Whole genome sequence and comprehensive data analysis of cancer genome

Akihiro Fujimoto

Laboratory for Medical Science Mathematics,
RIKEN Center for Integrative Medical Sciences,
Yokohama, 230-0045, Japan

Whole genome sequence (WGS) is the most effective and straightforward way for understanding the genetic variation in the human genome. On current platforms, accurate identification of variants is a critical but difficult task for application to personalized medicine. To construct an analysis pipeline for WGS, we have sequenced and analyzed whole genome sequence of a Japanese individual. We found 3,132,608 SNVs by a likelihood comparison method. Also, we identified 5,319 deletions smaller than 10kbp with high accuracy, as well as copy number variations and rearrangements. By *de novo* assembly of unmapped sequences, we identified contigs that showed high similarity with EB virus and other human reference genomes.

We sequenced and analyzed the whole genomes of 27 HCCs, including two sets of multicentric tumors. Although no common somatic mutations were identified in the multicentric tumor pairs, their whole-genome substitution patterns were similar, suggesting that these tumors developed from independent mutations, although their shared etiological backgrounds may have strongly influenced their somatic mutation patterns. Statistical and functional analyses yielded a list of recurrently mutated genes. Multiple chromatin regulators were mutated in ~50% of the tumors. Hepatitis B virus genome integration in the *TERT* locus was frequently observed in a high clonal proportion. Our whole-genome sequencing analysis of HCCs identified the influence of etiological background on somatic mutation patterns and subsequent carcinogenesis, as well as recurrent mutations in chromatin regulators in HCCs.

Akihiro Fujimoto
Laboratory for Medical Science Mathematics
RIKEN Center for Integrative Medical Sciences, Yokohama, Japan
E-mail: afujircb@src.riken.jp

EDUCATION

2008 Ph. D., Department of Human Genetics, University of Tokyo
2005 M. S., Department of Biological Science, Kyushu University
2003 B. A., Department of Biological Science, Kyushu University

PROFESSIONAL TRAINING

2012-current	Center for Genomic Medicine, RIKEN (Senior Researcher)
2011-2012	Center for Genomic Medicine, RIKEN (Researcher)
2010-2011	Center for Genomic Medicine, RIKEN (Special Postdoctoral Researcher)
2008-2010	Computational Science Research Program, RIKEN (Special Postdoctoral Researcher)

RECENT PUBLICATIONS

1. Fujimoto A, Totoki Y, et al. Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. ***Nat Genet*** 44: 760-764, 2012.
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