Determining the Prognostic Value of the DNA Methylation of the GYPC, NME1, and SLIT2 Genes in Human Lung Adenocarcinoma

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Lung cancer is responsible for the highest number of cancer-related deaths worldwide, and lung adenocarcinoma is its most common subtype. This study used statistical analysis to determine the prognostic value of GYPC, NME1, and SLIT2 DNA methylation for lung adenocarcinoma patients, which could aid in lung adenocarcinoma survival predictions and DNA methylation treatment. ANOVA was used to compare GYPC, NME1, and SLIT2 DNA methylation (as beta values) between tumor and non-tumor tissue and demographic features (age, sex, cancer stage, and smoking history). Kaplan-Meier survival analyses and log-rank tests were utilized to determine CpG sites associated with survival and detect differences in survival across demographic groups and DNA methylation levels of the three target genes. This study found significant differences between tumor and non-tumor methylation for two SLIT2 CpG sites ($p = 4.2279e-04$ and $p = 5.0077e-04$) and one GYPC CpG site ($p = 1.2376e-04$). There was also differential methylation based on cancer stage ($p = 0.0228$) and smoking history ($p = 0.0478$) for two SLIT2 CpG sites. Additionally, significant differences were identified in overall survival by cancer stage ($p = 0.0133$) and the methylation levels of a NME1 CpG site ($p = 0.0226$) and a GYPC CpG site ($p = 0.0379$). Lastly, 1426 survival-associated CpG sites were determined. This study achieved its purpose and identified two possible lung adenocarcinoma prognostic biomarkers from the three target genes, along with determining CpG sites that likely play a role in lung adenocarcinoma development and progression due to their differential methylation in tumor tissue.

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