Personalized Medicine in Cancer

Hiroyuki Aburatani

Research Center for Advanced Science and Technology,
The Univ. of Tokyo, Japan

Hiroyuki Aburatani

As the recent development of genomic technologies has enabled comprehensive analysis of gene expression, DNA methylation, and mutation screening, those data will be used to stratify the patients as well as to identify the therapeutic targets. Furthermore, as ultra high throughput sequencing strategies have enabled us to study the entire human genomes, we will be able to, or be required to, use the genomic information of each individual in medical practice within several years.

Cancer medicine has become more and more genome-based, particularly because each cancer genome is different. Since most of recent cancer therapeutics are designed against certain molecular targets, they should be given only to the appropriate patients, which requires development of biomarkers for patient stratification, e.g. HER-2 testing for trastuzumab. *KRAS* mutation status has been found to be a prediction marker for response to *cetuximab,* an anti-EGFR monoclonal antibody therapy.

In cancer genome sequencing, the International Cancer Genome Consortium (ICGC) has been formed, aiming to eventually sequence the full genomes of 25,000 tumor samples as well as those of the people from whom the tumors were taken, which would give 50,000 distinct genomes. Since the current cost of genome sequencing is still high, we would rather analyze many more cases by focusing on the coding regions of the genes, the exome, while completing the entire genome sequencing on a few cases. It is important to analyze many enough cases to distinguish the "driver" mutations, which are crucial in cancer development, from "passenger" mutations that just happen as a result of genetic instability in cancer.

Sequencing the targeted genomic regions has been enabled by sequence capture technology, where the target sequences, namely exonic sequences, are enriched by hybrid selection in solution. The ‘on-target’ efficiency was 50 to 80 %, while the concordance of SNP genotyping call on a HapMap individual was 99.4 %. The current progress of the cancer exome analysis will be presented.