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“Investigating microRNAs as a Biomarker for Analyzing Racial and Gender Disparities in B-cell ALL Patients”

Leukemias are hematologic malignancies. They develop due to failures in the process that creates normal leukocytes, causing an accumulation of immature, dysfunctional cells. The disease is typically classified based on cell differentiation and the cell primarily involved. Cell differentiation determines whether leukemia can be categorized as myelocytic or lymphatic. Leukemia is the eleventh leading cause of cancer deaths globally. According to the Leukemia and Lymphoma Society, in the United States, there are currently 376,508 leukemia patients either living with the disease or are in remission. There are four types of leukemia, and our research specifically focuses on B-cell acute lymphoblastic leukemia, which is caused by an excess of B lymphoblasts malignancies in the bone marrow.

One factor that can influence the initiation and further development of leukemia is epigenetic regulators, which include microRNAs and noncoding RNAs. Evidence reveals that miRNAs can be used as biomarkers in order to examine the early stages of leukemia as well as viewing the result of chemotherapy on the progression of the disease. A difference in microRNA expression is included in the epigenetic variations that impact the progression of leukemia. Specifically in acute myeloid leukemia, miRNA has been found to impact all parts of the progression of AML development: including a patient's survival rate, the differentiation in the progression of their disease, and cell proliferation.

Gender disparities in leukemia have not yet been well-studied; males are more affected by leukemia than females. In chronic myeloid leukemia, women are typically diagnosed at a later stage and have lower platelet counts compared to men. However, when diagnosed, men are found to have higher hemoglobin levels, a larger spleen size, and abnormalities in gene expression. In all blood cancers, which includes leukemia, White patients are diagnosed with blood cancers more frequently, yet Black and Hispanic patients with acute myeloid leukemia have a worse survival rate. We aim to analyze miRNA expression in B-cell acute lymphoblastic leukemia using the publicly available data set from TCGA. Due to the limitation of our data set, we limit our analysis among male and female, and Hispanic and non-Hispanic patients. We found differentially expressed miRNA signatures in the patients, including hsa-let-7a, hsa-mir-92a, hsa-mir-93, hsa-mir-103a, hsa-mir-181a, hsa-mir-28, hsa-mir-30d, and hsa-mir-30e. Differentially expressed miRNA signatures vary among male versus female and Hispanic versus non-Hispanic patients. Further analysis is ongoing to determine the association of miRNA signatures and survival of leukemia patients. The result of this project will help us to determine miRNA signatures as a biomarker of B-cell acute lymphoblastic leukemia.