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Title

Evaluation of gene expression profiles of CLL disease via bioinformatics analysis

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Introduction

chronic lymphocytic leukemia (CLL) is a type of cancer that affects the white blood cells, specifically the lymphocytes, the cells responsible for antibodies production. Chronic lymphocytic leukemia characterized by the excessive production of abnormal lymphocytes, which accumulate in the blood, bone marrow, and lymph nodes. The genetic differences between normal B cells and CLL cells play a crucial rule in the development and progression of the disease. In this research, our aim is to identify some of the genetic differences and therapeutic targets that could improve the patient outcomes.

Methodolgy

the study conducted a bioinformatics analysis of gene expression profiles in chronic lymphocytic leukemia (CLL) disease. We utilized three datasets from the Gene Expression Omnibus and merged them for meta-analysis. The differentially expressed genes were identified, and the pathways associated with these genes were determined. The results of meta-analysis were presented using heat maps to display both unregulated and downregulated genes. Pathway enrichment analysis was then conducted to identify the pathways to which these genes belonged. We utilized Venn diagram to display the overlapping pathways between the datasets.

Results

the findings showed that the MAP2K6 gene and PDGFD gene were unregulated in at least two of the three pathways we chosen. On the other hand, the IL6 gene, which is associated with cancer, we found to be downregulated in all three pathways. Further investigation revealed that according to a comparative study done in 2001, IL-6 was undetectable in 41% of CLL patients and that the detection of IL-6 resulted from previous treatment of the disease.

Conclusion

This study aimed to identify transcriptomic differences between CLL and normal B cells. By identifying the pathways associated with these genes, we aim to contribute to the treatment and prevention of the disease. Overall, the study successfully conducted a bioinformatics analysis of gene expression profiles in CLL. The use of meta-analysis and pathway enrichment analysis provided valuable insights into the genetic differences and pathways involved in CLL. The findings regarding the upregulation of MAP2K6 and PDGFD genes and the downregulation of IL6 gene contribute to the understanding of CLL and its potential treatment options.

Recommendation

Acknowledgements