



QBiC SEMINAR

Speaker

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Date &
Location

Tuesday, January 9, 2018, 10:00 - 11:00

Osaka QBiC Building A, 3F seminar room

(6-2-3Furuedai, Suita, Osaka)

There will be a TV broadcast at Kobe CDB Building A 7F seminar room

Title

A microfluidic tool for single-cell integrated nuclear and cytoplasmic RNA-seq

Abstract

Eukaryotes transcribe RNAs in nuclei and transport them to the cytoplasm through multiple steps of post-transcriptional regulation. Existing single-cell sequencing technologies, however, are unable to analyze nuclear (nuc) and cytoplasmic (cyt) RNAs separately and simultaneously. Hence, there remain challenges to discern correlation, localization, and translocation between them. Here we report a microfluidic system that physically separates nucRNA and cytRNA from a single cell and enables single-cell integrated nucRNA and cytRNA-sequencing (SINC-seq). SINC-seq constructs two individual RNA-seq libraries, nucRNA and cytRNA per cell, quantifies gene expression in the subcellular compartments and combines them to create a novel single-cell RNA-seq data enabled by our system, which we here term in-silico single cell. Leveraging SINC-seq, we discovered three distinct natures of correlation among cytRNA and nucRNA that reflected the physiological state of single cells: The cell-cycle-related genes displayed highly correlated expression pattern with minor differences; RNA splicing genes showed lower nucRNA-to-cytRNA correlation, suggesting a retained intron may be implicated in inhibited mRNA transport; A chemical perturbation, sodium butyrate treatment, transiently distorted the correlation along differentiating human leukemic cells to erythroid cells. These data uniquely provide insights into the regulatory network of mRNA from nucleus toward cytoplasm at the single cell level.

Host

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