**P2-025**  
**BSTB: Cancer Genetics Posters, Tue, Sept 4**

**The correlation of the differential expression of S100A4 gene (mts1) with the differentiation and metastasis of lung cancer**

Su, Lei; Zhi, Xiuyi; Xu, Qingsheng; Liu, Baodong; Zhang, Yi; Wang, Ruotian; Hu, Mu; Liu, Lei; Qian, Kun  
Department of Thoracic Surgery, Xuan Wu Hospital of Capital University of Medical Science, Beijing, China

**Background:** Invasion and metastasis are hallmarks of lung cancer and other malignant tumors. The activation of many genes has been shown to be important in tumor progression. We studied the corelationship of S100A4 gene (mts1) expression with the prognosis evaluation of lung cancer.

**Methods:** Total RNAs were extracted from 46 cases of patient with lung cancer, and 4 lung cancer cell lines (A549, GLC-82, NCI-H446, NCI-H460), S100A4 gene expressions were detected at mRNA level by reverse transcription-polymerase chain reaction (RT-PCR).

**Results:** Up-regulation of S100A4 gene was shown in 29 of 46 (63.0%) lung cancer patients and all of the lung cancer cell lines, especially in younger patients (89.5% vs 44.4%, p <0.01), poor differentiated lung cancer patients (81.0% vs 48.0%, p <0.05), mediastinum lymphonodus metastasis (77.3% vs 20%, p <0.05) and the IIIa stage patients (73.1% vs 0, p <0.05).

**Conclusions:** S100A4 gene played an important role in lung cancer progression, correlated well with the condition of the lung cancer differentiation, mediastinum lymphonodus metastasis, and the prognosis for the patients of lung cancer. It was likely that S100A4 gene as a prognostic, predictive, or even diagnostic factor in clinical practice.

**P2-026**  
**BSTB: Cancer Genetics Posters, Tue, Sept 4**

**Construction of antisense Slp2 gene and It’s effects on growth and proliferation of lung cancer cell lines**

Su, Lei; Zhi, Xiuyi; Xu, Qingsheng; Liu, Baodong; Zhang, Yi; Wang, Ruotian; Hu, Mu; Liu, Lei; Qian, Kun  
Department of Thoracic Surgery, Xuan Wu Hospital of Capital University of Medical Science, Beijing, China

**Background:** To study the effects of antisense Slp2 gene on the growth and proliferation in lung cancer cell lines.

**Methods:** Total RNAs were extracted from 4 lung cancer cell lines (A549, GLC-82, NCI-H446, NCI-H460), Slp2 gene expressions were detected at mRNA level by reverse transcription-polymerase chain reaction (RT-PCR); antisense Slp2 gene plasmid was constructed, and transfected into A549, GLC-82, NCI-H446, NCI-H460 cells with lipofectin. The expressions of Slp2 gene were analyzed by reverse transcription-polymerase chain reaction (RT-PCR). The correlation of the differential expression of Slp2 gene was positive expressed in A549, GLC-82, NCI-H446, NCI-H460 cell lines; The flow cytometry experiments presented here showed the transfected cells accumulation in the G2-phase of the cell cycle; The proliferation of GLC-82, NCI-H446, NCI-H460 cells were inhibited by antisense Slp2 gene conspicuously; Dramatic inhibition of colony formation in soft agar was observed in those transfected lung cancer cell lines.

**Conclusions:** Our results suggested that Slp2 gene might be a key gene in lung cancer cell growth and proliferation.

**P2-027**  
**BSTB: Cancer Genetics Posters, Tue, Sept 4**

**Comparison of genomic alterations by array comparative genomic hybridization and RT-PCR in early-relapse and non-relapse non-small cell lung carcinoma patients**

Sung Jae Suk1,2, Choi, Hyo Seon2, Jo, Uk Hyun2, Kim, Han Kyum3, Kang, Jason Jongho4, Kim, Yeul Hong1,2,5  
1 Department of Internal Medicine and Division of Brain Korea 21 Project for Biomedical Science, Seoul, Korea 3 Genetic Research Center for Lung and Breast/Ovarian Cancers, Seoul, Korea 4 Division of Pathology, Department of Internal Medicine, Korea University College of Medicine, Seoul, Korea 5 Department of Internal Medicine, Korea University College of Medicine, Seoul, Korea

**Lung cancer is the most common cause of cancer mortality in the worldwide.** Array Comparative Genomic Hybridization (CGH) is a recently introduced technology that measures variations in the gene copy number of hundreds of genes in a single experiment. It enables one to carry out genome-wide screening for regions of genetic alterations, such as chromosome gains and losses, or localized amplifications and deletions.

In this study, we have utilized the array CGH to elucidate the difference of the genome-wide alterations between early relapse and non-relapse Non-small cell lung carcinoma (NSCLC) patients after surgical resection. A total of 49 frozen tissues provided from the Korea Lung Tissue Bank were used in this study. Twenty five patients had distant relapse within 2 years of resection (Early-relapse group) and 24 patients were alive without disease at least 2 years after treatment (Non-relapse group). Genomic alterations were analyzed using 1,440 BAC clones in the chromosomes and differences between 2 groups were noted in 126 clones.

The different DNA copy number variations observed in the between Non-relapse and Early-relapse groups were noted on chromosomes 1p36, 1q41, 3q26, 5q35, 7p15, 8q24, 8p22, 17p11, 18q21, 19p13 and 20p12. To confirm the array CGH results, RNA expression level of gene located in each was evaluated by RT PCR in tumor samples. With RT-PCR of TP73, TGFb2, SNO, MYC and DCC genes, a positive correlation was found between gene copy number variation (aCGH) and mRNA expression (RT-PCR).

We will further try to identify high relapse risk group using more tumor tissues and to identify prognosis related genes. And, we will consider the various platforms that used logistic analysis.

This study on defining the gene involved in Early-relapse may thus be of value in understanding the prognosis of NSCLC after surgical resection.

*This study was supported by a grant of the Korea Health 21 R&D project, the Ministry of Health & Welfare, Republic of Korea (A010250)