Dr. Chung Chau Hon**

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Date : Thursday, November 26th, 2020
Time : 13:00〜13:40
Venue: C108 room, School of Applied Biological Science
生物生産学部　第一会議室

Our genome is pervasively transcribed into RNAs, the majority of which are non-coding RNAs (ncRNAs) of unknown function. Many of these ncRNAs derive from gene distal DNA regions that regulate gene expression (cis-regulatory elements, CRE), known as enhancers. These enhancers harbor a large fraction of the genetic variants associated with diseases, which contribute to the disease predispositions through regulation of gene expression. Thus, mapping these non-coding transcription events can serve as a proxy to understand enhancer activities and their contributions to genetic predispositions. To build an accurate transcription map of our genome, we have developed molecular and bioinformatic methods to quantify transcription initiation events genome-wide, revealing the extensively intertwining transcription units, prompting us to reimagine the definition of a gene. Systematic knockdown of randomly selected ncRNAs revealed a significant fraction of them are potentially functional. To identify potentially functional ncRNAs with disease contexts, using Parkinson's disease as a model, we integrated the transcriptomic data of cellular disease models with genome-wide association studies data for prioritization of disease relevant ncRNAs at genetic risk loci. To understand the biological contexts of ncRNAs from enhancers (eRNAs), we developed methods for detecting their transcription at single-cell resolution. By applying these single-cell methods to detect eRNA transcription in various immune cell types, we demonstrate its applications for interpreting immunologic trait associated variants in cell-type specific contexts, providing insights to the genetic predispositions of immune diseases. Finally, I will discuss the grand perspectives of building a transcribed CRE atlas of the human body at single cell resolution and its values for understanding the molecular basis of genetic predispositions.

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