P-316 Frequent Aberrant Methylation of gene SAMD 14 in Human Pulmonary Adenocarcinoma

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Methylation is known to play an important role in neoplasia by inactivating tumor suppressor genes. The aim of this study is to detect the abnormally methylated gene in the adenocarcinogenesis using A/J mouse lung adenoma tissue. The PCR-based methylated CpG island amplification technique, modified suppression subtractive hybridization and differential screening were used to identify the differentially methylated sequence. Four genes were identified from A/J mouse adenoma tissue. These were Kif21a, Samd14, EG436235 and Vwa1.Quantitative RT PCR result showed differences in expression level between A/J mouse normal lung tissue and adenoma tissue for Kif21a ($p<0.005$), Samd14 ($p<0.005$) and EG436235 ($p<0.01$) genes. Using homoloGene software, human homologue genes were detected. Further study of the human homologues of KIF21A ($p=0.045$) and SAMD14 ($p=0.007$) showed that they were expressed in normal lung tissue but markedly down-regulated in lung adenocarcinoma tissue. Bisulfite sequencing and MSP revealed that the promtor region of SAMD14 in human lung adenocarcinoma was methylated more frequently than that of its normal counterpart. These data suggest that promotor methylation of this gene is a specific event in pulmonary adenocarcinogenesis, and that their down-regulation may be functionally associated with malignant progression of lung adenocarcinoma.