

Clinical application of expression profiling in colorectal cancer

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Colorectal cancer (CRC) is one of the most common causes of cancer-related deaths, and it causes death primarily through liver metastasis. Recent progress in diagnosis and treatment has enabled clinicians to save the lives of many patients at early stages of the disease, but the prognosis for patients at advanced stages or with systemic metastasis is still very poor. The biologic heterogeneity of the tumor is the major obstacle to the effective treatment of CRC because of various clinical patterns and treatment efficacies. To gain a more comprehensive understanding of molecular pathophysiology and to identify various bio-markers to determine prognosis and treatment efficacy, cDNA microarrays could be a useful, high-throughput technology for detecting complex genetic changes. However, for the proper usage of those molecular information in the standard practice, there are several issues to consider; 1) availability of fresh tissue samples with adequate amount, 2) standardization of experiment technique, analysis methods and evaluation criteria, 3) acceptable sensitivity and specificity of the test, 4) rigorous clinical validation with large number of in prospective trials, 5) adequate study design for the purposes, and 6) cost-effectiveness. Here, I will introduce the current genomic approaches in colorectal cancers for the future clinical application in various ways; 1) understanding molecular pathophysiology of CRC, 2) diagnostic biomarkers/cancer classifier, 3) prognostic signatures, 4) predictive signatures as pharmacogenomics, and 5) potential therapeutic targets.