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Integrated analysis of DNA methylation profiling and gene expression profiling identifies novel markers in lung cancer in Xuanwei, China

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Summary: Background: Aberrant DNA methylation occurs frequently in cancer. The aim of this study was to identify novel methylation markers in lung cancer in Xuanwei, China, through integrated genome-wide DNA methylation and gene expression studies. Methods: Differentially methylated regions (DMRs) and differentially expressed genes (DEGs) were detected on 10 paired lung cancer tissues and noncancerous lung tissues by methylated DNA immunoprecipitation combined with microarray (MeDIP-chip) and gene expression microarray analyses, respectively. Integrated analysis of DMRs and DEGs was performed to screen out candidate methylation-related genes. Both methylation and expression changes of the candidate genes were further validated and analyzed. Results: Compared with normal lung tissues, lung cancer tissues expressed a total of 6,899 DMRs, including 5,788 hypermethylated regions and 1,111 hypomethylated regions. Integrated analysis of DMRs and DEGs identified 45 tumor-specific candidate genes: 38 genes whose DMRs were hypermethylated and expression was downregulated, and 7 genes whose DMRs were hypomethylated and expression was upregulated. The methylation and expression validation results identified 4 candidate genes (STXBP6, BCL6B, FZD10, and HSPB6) that were significantly hypermethylated and downregulated in most of the tumor tissues compared with the noncancerous lung tissues. Conclusions: This integrated analysis of genome-wide DNA methylation and gene expression in lung cancer in Xuanwei revealed several genes regulated by promoter methylation that have not been described in lung cancer before. These results provide new insight into the carcinogenesis of lung cancer in Xuanwei and represent promising new diagnostic and therapeutic targets.

Associated Publications: Wang J, Duan Y, Meng Q, Gong R, Guo C, Zhao Y, Zhang Y (2018) Integrated analysis of DNA methylation profiling and gene expression profiling identifies novel markers in lung cancer in Xuanwei, China. PLoS ONE 13(10): e0203155. doi: [10.1371/journal.pone.0203155](https://doi.org/10.1371/journal.pone.0203155)

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