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ORIGINAL ARTICLE

Identification of Potential Biomarkers of EGFR Mutation in Pleural Effusion of Non-Small Cell Lung Cancer Patients Based on Metabolomics

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SUMMARY

Background: **Malignant pleural effusion (MPE) is a common complication of non-small cell lung cancer (NSCLC). Patients with NSCLC exhibit a high rate of epidermal growth factor receptor (EGFR) mutations. The detection of EGFR mutations is usually time-consuming and costly. This study aimed at identifying potential biomarkers of EGFR mutations in MPE of NSCLC patients by metabolomics.**

Methods: **In total, 58 MPE samples from 30 EGFR mutant and from 28 wild-type NSCLC patients were collected and analyzed by using hydrogen nuclear magnetic resonance (^{1}H NMR) based metabolomics and UPLC-MS/MS based amino acid analysis.**

Results: **Our ^{1}H NMR study showed a significant increase in the lysine levels but a significant decrease in the alanine levels in MPE of NSCLC patients with EGFR-mutant. Twelve amino acids in MPE were further determined by UPLC-MS/MS. It showed that alanine in MPE (6.34 ± 1.88 vs. 8.73 ± 3.68) were significantly decreased and leucine (3.13 ± 0.57 vs. 2.22 ± 0.13), lysine (2.19 ± 0.50 vs. 1.53 ± 0.40), and tyrosine (2.69 ± 0.71 vs. 1.89 ± 0.46) were increased in the EGFR mutation group; leucine (2.19 ± 0.50 vs. 1.53 ± 0.40), methionine (2.19 ± 0.50 vs. 1.53 ± 0.40), and threonine (2.19 ± 0.50 vs. 1.53 ± 0.40) in MPE were significantly lower in the EGRF 19 mutation compared with 21 mutation patients. The area under the receiver operating characteristic curve of 0.851 and 0.931 would be achieved by the logistic model for classification of EGFR-mutant patients from the wild-type controls or the exon 19 from exon 21 mutant patients.**

Conclusions: **Amino acids in MPE are significantly altered and helpful in the diagnosis of EGFR-mutant patients from the wild-type controls or the exon 19 from exon 21 mutant patients with high accuracy, which is worthy of further study.**

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Supplementary Data

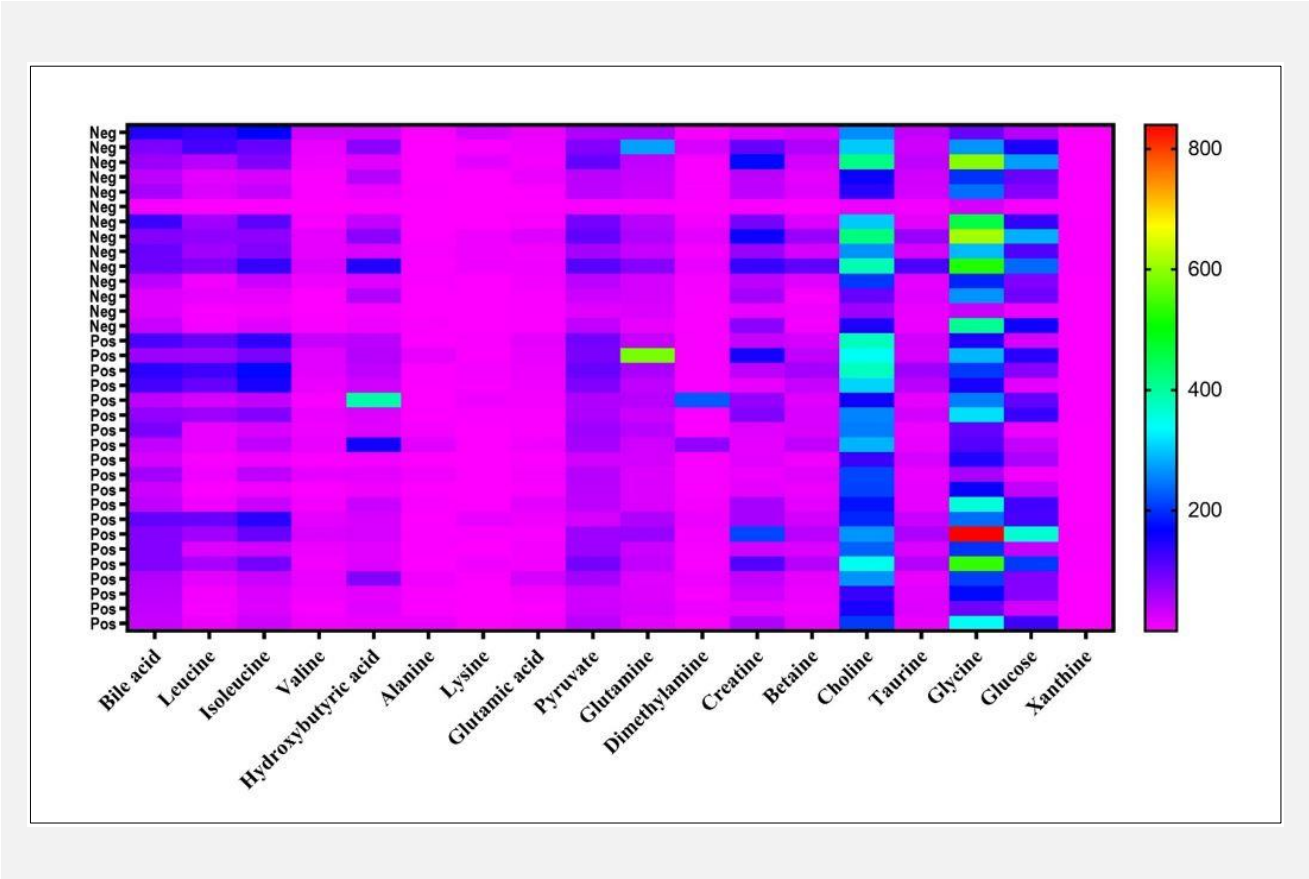

Figure S1. Heat map of metabolite levels based on ^{1}HNMR data in MPE for classification of EGFR mutant (pos) and wild-type (neg).