

ERCC1 Expression in stage IIIA Non-Small Cell Lung Cancer and Platinum-based Neoadjuvant Concurrent Chemoradiotherapy

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Background : Excision repair cross-complementation group 1 (ERCC1) overexpression is associated with resistance to cisplatin-based chemotherapy in non-small cell lung cancer (NSCLC) patients. Preliminary study also suggests that ERCC1 expression was associated with radioresistant in the lung cancer cells. **Objective :** Aim of our study was to evaluate the prognostic value of ERCC1 expression in Stage IIIA, N2 positive NSCLC patients treated with platinum-based neoadjuvant concurrent chemoradiotherapy (CCRT) followed by surgery. Method Sixty eight patients with mediastinoscopic biopsy-proven N2 positive NSCLC were enrolled between August 1997 and September 2003. ERCC1 expression was assessed by immunohistochemistry. The correlation of ERCC1 expression with various clinicopathological factors, including response rate, progression free survival (PFS) and overall survival (OS) was also analyzed. **Result :** Among 68 specimens, ERCC1 expression was positive in 31 (46%). At a median follow-up of 61.8 months (range: 34.3-108.8 months), the median PFS and OS were 18.0 months (95% CI: 13.9-22.1 months) and 29.0 months (95% CI: 17.9-40.1 months), respectively in all patients. In univariate analyses, ERCC1-negative group, as compared with ERCC1-positive group, showed significantly prolonged OS (89.2 vs 26.0 months, $p=0.014$). In multivariate analyses, negative ERCC1 expression ($p=0.041$) and achieving downstage after CCRT ($p=0.005$) were statistically significant independent prognostic factors for prolongation of survival. **Conclusion :** These results suggest that stage IIIA, N2 positive NSCLC patients with ERCC1-negative tumors showed survival benefit from CCRT with platinum-containing regimen, indicating ERCC1 expression would be a useful prognostic marker.

Whole genome analysis for liver metastasis gene signatures in colorectal cancer

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Liver metastasis is one of the major causes of death in colorectal cancer (CRC) patients. To understand this process, we investigated whether the gene expression profiling of matched colorectal carcinomas and liver metastases could reveal key molecular events involved in tumor progression and metastasis. We performed experiments using a cDNA microarray containing 17,104 genes with the following tissue samples: paired tissues of 25 normal colorectal mucosa, 27 primary colorectal tumors, 13 normal liver and 27 liver metastasis, and 20 primary colorectal tumors without liver metastasis. To remove the effect of normal cell contamination, we selected 4,583 organ-specific genes with a false discovery rate (FDR) of 0.0067% by comparing normal colon and liver tissues using significant analysis of microarray, and these genes were excluded from further analysis. We then identified and validated 46 liver metastasis-specific genes with an accuracy of 83.3% by comparing the expression of paired primary colorectal tumors and liver metastases using prediction analysis of microarray. The 46 selected genes contained several known oncogenes and 2 ESTs. To confirm that the results correlated with the microarray expression patterns, we performed RT-PCR with WNT5A and carbonic anhydrase II. Additionally, we observed that 21 of the 46 genes were differentially expressed (FDR = 2.27%) in primary tumors with synchronous liver metastasis compared with primary tumors without liver metastasis. We scanned the human genome using a cDNA microarray and identified 46 genes that may play an important role in the progression of liver metastasis in CRC.