Abstract of Presentation

Presentation Title:

Regulatory genomics: allelic variation in transcriptional regulation

Abstract :

Since the completion of the Human Genome Project, there have accumulated much knowledge on the human genetic variation, e.g. SNPs and copy number variations (CNVs)[1]. Furthermore, recent progress in high throughput sequencing will provide much precise information on the structural variation of our genomes. On the contrary, less is known about the molecular mechanisms that control expression of human genes, and about the variations in gene expression that underlie many pathological processes, including drug responses. Through the global epigenomic analysis using whole genome DNA microarray and high throughput DNA sequencing technologies, we have begun to understand the regulatory genetic codes, which are composed of maps of transcription factor binding, histone modification and DNA methylation. Deciphering these regulatory codes will be crucial in understanding individual variation in drug responses, where little is known about the mechanisms how genetic variations will affect transcriptional regulation. We have recently developed a novel method, called ExpressGenotyping to analyze allelic variation in gene expression and observed allelic difference is not a rare event.

I will present how we can apply genomic and epigenomic information to monitor the transcriptional variation in drug responses.

[1] Redon R, Ishikawa S, et al. Global variation in copy number in the human genome. **Nature**. 444:444-454. 2006