10-31-2023

Analyzing prominent genes in Acute Lymphocytic Leukemia (ALL)

shima z. omar
Georgia Southern University

Analyzing prominent genes in Acute Lymphocytic Leukemia (ALL)

An Honors Thesis submitted in partial fulfillment of the requirements for Honors in *Department Biology.*

By
Shima Omar

Under the mentorship of *Professor Aaron Schrey*

ABSTRACT
Acute lymphocytic leukemia (ALL) is the most common type of childhood cancer. Leukemia is a type of cancer that involves the bone marrow and blood. This research study examined prominent genes in the disease. Two groups of genes, tumor suppressor and cell differentiation, were compared using statistical analysis to compare their binding potential and epigenetic potential. It is most likely that I failed to detect significant differences either because these genes' function in the disease etiology is not strongly contexed to changes in expression, or that the magnitude of the differences were too slight to be detected with these methods. Childhood cancer is the number one cause of disease in children in the United States yet receives only 4% of funding per year. This lack of funding could potentially close the door on discovering new, safer treatments for children.

Thesis Mentor: *Dr. Aaron Schrey*

Honors Dean: Dr. Steven Engel

November 2023
Biology Department
Honors College
Georgia Southern University

Introduction

Acute Lymphocytic Leukemia (ALL) is a type of illness that impacts children and adults all around the world. I've personally seen how it impacts children and families at my workplace. While working at the local children's hospital, I've noticed how some children would stay in remission successfully while other would relapse with the cancer coming back worse. Forming relationships with patients and the families that have been impacted by ALL has made me interested in researching its genetics. In particular, I am interested in the genetics of leukemia and what parts of the human genome the disease attacks.

Leukemia is a type of cancer that involves the bone marrow and blood. Acute lymphocytic leukemia (ALL) is the most common type of childhood cancer. Around ¾ children diagnosed with leukemia are diagnosed with ALL (Terwilliger & Abdul-Hay, 2017). It is most common during early childhood around the ages 2-5. This occurs when there is a mutation in the cell that develops into bone marrow. The rate at which these cells grow become uncontrollable and bone marrow creates immature cells called lymphoblasts. These cells are dysfunctional and impact other healthy cells (Terwilliger & Abdul-Hay, 2017).

Methods

To study the genetics of Leukemia, 6 prominent genes that are associated with the disease were researched and found to be NPM1, KRAS, TP53, GATA2, CEBPA, and ASXL3 (Yokota & Kanakura, 2016). Characters such as being tumor suppressors or being able to differentiate blood cells were noted. The three tumor suppressor genes found to be prominent in ALL are TP53, NPM1, and *KRAS* (*Genes*, 2023). The three cell differentiation genes were GATA2, *CEBPA*, *ASXL3* (*Genes*, 2023).

Using GenBank, the genome sequence for the promoter was identified for each gene. The epigenetic potential and biding site potential were found for each gene. To find the epigenetic potential, which is the capacity for environmentally induced phenotypic change, the number of CG bases was divided by the number of total bases. To find the binding site potential, which is the region where a transcription factor may bind, the online program "Alibaba2" An unpaired T-test was performed to compare the binding site potential and epigenetic potential between the three tumor suppressor genes and the three cell differentiating genes.

Results

The t test revealed that the difference between the tumor suppressor genes and epigenetic potential, for both the binding site potential and epigenetic potential, were non-statistically significant ($P > 0.05$). The *t* test P-value for binding potential was 0.23 while the *t* test P-value for the epigenetic potential was 0.6215. This suggests that these genes have similar regulatory potential.

Discussion

It is most likely that I failed to detect significant differences either because these genes' function in the disease etiology is not strongly contexed to changes in expression, or that the magnitude of the differences were too slight to be detected with these methods. Childhood cancer is the number one cause of disease in children in the United States yet receives only 5.5% of funding in 2022 (*NCI Budget Fact Book*, 2023). This lack of funding could potentially close the door on discovering new, safer treatments for children.

Works Cited

Genes. MedlinePlus. https://medlineplus.gov/genetics/gene/

NCI Budget Fact Book. National Cancer Institute. https://www.cancer.gov/about-nci/budget/fact-book

Terwilliger, T., & Abdul-Hay, M (2017). Acute lymphoblastic leukemia: A comprehensive review and 2017 update. *Blood Cancer Journal*. https://doi.org/10.1038/bcj.2017.53

Yokota, T., & Kanakura, Y. (2016). Genetic abnormalities associated with acute lymphoblastic leukemia. *Cancer Science*. https://doi.org/10.1111/cas.12927