Systemic analysis of transcriptional network in cancer

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【 Outline of survey 】

Integrated Biology, which analyzes the multiple biological information systemically, is one of the main topics in the post-genome biology. Integrated analysis should be required to understand the cross talks between the signaling pathways. In our project, we attempt to elucidate the abnormality in transcriptional network in cancer with the global analysis of gene expression profiles and mutation detection. Recent progress in genome analysis technology allows us to establish the Clinical Genomics, namely comprehensive gene expression and mutation detection analysis of the tiny amount of clinical specimens. By integrating together the gene expression profiles, epigenetic changes and chromosomal aberration data, we will be able to better clarify the carcinogenesis process from its beginning to the advanced stages. Based on the data collected above, we aim particularly at systemic analysis of transcriptional network in cancer.

【 Expected results 】

Identification and validation of the pathway involved in carcinogenesis will help us develop a novel therapeutic strategy for cancer in personalized medicine. For example, a new biomarker for early cancer detection and clinical monitoring, which is likely to show specific expression in cancer, will be developed.

【 References by the principal researcher 】

Hippo Y, Watanabe K, Watanabe A, et al. Identification of Soluble Amino Terminal Fragment of Glypican-3 as a Serological Marker for Early Stage Hepatocellular Carcinoma. **Cancer Research** 64 (7): 2418-2423. 2004

Tsutsumi S, Taketani T, Nishimura K, et al. Two distinct gene expression signatures in pediatric acute lymphoblastic leukemia with *MLL* rearrangements. **Cancer Research** 63(16):4882-7, 2003

【 Term of project 】 ＦＹ 2004 － 2008	**【 Budget allocation 】** 87,100,000 yen

【 Homepage address 】

http://www2.genome.rcast.u-tokyo.ac.jp/
http://www.lsbm.org