Identification of proteomic differences between squamous cell carcinoma of the lung and bronchial epithelium.

Proteins that exhibit different expression levels in normal and malignant lung cells are good candidate biomarkers to improve early diagnosis and intervention. We used a quantitative approach and compared the proteome of microdissected cells from normal human bronchial epithelium and squamous cell carcinoma tumors of histopathological grades G2 and G3. DIGE analysis and subsequent MS-based protein identification revealed that 32 non-redundant proteins were differentially regulated between the respective tissue types. These proteins are mainly involved in energy pathways, cell growth or maintenance mechanisms, protein metabolism, and the regulation of DNA and RNA metabolism. The expression of some of these proteins was analyzed by immunohistochemistry using tissue microarrays containing tissue specimens of 55 patients, including normal bronchial epithelium, squamous cell carcinomas, adenocarcinomas, and large cell carcinomas. The results of the immunohistochemical studies correlated with the proteome study data and revealed that particularly HSP47 and a group of cytokeratins (i.e. cytokeratins 6a, 16, and 17) are significantly co-regulated in squamous cell carcinoma. Furthermore cytokeratin 17 showed significantly higher abundance in G2 grade.
compared with G3 grade squamous cell carcinomas in both the gel-based and the immunohistochemical analysis. Therefore this protein might be used as a marker for stratification between different tumor grades.