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Alterations in the Genes Expression Profile of Hematopoietic Stem Cell led to Pediatric B-Cell Acute Lymphoblastic Leukemia

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Background

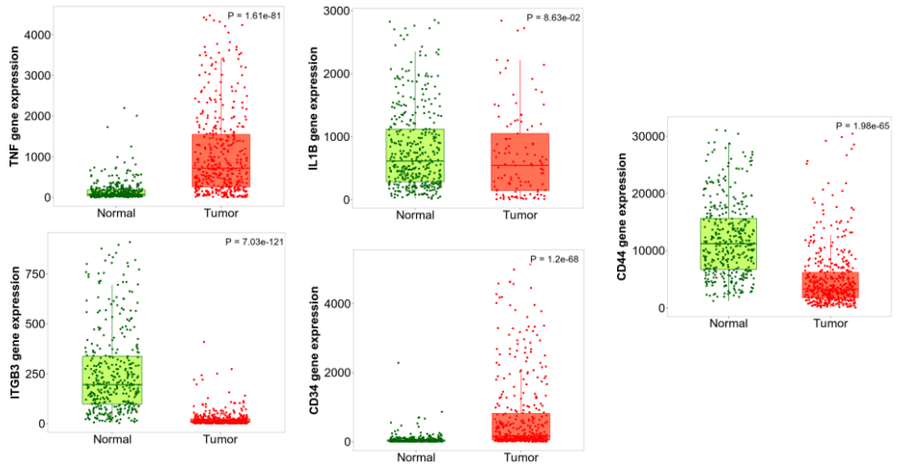
- Pediatric B-cell acute lymphoblastic leukemia (B-ALL) is characterized by the lymphoid progenitor cells' exponential proliferation inside the bone marrow.
- Numerous studies conveyed that the tumorigenesis of B-ALL is associated with several mutations, including ETV6-RUNX1, BCR-ABL-1, RAS, and PI3K, that are leading to cell cycle dysregulation.
- One of the important things to mention is that perturbation of hematopoietic stem cells (HSCs) homeostasis leads to malignancy.
- In this study, we analyzed online databases to find novel biomarkers in patients with pediatric B-ALL.

Materials and Methods

- The GEO database was searched for pediatric B-ALL, the expression array with accession number GSE128254 was selected. Afterward, via the GEO2R, the data of patients with ALL were compared with normal controls. The genes with altered expression (|logFC| >1) were analyzed by Cytoscape 3.8, and hub genes were demonstrated. Differentially expressed genes (DEGs) were analyzed to reveal the genes ontology and protein-protein interaction.

Results

- The KEGG pathway analyses conveyed that DEGs were strongly associated with the proteoglycans in cancer, focal adhesion, and programmed cell death.
- Interestingly, most of these genes are in the extracellular region part with protein binding function. Nine hub genes were identified from the PPI network in which five genes (CD44, CD34, TNF, ITGB3, and IL1B) had a potential impact on the hematopoietic cell lineage differentiation pathway were selected.
- Ultimately, gene expression analyzes revealed that CD44 and ITGB3 were significantly downregulated. On the other hand, CD34 and TNF were significantly upregulated, while the expression of IL1B was not significantly altered in tumoral cells compared to normal cells.



Conclusion

- These results revealed that perturbations in the hematopoietic cell differentiation could be one of the main reasons for tumorigenesis in lymphoid progenitor cells and could be served as potential biomarkers.

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