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Detection of gene mutations in gastric cancer tissues by sequencing panel

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Companion diagnostics provide information of the effective use of a drug or biological product to help physicians to decide appropriate treatment to the patients. Especially, in cancer field, new technologies such as next generation sequencing, are used to identify nucleotide mutation in the genome of biopsy tissue. Cancer Panel analysis (Illumina) provides pre-designed, optimized oligonucleotide probes for sequencing mutational hotspots in > 35 kilobases (kb) of target genomic sequence. Forty-eight genes are targeted with 212 amplicons in a highly multiplexed, single-tube reaction. We performed mutation analysis of the fresh Gastric cancer tissues from 4 patients by Cancer Panel analysis using next generation sequencer (MiSeq). We found three hotspots mutations from two patients by comparison with normal tissues, and those mutations would be correlated with their clinical information.
Also, Cancer Panel analysis was successful for same tissues which were fixed by 5% of formalin within one day. Nucleic acid transition appeared in samples fixed for more than 3 days, but such error was not detected for samples fixed within a day. These results would be useful to establish guidelines of tissue fixation for protocols of DNA analysis.

Biography

Dr. Tomoaki Ito was received the M.D. in 2000 and the Ph.D. in medical science from Juntendo University, Tokyo, Japan. and postdoctoral studies from Stanford University School of Medicine. He is an assistant professor of Department of Surgery, Juntendo Shizuoka Hospital, Juntendo University School of Medicine, Shizuoka, Japan. His reseach interest includes Oncology and Cancer Biomarker.

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