The Role of QRSL1 in Clinical Subtypes and Prognosis of Childhood B-cell Acute Lymphoblastic Leukemia

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Abstract

B-cell acute lymphoblastic leukemia (B-ALL) is the most common leukemia in the pediatric population, caused by a malignant clonal proliferation of B lymphoid progenitor cells. Identifying new molecular markers related to B-cell development is helpful for investing the pathogenesis of B-ALL, and is potentially important for clinical prognosis. We found that B cells showed the highest expression of glutaminyl-tRNA amidotransferase subunit QRSL1 (QRSL1) compared with other cells during the differentiation and development of hematopoietic stem cells and the expression of QRSL1 also gradually increases with the development of human fetal B-cell. Moreover, QRSL1 expression was higher in the tissues and cell lines extracted from patients with B-ALL than in corresponding control tissues. In the TARGET cohort, EFS and OS decreased in B-ALL with high expression of QRSL1, suggesting that QRSL1 was an independent prognostic factor. And high QRSL1 expression is associated with more bone marrow sites of relapse and TCF3-PBX1 gene fusions. Then analyzing the gene expression of the TCF3-PBX1 gene fusion subgroup, the significantly different gene expression between the QRSL1 ^{low} group and QRSL1 ^{high} group exhibited enrichment in cell development, suggesting that QRSL1 may participate in leukemic cell development in childhood B-ALL. Therefore, QRSL1 may be a molecule related to B cell development and is associated with molecular subtypes of B-ALL. The high expression of QRSL1 is associated with poor prognosis in patients with B-ALL, showing its potential as a prognostic marker of B-ALL leukemia.

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