



Identifying differentially expressed genes and pathways in two types of non-small cell lung cancer: adenocarcinoma and squamous cell carcinoma

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ABSTRACT. Non-small cell lung carcinoma, NSCLC, accounts for 80-85% of lung cancers. NSCLC can be mainly divided into two types: adenocarcinoma (ADC) and squamous cell carcinoma (SCC). The purpose of our study was to identify and differentiate the pathogenesis of ADC and SCC at the molecular level. The gene expression profiles of ADC and SCC were downloaded from Gene Expression Omnibus under accession No. GSE10245. Accordingly, differentially expressed genes (DEGs) were identified by the limma package in R language. In addition, DEGs were functionally analyzed by Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathway enrichment. A total of 4124 DEGs were identified, including CDK1, CDK2, CDK4, and SKP2. The DEGs were mainly involved in 16 pathways related to cell proliferation, cell signal transduction and metabolism. We conclude that the molecular mechanisms of ADC and SCC are considerably different, and that they are involved in immune response, cell signal transduction, metabolism, cell division, and cell proliferation. Therefore, the two diseases should be

treated differently. This study offers new insight into the diagnosis and therapy of these two types of lung cancer.

Key words: Non-small cell lung cancer; Adenocarcinoma; Squamous cell carcinoma; Differentially expressed genes