Identification of Prognostic mRNA Markers in Colorectal Cancer Patients

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Background：Colorectal cancer (CRC) is the third most commonly diagnosed cancer in Taiwan, with an estimated >10,000 new cases and > 4,000 deaths per year. The introduction of newer agents in combination with 5-FU has increased response rates to 40% to 50% in advanced disease and improved overall survival. The development of monoclonal antibodies targeting has demonstrated additional clinical benefit for patients with metastatic disease. However, the utility of individual markers of response, toxicity, and disease recurrence remains in question. In the present study, we aimed to investigate the prognostic mRNA markers in CRC patients.
Materials and Methods：Blood specimens were collected from 156 colorectal cancer patients. RNA were extracted from whole blood samples and then applied to Weighted Enzymatic Chip Array (WEnCA) which contained 31 candidate genes selected from microarray in 10 pairs of CRC cancer tissue specimens. The Chi-square test was used to analyze the correlation between direct sequencing and WEnCA analysis results.
Results：The expression level of *MYC*, *CA9* and *CHRNB1* genes were respectively correlated with vascular invasion (P=0.012) and perineural invasion (P<0.05). The specificity of *MYC* predicting the vascular invasion was 83.3%. The sensitivity of both *CA9* and *CHRNB1* to predicting the vascular invasion were 85.71%.
Discussion：These genes have the potential to be the predictive prognostic markers in CRC after further validation. Moreover, WEnCA platform may be the alternative detection method for clinical application.