

“Precision Cancer Medicine and Super-computing System”

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Precision Cancer Medicine: Tumors are classified into several molecular subtypes by Genomic Sequencing. Comprehensive targeted-gene panel provides more therapeutic options. CANCERPLEX-JP version 4.0 includes 435 actionable genes, which clinical approaches are available. Utilizing the gene panel platform, we assessed the genes and pathways most frequently altered in Japanese and US cases (Genome Med 2016;8:136). We demonstrate concordance of CANCERPLEX-JP with whole-exome sequencing from the TCGA in identifying hypermutated samples and microsatellite instability in multiple cancer types, such as colorectal and gastric cancer. We introduced our activity for precision medicine at 4th US-Japan Clinical Trials in Oncology Workshop sponsored by Embassy of Japan, at Washington DC, held in June 9, 2016. We highlight the clinical utility of CANCERPLEX-JP (435 genes) in guiding treatment strategies with targeted therapy in solid tumors, thus providing rationale for Comprehensive Genomic Sequencing in actualizing precision medicine. The goal of Precision Medicine is cost effectiveness and realization of genome drug discovery.

Super-computing System: This introduction plan is based on the massive medical big data (cancer gene mutation information, genomic data, image data, etc.) possessed by Niigata Prefecture and Niigata University, to construct an integrated analysis system incorporating deep learning, and introduces a high-performance computer system for the development and activation of related industries. Therefore, it is necessary to have an operation system that can connect to the hospital electronic medical record without interference.