Innovative approaches in metabolomics for understanding drug resistance in breast cancer

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Breast cancer is one of the leading causes of death worldwide. In Pakistan, prevalence of this ailment is highest amongst all types of cancer i.e. 38.5%. Major clinical setback is drug resistance in breast cancer. Metabolomics is an emerging field that utilizes information of cellular biochemistry for the early detection, diagnosis and establishment of predictive biomarkers of breast cancer. This review highlights potential metabolomics applications to clinical pharmacology. The methodology is based on inclusion exclusion criteria. Literature survey and questionnaire were included while clinical trial was excluded. This report provides a review of 12 articles out of few were excluded. The objective was to explore 1) early breast cancer detection, 2) increasing life expectancy of cancer patients and 3) mechanisms for breast cancer drug resistance. According to the survey, the average response rate of a cancer drug is the lowest at 21%, suggesting that 79% of patients with cancer are over-dosed. While according to an international study, 40%–50% of breast tumors will display acquired resistance. When specific therapies are chosen on the basis of a patient’s metabolomics profile, it will give rise to customized medicine and personalized tailored treatment. Using high-throughput information using metabolomics to clinical diagnosis and treatment can help accelerate the patient safety, quality of life and survival rate by identifying pathways involved in drug resistance. Metabolomics is future of anti-cancer pharmacology; following “the right drug for the right patient at the right time” can offer safety, quality and effectiveness of anti-cancer treatment.

Evaluation of Rac1 and Rac1b in serum of non-small cell lung cancer

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Rac proteins are found to play major role in tumorogenesis. This study aimed to quantify Rac1 and Rac1b in serum of non-small cell lung cancer (NSCLC) patients. The blood of 77 NSCLC patients and 52 healthy controls were collected and the concentration of Rac1 and Rac1b was quantified mainly by surface plasmon resonance and was verified by Western blot analysis. Statistical analyses of all the data were performed by Graph Pad Prism version 5.0. Rac1 and Rac1b both were found to be significantly over expressed in lung cancer patients compared to healthy controls. The levels of Rac proteins were found to be elevated in all stages of cancer. Despite the low survival rate, we managed to collect serum sample of the 18 follow up patients after the therapy, where 11 patients of CR+PR group showed down regulation of the Rac protein after therapy and unfortunately 80% patients died during the study period. This study first time reported the elevated level of Rac protein in serum of NSCLC patients. The high specificity and sensitivity obtained from ROC analysis for Rac1 and Rac1b envisaged it to be used as a serum diagnostic marker in early stage of cancer.

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