

## **Genome project and the future medicine**

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The human genome project is now considered to be the most important project in biological and medical research. The discovery of entire human genes that are estimated to be 70,000-150,000 in our genome, through this project must revolutionize biological medicine including molecular diagnosis of various diseases and development of novel treatment.

In this regard, analysis of expression profiles and SNPs (single nucleotide polymorphisms) using "microarray" or "DNA-chip" is quite important. "Microarray" or "DNA chip" technology has made it possible to examine expression levels of thousands of genes and genotype a huge number of SNPs by a single experiment. We have been applying microarray analysis for screening of genes involving in colorectal, hepatocellular, and ovarian carcinogenesis as well as those related to responsiveness to anti-cancer drugs and those involving in various signal transduction pathways of medical importance. We have so far established a system to analyze 30,000 genes and are accumulating the expression profile data of various types of cancer cells. For example, we analyzed cancer tissues of 26 esophageal cancer patients who were treated by the same chemotherapy after their operation and established the DRS (drug sensitivity score) system to predict the efficacy of the treatment.

In addition to the expression profile analysis, we undertook a systematic survey of genomic DNA for SNPs located not only in coding sequences but also in non-coding regions (e.g introns and 5' flanking regions) of genes of medical interest. Using DNA samples from Japanese individuals, we have so far identified about 36,000 SNPs and are adding nearly 2000 SNPs every week.

In the meeting, I introduce the recent progress and future direction of human genome analysis and its impact on the medical science.