translational research

**1606P CBX3 AND CRABP2 ANALYSIS BY RNA SEQUENCING IN NON-SMALL CELL LUNG CANCER**

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**Aim:** Complete sequencing of the human genome and the concurrent development of technologies can help us to understand cancer biology. Here, we used RNA sequencing (RNA-Seq) to find new genes associated with non-small cell lung cancer (NSCLC). And then we investigated the relationship between survival rate and the genes that we found out.

**Methods:** We enrolled 88 male patients with NSCLC. RNA-Seq was performed on 88 pairs of NSCLC tumor tissue and non-tumor tissue from 54 patients with adenocarcinoma and 34 patients with squamous cell carcinoma. After RNA-Seq analysis, we validated the analysis by immunohistochemistry (IHC) in a different NSCLC group. And then we performed the survival analysis.

**Results:** In RNA-Seq analysis, we found two upregulated genes, such as CBX3 (chromobox homolog 3) and CRABP2 (cellular retinoic acid binding protein 2), not previously reported in lung cancer, and these were studied further. Their altered expressions about four genes were verified by immunohistochemistry in a different set of NSCLC tissues (n=154). CBX3 was positive in 90.3% (139 cases), CRABP2 in 72.1% (111 cases). We divided the NSCLC group into two groups according to the median FPKM (fragments per kilobase of exon per million fragments mapped) and then performed Kaplan-Meier survival analysis. However, CBX3 and CRABP2 showed the tendency that the overall survival rate increased as median FPKM was low, although it did not reach the statistical significance (p=0.109 for CBX3, and p=0.104 for CRABP2).

**Conclusions:** CBX3 and CRABP2 expression was markedly increased in NSCLC tissues. However, the FPKM levels of CBX3 and CRABP2 in tissues were not related to survival.

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