Bioinformatics Studies for Biomarker Identification in Chronic Lymphocytic Leukemia (CLL)

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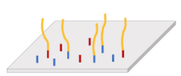
Abstract

Chronic Lymphocytic Leukemia (CLL) is a serious blood cancer. CLL affects white blood cells, mainly B cells. CLL cancer cells spread through the blood and bone marrow of the host. Eventually CLL can cause the bone marrow to lose its function. The main factors that cause Chronic Lymphocytic Leukemia are not known. It is unclear if certain chemicals cause or increase CLL. Hopefully in the future, researchers will be able to find out the main risk factors of CLL. The problem is that CLL cases are consistently rising and getting harder to understand, Also if we don't find a way to reduce the risk it can only get worse from here. The purpose of this project is to identify some of the major elements that cause CLL. CLL usually affects older adults, mainly people over the age of 60. It is more common in Men than Women. Some people with CLL have family members with the same disease, basically stating that CLL can be passed on down generations.

Background

CLL is a type of cancer that affects the white blood cells, specifically the lymphocytes. It is the most common type of leukemia in adults, particularly in older individuals. CLL is characterized by the accumulation of abnormal lymphocytes in the blood, bone marrow . In early-stage CLL or when there are no significant symptoms, the doctor may recommend close monitoring of the disease without immediate treatment. Chemotherapy with drugs that kill cancer cells may be administered orally or intravenously. Targeted therapy can be medications that specifically target certain molecules or pathways involved in CLL cells' growth and survival. Immunotherapy include drugs that enhance the body's immune system to recognize and attack cancer cells. In some cases, a stem cell transplant may be considered, particularly for younger patients or those with high-risk disease.

Next Gen Sequencing



Next-generation sequencing (NGS) is a massively parallel sequencing technology that offers ultra-high throughput, scalability, and speed. The technology is used to determine the order of nucleotides in entire genomes or targeted regions of DNA or RNA.

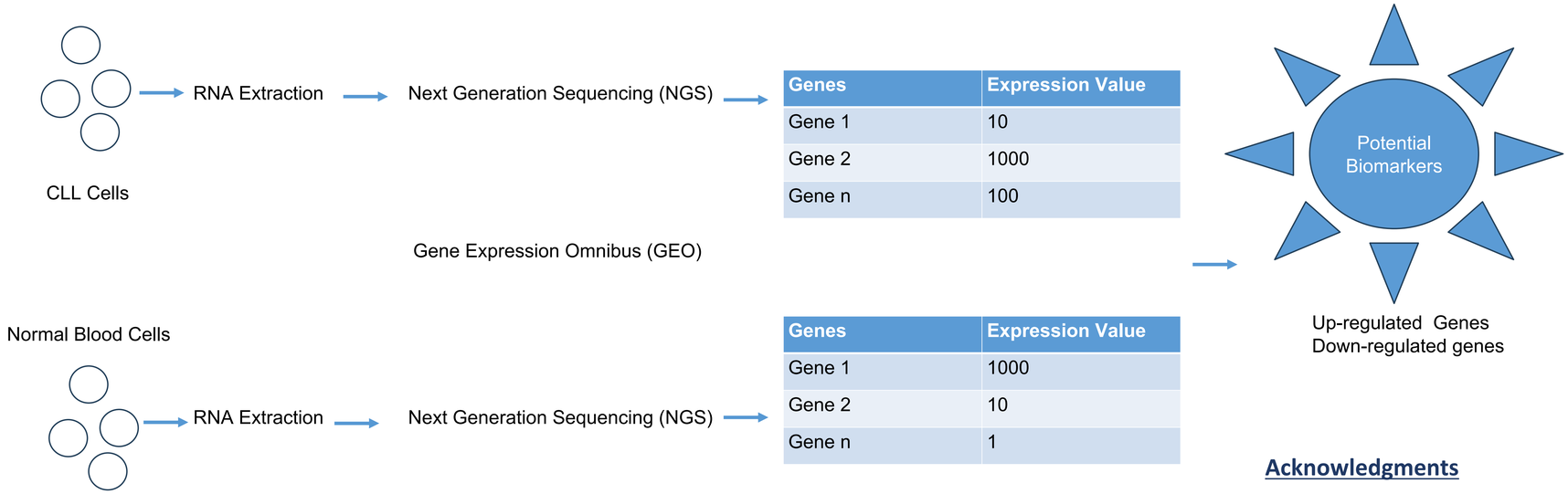
Below chart #1 shows the survival rate of CLL split into the different races. White Americans have a higher rate of obtaining CLL than any other race. To be exact 87%-89% of CLL patients are white.

SEER 22 5-Year Age-Adjusted Incidence Rates, 2015-2019‡	
White	5.1 per 100,000
Black	3.2 per 100,000
Hispanic (any race)	2.1 per 100,000
Asian	1.1 per 100,000

‡ From publicly available SEER*explorer data

Chronic lymphocytic leukemia prognosis and results might vary greatly from person to person. The results are influenced by factors such as the stage and intensity of the disease, genetic variations, age, general health, and response to treatment.

Analysis Pipeline



Conclusion

CLL is a form of cancer that affects white blood cells known as lymphocytes. It typically affects elderly people and is identified by an increase of abnormal lymphocytes in the blood, bone marrow, and lymph nodes. While CLL is typically thought to be a slow-progressing disease, the course can vary from person to person, and some people may suffer a more severe version of the disease. CLL is diagnosed using a series of procedures, including blood testing, bone marrow biopsies, and imaging studies. Treatment choices are determined by standards such as illness stage, general health, and personal preferences. These may include observation, chemotherapy, targeted treatment, immunotherapy, and, in certain situations, stem cell transplantation.

Using the bioinformatics analysis pipeline shown below, differentially expressed up and down-regulated genes can be analyzed comparing CLL and normal cells utilizing NGS technology. The selected genes can predict the prognosis of CLL patients, further they can also be used to study downstream pathways or proteins affected in these patients for developing effective drug targets.

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