Global profiling studies in tumor bearing mouse models using high mass accuracy MSn analysis

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Overview

Global metabolic profiling provides an insight into the phenotype of biological systems and the pathophysiologic processes related to disease. In this paper, we describe the application of a LC/MS-IT-TOF to metabolic profiling in several colorectal and non small cell lung cancer cell tumors.

Results

Table 1: Sample and compound identification rates for UPLC-MS/MS analysis of tumor tissue extracts. The confidence level of each compound was calculated from a combination of data on the reconstructed exact mass of the precursor, fragment ions, and retention time. For the sample with the highest number of compounds identified, the confidence level was 99.9999%

Table 2: Relative changes in the levels of amino acids and lipids accounted for changes in the tumor extracts. The PCA analysis shows clear differentiation between NSCLC cell line (CALU6) and CRC cell lines.

Discussion and Conclusion

Integrative global metabolic profiling has been applied to analysis of endogenous metabolite levels in colorectal and non small cell lung cancer tumors implanted in mice. The changes in amino acid and lipid levels provide a useful framework to differentiate the tumor cell lines. The PCA analysis shows clear differentiation between NSCLC cell line (CALU6) and CRC cell lines.