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"Comparative miRNA Profiling in Breast Cancer Tissue and Plasma"

Micro-RNAs (miRNAs) have been shown to regulate oncogene and tumor suppressor pathways and are often dysregulated in breast cancer impacting progression of malignancies. Their presence in circulation has led to interest in their potential use as non-invasive tumor biomarkers. This study aims to characterize miRNA expression patterns in breast cancer tissues and compare them across clinical and demographic subgroups, along with the future aim of comparing tumor expression and plasma levels.

Archived formalin-fixed paraffin-embedded (FFPE) breast cancer samples (n=106) are currently being processed using the Qiagen AllPrep DNA/RNA FFPE Kit. Total RNA is quantified and quality assessed by Nanodrop, converted to cDNA via reverse transcription, and analyzed via quantitative PCR (qPCR). Expression patterns of 9 candidate miRNAs are measured using miR-16 as loading control. Delta Ct values were compared between tumor and normal tissues, as well as across clinicopathologic subgroups using independent t-tests with Welch's correction. Fold changes were calculated from delta-delta Ct values.

To date, analysis has been completed for a subset of samples (n≈30). In comparison of patient matched tumor and healthy tissue, multiple miRNAs showed altered trends in expression, with let-7d particularly showing a strong trend toward significant down regulation (p=0.051, n=12 vs 11). Furthermore, exploratory subgroup analyses suggest differences by nodal status, tumor laterality, and race. Exploratory results showed miR-192 downregulation in node-positive tumors compared to node-negative tumors (p=0.097, n=3 vs 3), miR-23a upregulation in left-sided tumors compared to right-sided tumors (p=0.022, n=3 vs 4), and miR-192 upregulation in African American patients compared to Caucasian patients (p=0.033, n=2 vs 6). Initial exploratory findings are limited by subgroup sizes and potentially confounding variables but represent potential directions for further investigation as the project progresses.

Our preliminary analyses suggest that let-7d, miR-192, and miR-23a may play roles in breast cancer biology, with expression differences observed by tumor presence, nodal status, laterality, and race. While plasma analyses and expanded clinical correlations are ongoing, these early findings highlight biological signals of interest with continued processing and analysis underway.