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Analysis of Differentially Expressed Proteins in Self-Paired Sera of Advanced Non-small Cell Lung Cancer Patients Responsive to Gefinitib

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摘要

Background and objective All the advanced NSCLC patients that received EGFR-TKI therapy will eventually relapse after a period of efficacy. The aim of this study is to investigate the serum biomarkers as potential predictive factors for the efficacy of epidermal growth factor receptor (EGFR) tyrosine kinase inhibitor (TKI) targeted therapy in advanced non-small cell lung cancer. Methods Twenty self-paired serum samples were collected from 9 advanced NSCLC patients that evaluated as disease control (SD or PR) after gefinitib therapy, at the time points of before and after gefinitib treatment but 2 weeks before being evaluated as disease progress. All samples were pre-separated by WCX microbeads, and then detected on the MALDI-TOF-MS platform of Bruker AutoflexTM. ClinProTools (Version: 2.1) was used to analyze the differentially expressed proteins. Results There were 7 protein peaks (m/z), 3 242.09, 8 690.36, 2 952.64, 3 224.04, 1 450.51, 1 887.8 and 3 935.73 found statistically differentially expressed between the self-paired samples. Three proteins (3 242.09, 2 952.64 and 3 224.04) were down-regulated and four proteins (8 690.36, 1 450.51, 1 887.8 and 3 935.73) up-regulated in gefinitib treated sera. Conclusion The data here suggest that several specific protein peaks might indicate gefinitib resistance, yet the identities of these proteins and the mechanisms underlying the responsiveness to gefinitib treatment need further investigation.

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