Expression of microRNA Change after Chemotherapy in Breast Cancer Patients

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Abstract:

Background

Breast Cancer continues to be the second leading cause of cancer related death in women in the United States only after lung cancer. Even with early detection and new treatments, some patients, unfortunately, have further progression of disease even on definitive treatment or have a recurrence of their cancer within a short period of time. There continues to be a need for new targets for therapy and new markers for early identification of disease or monitoring treatment success. MicroRNAs (miRNA), small non-coding RNAs, function in gene regulation and proper cell function. *In* vitro experiments have linked miRNAs including 23b, 27b, and let-7a to breast cancer metastasis and may play a role in the pathogenesis and progression of cancer. Our lab has recently shown there was increased miRNA expression of let-7a and 125a in patients with breast cancer compared to controls without any known cancer. In this study, we look to examine the differential expression of miRNA before chemotherapy and after definitive treatment. We hope to identify molecular markers that may serve to identify early recurrence of disease which may help patients make informed decisions about their treatment options.

Study Design: Several newly diagnosed breast cancer patients were recruited between April 2021 to December 2022 at the University Medical Center New Orleans. Plasma samples were collected at diagnosis and after their last chemotherapy treatment. Plasma miR-125-3p, 23b, 27b, let-7a, 192-5p, 451a were isolated and their expression was measured using qRT-PCR method.

Results:

Expression of miR-let-7a and miR-451a was significantly decreased in circulating plasma for breast cancer patients' post-chemotherapy compared to their baseline plasma at diagnosis. However, there was no significant differential expression of miRNA 125-3p, 23b, 27b, and 192-5p.

Conclusion:

Circulatory miRNAs represent the potential to serve as diagnostic biomarkers, markers for molecular identification of residual disease, stratification of risk of recurrence and monitoring of treatment. The role of miRNAs expression after chemotherapy should be further explored with a larger patient population. We plan to expand our study to include a larger patient population including patients from another institution. We also hope to explore the differential expression of miRNA in paraffin tissue sections and how it differs from plasma samples.

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