

COMPARATIVE GENOMIC PROFILING OF PRIMARY TUMOR TISSUE AND CIRCULATING TUMOR DNA IN COLORECTAL CANCER

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Background: Genomic profiling of tumor tissue is an effective approach for detecting mutations, single-nucleotide variants (SNVs), copy number variations (CNVs), and gene fusions that contribute to cancer progression. Circulating tumor DNA (ctDNA) has recently emerged as a minimally invasive alternative for the early detection and monitoring of cancer. However, its accuracy compared to tumor tissue sequencing remains to be investigated. The present study aimed to compare the mutational profiles of colorectal cancer (CRC) tumor tissue and ctDNA.

Materials and Methods: Three CRC samples from KazIOR were analyzed. Biological material included paraffin-embedded tumor blocks and ctDNA isolated from blood plasma. DNA was extracted using the ReliaPrep™ FFPE gDNA Miniprep System and QIAamp MinElute ccfDNA Kits. Library preparation was performed using the Illumina TruSight Oncology 500 High-Throughput kit, and the quality of cfDNA was evaluated by spectrophotometric and fluorometric methods.

Results: In sample BR115, the PGR mutation (NM_000926.4:c.2657A>G) was detected in both tumor tissue and ctDNA. Additional pathogenic variants in PMS2, CDKN2A, KRAS, and TP53 were identified in tumor tissue but were absent in ctDNA. In sample BR121, metastatic disease was confirmed, with KRAS and IRS2 mutations found

in both tumor and ctDNA. Notably, a somatic pathogenic mutation in IRS2 (NM_000038.5:c.994C>T) was identified only in ctDNA, not in tumor tissue.

Conclusion: The study demonstrates that ctDNA can mirror tumor mutational profiles and occasionally reveal additional variants undetectable in tissue, underscoring its potential as a non-invasive biomarker for early CRC detection and real-time disease monitoring. Unique mutational patterns also support the use of ctDNA for personalized treatment strategies.

Key words: Colorectal cancer (CRC); solid tumors (ST); cell-free DNA (cfDNA)

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Acknowledgements: Study was supported by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan (Grant No. AP23489913, AP22788205, BR24992841, BR24993023)