医学・生命科学セミナー
Medical and Life Science Seminar

Whole genome sequencing analysis of cancer, forwarding to personalized medicine

Dr. Hidewaki Nakagawa
講師：中川　英刀　先生

RIKEN Center for Integrative Medical Sciences, Laboratoy for Genome Sequencing Analysis, Tokyo, Japan

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会場：医学教育図書棟４階　第３講義室
(Med. Edu. Lib. Bldg., 4th FL., Lecture Room 3)

Abstract

Cancer is essentially a “disease of genome” which evolves with the accumulation of a variety of mutations, and some of the driver mutations have been targeted for cancer treatment and diagnosis. Recent explosive advances of next-generation sequencing technology (NGS) and bioinformatics/biomathematics enable us to comprehensively analyze a number of cancer genomes by whole genome sequencing (WGS), whole exome sequencing (WES), or RNA sequencing (RNAseq). Now many types of cancer genomes have been sequenced whole world, including ICGC (International Cancer Genome Consortium), to explore cancer genomic alterations and diversity[1], and we have been performing WGS analysis focusing on liver cancers as one of the ICGC projects[2]. Liver cancer is one of the most common and deadly cancers worldwide, especially in Asia, and has no effective treatment, yet its molecular mechanism remains largely unknown. Now WGS by NGS and mathematics approach for liver cancers is demonstrating comprehensive landscape of various phenotypes of liver cancers with multiple etiological backgrounds (HBV-infected, HCV-infected, and non-virus, HCC and biliary phenotype) for point mutations, short indels, copy-number alterations, structural variations, and virus integrations. Comparison among whole genomic pictures of these heterogeneous cancers can clarify the underlying carcinogenesis and achieve molecular sub-classification, which facilitates its genomic biomarkers discovery and personalized cancer medicine.

References

1. Alexandrov LB, et al. Nature 500:415-421 (2013)

2. Fujimoto et al. Nat Genet 44:760-764 (2012)

【共催】がんプロフェッショナル養成基盤推進プラン

【連絡先】：免疫識別学分野　西村　泰治　内線：5310（教授室）、5313（秘書室）
For details, call ex.5313 or e-mail to mxnishim@gpo.kumamoto-u.ac.jp.