Metabolic reprogramming in breast cancer patients as revealed by 1H NMR spectroscopy

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Presenter Information (List ALL Authors)

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Background: Breast cancer is a global health concern among women. Several metabolic pathways are dysregulated in breast cancer cells, including alterations in energy metabolism, amino acid metabolism, and lipid metabolism. Reprogramming of metabolic pathways may facilitate inappropriate proliferation of cancer cells and adaptation to the tumor microenvironment. Long non-coding RNAs (lncRNAs) have emerged as important regulatory targets in the process of tumorigenesis. However, the role of lncRNAs in the process of metabolic reprogramming is not properly known. Exploring metabolic alterations and its association with lncRNAs expression might be helpful for developing new biomarkers and therapeutic targets for cancer management.

Objectives: Serum from 43 breast cancer patients and 13 healthy individuals were used for the analysis of metabolic profile.

Methods: For the identification and quantification of metabolites, ^{1}H NMR spectroscopy was used while for lncRNAs expression, q-RT-PCR was used.

Results: Metabolites such as amino acids, lipids, membrane metabolites, lipoproteins, and energy metabolites were observed in the serum of both patients and healthy individuals. The serum of patients and healthy individuals produced measurable amounts of metabolites related to lipoproteins, amino acids, membrane, lipids, and energy. The unsupervised PCA, supervised PLS-DA, supervised OPLS-DA, and random forest classification analyses revealed alterations in more than 25 metabolites. Further analysis of metabolites with AUC value >0.9 revealed significant elevation in the levels of LPR, glycerol, and lactate, while the levels of succinate, glucose, and isobutyrate was reduced in comparison to healthy control. The advanced stage breast cancer patients revealed alterations in these metabolites (except LPR) in comparison to early breast cancer patients. Over 25 metabolic signaling pathways were associated with altered metabolites. Further, a dysregulation in MEG3, H19, and GAS5 lncRNAs were observed in the breast tumor tissue in comparison to normal adjacent tissue.

Conclusion: The study reveals that metabolic pathways are altered in breast cancer patients. The study also opens a window for examining the association of lncRNAs with metabolic patterns in patients.