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Evaluation of *GAB1* role in pediatric B-cell acute lymphoblastic leukemia

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Abstract

Backgrounds: Acute lymphoblastic leukemia (ALL) is a malignancy in which excessive proliferation of immature lymphoid cells leads to reduction of normal bone marrow cells. It most commonly affects B lymphoblasts where it results in B-ALL and is the most frequent pediatric cancer. A better pathophysiological understanding of this cancer may help create treatment options with less side effects and toxicity. Thus, *GAB1* (Grb2-associated binder 1), an adaptor protein involved in intracellular signal transduction by receptor tyrosine kinases, may be of special interest as it plays an important role in the development of various cancers. However, its role in B-ALL is still unclear. Differential gene expression (DGE) and co-expression analyses may help to explain the role of *GAB1* in this malignancy.

Materials and Methods: RNA-seq raw data samples were obtained from 4 datasets of BioProject at NCBI database. After pre-processing, data normalization and DGE analysis were performed using the DESeq2 package in R. Then, for gene co-expression and correlation analysis of *GAB1*, WGCNA (Weighted correlation network analysis) package in R and GraphPad Prism were utilized, respectively.

Results: *GAB1* was differentially expressed in B-ALL patients compared to the control group (log2FC= 4.90, p< 0.0001). Based on the WGCNA algorithm, *PXDN*, *RN7SL1*, *LEF1, NRIP1* and *UBASH3B* genes had the most significantly related co-expression with *GAB1*. Also, their positive correlation confirmed in GraphPad Prism.

Conclusion: Based on our findings, overexpression of *GAB1* may result in upregulation of genes responsible for cell growth and proliferation. Indeed, *GAB1* may play an important role in increasing the proliferation of immature B cells.

Keywords: *GAB1*, RNA-seq, Differential expression, B-ALL