Integrated analysis of transcriptional regulation in cancer

Hiroyuki Aburatani
(The University of Tokyo, Research Center for Advanced Science and Technology, Professor)

【Outline of survey】

In the course of malignant transformation, there accumulate various genetic mutations, structural aberrations and epigenetic changes. To identify those mutations in the cancer genome, systematic analysis of genome, transcriptome and epigenome will be required. I will develop novel applications for such genomic analysis on the high-throughput technologies, e.g. next generation sequencers. Through the integrated analysis of various types of genomic information, I will elucidate the network orchestrated by transcriptional factor complexes involved in cellular proliferation and survival, and the epigenetic regulation in development and differentiation. Furthermore, it will be crucial to integrate 'genetics' and 'genomics', where I will investigate individual differences in transcriptional regulation. Finally, I aim to identify the signaling pathways that drive the cancer cells, which will be potential targets for cancer treatment.

【Expected results】

Through systematic genomic and epigenomic analysis of cancer genome, this research project will provide fundamental information related to carcinogenesis and may identify novel therapeutic targets and biomarkers for cancer. By integrating information on genetic variation, we may develop the prediction system for drug responses, which will enable the personalized medicine by patient stratification.

【References by the principal investigator】

- Redon R, Ishikawa S, et al. Global variation in copy number in the human genome. ***Nature***. 444(7118): 444-454. 2006
- Komura D, et al. Genome-wide detection of human copy number variations using high-density DNA oligonucleotide arrays. ***Genome Res***. 16(12):1575-1584, 2006
- Wendt KS, Yoshida K, et al. Cohesin mediates transcriptional insulation by CCCTC-binding factor. ***Nature***. 451(7180): 796-801. 2008

【Term of project】 FY2008− 2012	【Budget allocation】 **161,400,000 yen** (direct cost)

【Homepage address】 http://www.genome.rcast.u-tokyo.ac.jp/