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Comparative Proteomic Analysis of Human Lung Adenocarcinoma Cisplatin-resistant Cell Strain A549/CD

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摘要

Background and objective Chemotherapy plays an important role in the comprehensive therapy of lung cancer. However, the drug-resistance often causes the failure of the chemotherapy. The aim of this study is to identify differently expressed protein before and after cisplatin resistance of human lung adenocarcinoma cell A549 by proteomic analysis. Methods Cisplatin-resistant cell strain A549/CDDP was established by combining gradually increasing concentration of cisplatin with large dosage impact. Comparative proteomic analysis of A549 and A549/CDDP were carried out by means of two-dimensional gel electrophoresis. The differentially expressed proteins were detected and identified by MALDI-TOF mass spectrometry. Results Eighty-two differentially expressed proteins were screened by analysis the electrophoretic maps of A549 and A549/CDDP. Six differential proteins were analyzed by peptide mass fingerprinting. Glucose regulating protein 75, ribosomal protein S4, mitochondrial ATP synthase F1 complex beta subunit and immunoglobulin heavy chain variable region were identified. All four differentially expressed proteins were over-expressed in A549/CDDP, whereas low-expressed or no-expressed in A549. Conclusion These differentially expressed proteins give some clues to elucidate the mechanism of lung cancer cell resistant of cisplatin, providing the basis of searching for potential target of chemotherapy of lung cancer.

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