

EDITORIAL



Integrative cancer genomics in the *era* of precision cancer medicine

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Cancer is a disease caused by genomic and epigenome abnormalities, and the accumulation of such abnormalities and errors results in cancer evolution. The development of next-generation sequencers (NGSs) led to a large-scale cancer genome sequence project, which revealed the existence of a huge number of nucleic acid sequence alterations in the genomes of various cancer cells.

Among them, the mutation that contributes to actual carcinogenesis is called a cancer driver mutation. When a protein product translated by a mutated gene has the ability of oncogenesis, a specific inhibitor for that product has a remarkable cancer inhibitory effect, that is, molecular target therapy. Many genetic abnormalities responsible for such carcinogenesis have been identified in various cancers. Molecular target therapies have demonstrated remarkable clinical success in the treatment of various cancers including breast, colorectal, lung, gastric, liver, and gynecologic cancers. Currently, with the aim of selecting effective therapeutic drugs, genetic diagnosis of cancer not only uses a system that comprehensively diagnoses many genetic mutations simultaneously with tissues obtained by surgical resection, a so-called cancer gene panel, but also a liquid biopsy method that reduces invasion of patients using DNA leaking from cancer cells and cancer cells circulating in the patient's peripheral blood.

NGS has also revealed the presence of age-related somatic mutations in the human genome, which are important for understanding the background of different cancer developments among environments, races, and countries. Immunogenomics has developed in the field of clinical implementations of immune-checkpoint inhibitors, CAR-T-cell therapy and cancer vaccines.

Increasing evidence on the functional roles of noncoding miRNAs in cancer progression has revealed the potential of miRNA therapeutics in cancer. Furthermore, recent advances in single-cell sequencing enables an omics approach at the single-cell level to reveal the complex interplay between genotype and phenotype. Elucidation of intra-tumor heterogeneity by single-cell DNA sequencing and multi-omics will greatly contribute to the research leading to precision medicine, such as elucidation of the mechanism of cancer recurrence and drug resistance, and development of new methods of cancer therapy.

In the *era* of "Precision Cancer Medicine," where "whole genome analysis" and "whole exome analysis," that comprehensively analyze an individual's genome sequence (personal genome), are widely used to elucidate the causes of cancers as the monogenic or multifactorial diseases, it is important for us to understand ethical issues such as privacy issues, the management of secondary findings, and challenges in data storage and sharing.

In this special issue of Cancer Genomics, we invite established leaders in cancer omics and/or integrative cancer genomics, most of them are active researchers to discuss about cancer genomics studies and their future perspectives. We hope that this collection of review articles contributes to equip the readers for the *era* of precision cancer medicine.

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