mutation. There was no gender difference in ER expression. The survival time for patients with the ER mutation was longer (median survival time 44.5 months versus 23.5 months), however these differences were not statistically significant.

Conclusions: There were strong correlation between ERβ and ERCC1 expression. These expressions may play a role simultaneously in the development of adenocarcinoma of the lung.

P3-008 **BSTB: Molecular Pathology Posters, Wed, Sept 5 – Thur, Sept 6**

Identification of DNA methylation markers for NSCLC and adjacent normal lung tissue using Hpall-Mspl Methylation chip

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Introduction: Epigenetic alterations in certain genes are now known as at least important as genetic mutation in pathogenesis of cancer. Especially abnormal promotor region methylation in tumor suppressor genes is known to result in gene silencing and therefore loss of gene function. Objective We, the authors, wanted to search for new lung cancer-specific tumor suppressor genes through the study, and to figure out the roll of known tumor suppressor genes of other kinds of cancer for NSCLC as well.

Material and Methods: Cancer tissue & adjacent normal tissue were obtained from 10 patients who diagnosed with NSCLC and underwent surgery in Konyang university hospital in 2005. NotI-MseI Methylation chip was used to analyze DNA methylation on promoter region of 27 genes in tumor tissue & nearby normally-appearing tissue. The rate of methylation was measured and compared for both groups to find out the genes associated with tomorigenesis. Also the patients were grouped by age, gender, history of smoking, and cell type of NSCLC, and compared between groups. And as normal control group we obtained lung tissue from two young patients with pneumothorax during their bullectomies, methylations were examined in the same way and compared with tumor and non-tumor tissue from NSCLC patients.

Result: Among the 27 genes, the higher rate of methylation for tumor tissue than that of non-tumor tissue were observed in 14 genes, and 6 genes including AR, HTR1B, CFTR from those 14 genes in normal lung tissue were not methylated, suggesting the possibility of the role for TSG(tumor suppressor gene) of NSCLC.

P3-009 **BSTB: Molecular Pathology Posters, Wed, Sept 5 – Thur, Sept 6**

Immunohistochemical study for the expression of DR5 TRAIL receptor in non-small cell lung cancer

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Background: KILLER/DR5 is a recently identified p53-regulated death recpetor gene that was induced by doxorubicine only in cells with wild-type p53 status. KILLER gene was also independently identified as a TRAIL (TNF-related Apoptosis-inducing Ligand) death receptor, DR5. KILLER/DR5 is now considered as one of the p53-dependent apoptotic genes such as fas, bax, or insulin-like growth factor-binding protein 3. However, examination of KILLER/DR5 in primary tumour tissue has not yet been reported. In this study, we demonstrate that KILLER/DR5 expression is dependent on wild-type p53 status in non-small cell lung cancer (NSCLC).

Methods and Materials: Immunohistochemical analysis using the avidin-biotinylated horseradish peroxidase complex was carried out in eighty-nine surgically resected NSCLC formalin-fixed paraffin-embedded tissue sections. As primary antibodies, we used anti-DR5 polyclonal antibody (Pro Sci Inc., Poway, CA) and anti-p53 monoclonal antibody (DO-7, Novocastra, Inc, Manhasset, NY). A negative control was processed with each slide; it excluded the primary antibody but included all other steps of the procedure. Positive tumor cells were quantified twice, expressed as a percentage of the total number of tumor cells, and the intensity of immunostaining: 1+, weak and diffuse(>50%) or focal (<50%) or moderate and focal; 2+, strong and focal or moderate and diffuse; 3+, strong and diffuse. The analysis of DR5 expression was done separately in tumor area and regional normal area.

Results: DR5 expression was high (> 2+) in bronchial epithelium (89% of cases) but almost absent in type I & II pneumocytes, lymphocytes, and smooth muscle cells. High DR5 expression rate in tumor was 28% (15/53) in squamous cell carcinoma, 47%(15/32) in adenocarcinoma, and 50% (2/4) in large cell carcinoma, overall 36%. DR5 expression did not show any statistical significance with T stage, N stage, and survival. However, DR5 expressiont showed significant inverse correlation with p53 expression. ($p < 0.01$). If p53 expression was high, there was no expression in DR5 and vice versa.

Conclusions: This significant in vivo correlation between p53 expression and KILLER/DR5 expression is highly suggestive for the fact that KILLER/DR5 is one of important p53-dependent apoptotic genes.

P3-010 **BSTB: Molecular Pathology Posters, Wed, Sept 5 – Thur, Sept 6**

Using immunohistochemistry to evaluate protein expression levels of female sex hormone receptors (ER, PR) and epidermal growth factor receptor family members (EGFR, HER2) in East Asian non-small cell lung cancers (NSCLC)

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Background: The non-smoking East Asian female with lung adenocarcinoma is a phenotype that has been correlated with higher frequencies of EGFR mutations, with corresponding increased tumor response to tyrosine kinase inhibitors. We hypothesize that estrogen receptor (ER) has a role in the biological mechanism underlying this clinical entity, in a combinatorial fashion with other signaling transduction components. Here, we examine the protein expression levels via immunohistochemistry of isoforms of ER, namely ERα and ERβ, progesterone receptor (PR), EGFR and HER2.

Methods: Tissue microarrays (TMA): These were constructed from paraffin-embedded blocks of surgically resected tissues. Each array was targeted to contain replicates of 33 adenocarcinomas and 16 squamous cell carcinomas, of which 26 and 2 had matched normal lung tissues, respectively.

Immunohistochemistry: Commercially available antibodies identifying ERα, ERβ, PR, EGFR and HER2 were used for staining and detection, according to the manufacturers' protocols. The ER, PR and HER2 analyses used breast invasive ductal carcinomas as positive controls. Extent (% of cells) and intensity of staining were scored on a scale of