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B-Cell Specific Gene Expression Pathways Show No Significant Change from Stage I to Stage IV in Diffuse Large B-Cell Lymphoma

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B-cell specific gene expression pathways show no significant change from stage I to stage IV in diffuse large B-cell lymphoma

Rachel Skabelund, Stephen Piccolo, Kim O’Neill

Introduction

Diffuse large B-cell lymphoma (DLBCL) is a type of non-Hodgkin’s lymphoma that affects over 18,000 new patients every year. It is characterized by aggressive growth in B-cell populations and can form tumors in any organ in the body.

Previous studies in other cancer types have analyzed changes in gene expression between the stages of cancer to understand how the disease progresses from stage I to stage IV. However, very little research is available for DLBCL. Survival analyses show that patients diagnosed with higher stages DLBCL have significantly worse outcomes for both the Ann Arbor clinical staging method and the International Prognostic Index (IPI) staging method. This indicates that DLBCL stages must have different underlying factors that lead to poor patient outcomes.

Using gene set omics analysis (GSOA), we analyzed B-cell specific gene expression pathways in consecutive stages of diffuse large B-cell lymphoma to understand if there were specific pathways that changed their expression from one stage to the next.

Methods

GSOA Algorithm:

1. The researcher inputs two distinct groups, omic data, and a list of gene expression pathways into the algorithm
2. The algorithm attempts to differentiate between the two groups by comparing the gene expression levels of each gene in that pathway
3. If the algorithm successfully differentiates between the two groups, that pathway is considered significantly different between the groups and further research can then be done to determine why there’s a difference.

Results

Although the survival analyses showed significant differences between the stages of DLBCL, the GSOA algorithm did not find any significant changes in B-cell specific gene expression pathways between each stage in either staging system.

Future Directions

While this study didn’t find any statistically significant gene expression pathways, future studies may be able to discover changes in gene expression between different stages of diffuse large B-cell lymphoma. The current analysis focused on B-cell specific gene pathways, and future analyses should examine a broader range of pathways that are common between B-cells and other cell types.

Previous research has determined that diffuse large B-cell lymphoma is made up of two main subtypes, germinal B-cell (GBC) and activated B-cell (ABC). These two subtypes originate from different points in the life of a B-cell, and likely have different molecular pathways that are affected during tumorigenesis. The current analysis didn’t differentiate between the two subtypes, and that could have been a confounding factor in the experiment. To account for this, further analyses should be run using only GBC or ABC subtypes, and other clinical factors such as age, comorbidity, or treatment type should also be analyzed to determine if these variables affect gene expression or survival rates.

Key Terms

Omic Data: Quantitative data describing the components of a cell, i.e. genomic, transcriptomic, proteomic, etc.

Ann Arbor Clinical Staging: Defines cancer stage based on how much it has spread in the body. Stage I shows cancer in one lymph node, stage IV shows cancer spread throughout the body

IPI Staging Method: A newer staging method that includes cancer location, age of the patient, and other risk factors

References