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Metabolomics Profile Recognition for Cancer Diagnostics

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Abstract : Metabolomics has become a rising field of research for various diseases, particularly cancer. Increases or decreases in metabolite concentrations in the human body are indicative of various cancers. Further elucidation of metabolic pathways and their significance in cancer research may greatly spur medicinal discovery. We analyzed the metabolomics profiles of lung cancer. Thirty-three metabolites were selected as significant. These metabolites are involved in 37 metabolic pathways delivered by MetaboAnalyst software. The top pathways are glyoxylate and dicarboxylate pathway (its hubs are formic acid and glyoxylic acid) along with Citrate cycle pathway followed by Taurine and hypotaurine pathway (the hubs in the latter are taurine and sulfoacetaldehyde) and Glycine, serine, and threonine pathway (the hubs are glycine and L-serine). We studied interactions of the metabolites with the proteins involved in cancer-related signaling networks, and developed an approach to metabolomics biomarker use in cancer diagnostics. Our analysis showed that a significant part of lung-cancer-related metabolites interacts with main cancer-related signaling pathways present in this network: PI3K–mTOR–AKT pathway, RAS–RAF–ERK1/2 pathway, and NFKB pathway. These results can be employed for use of metabolomics profiles in elucidation of the related cancer proteins signaling networks.

Keywords: cancer, metabolites, metabolic pathway, signaling pathway

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