Expression Analyses of Genes and Neuroendocrine Markers Recognize Long Survival Subtype of Small Cell Lung Carcinoma.

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Abstract:

Purpose: Although small-cell lung carcinoma (SCLC) has high chemo-sensitivity, but recurrence by distant metastasis causes unfavorable prognoses. We previously reported that gene expression profiling could identify a good-prognosis subtype of SCLC. Here, we evaluated the subtype using immunohistochemistry to obtain appropriate biomarkers.

Methods and Results: Surgical specimens of 30 SCLCs were employed for the comprehensive gene expression analysis using an Affymetrix HG U133 plus 2.0 chips. This analysis successfully duplicated the subtype with significantly good prognosis. We subsequently evaluated the protein expression of neuroendocrine (NE) and basal cell (BA) markers with cases of 39 SCLCs. NE negative patients (n=7) had better survival than NE positive patients (p=0.026), whereas there was no survival difference by BA marker expression.

Conclusion: The gene expression analysis of SCLC revealed that surgical SCLC had a subset of cases with good prognosis, and this subtype was identified by low NE marker expression.

Key words : SCLC, gene expression profiling, protein expression, prognosis