

INVESTIGATING KIAA0125 AS A MOLECULAR MARKER IN PEDIATRIC ACUTE LYMPHOID AND MYELOID LEUKEMIAS

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Introduction: Hematopoietic neoplasms represent a public health concern, as they are the most common type of cancer in children worldwide. Patients afflicted with this illness often face various complications, including resistance to the available therapy regimens and severe associated side effects, as well as frequent relapses and emotional distress. In light of these challenges, there is an urgent need for intensified research focused on early diagnosis and more precise therapeutic targeting. From this perspective, long non-coding RNAs (lncRNAs) are recognized for their multiple functions in cellular metabolism and their key involvement in cancer biology. Among them, lncRNA KIAA0125 has been proposed as a potential biomarker for prognosis prediction and risk stratification in Acute Myeloid Leukemia (AML) and Acute Lymphoblastic Leukemia (ALL) of B (B-ALL) and T (T-ALL) cells, thus highlighting its promise as a research target to improve the therapeutic landscape of AL. **Objectives:** The present study aimed to evaluate the impact of KIAA0125 expression levels on patients with AL. **Methods:** For this research, 91 peripheral blood (PB) or bone marrow samples from AL patients (AML = 10; ALL = 81; B-ALL = 70; T-ALL = 11) and 8 PB samples from healthy volunteers (CAAE = 30307820.7.0000.5634) were used. Groups consisted of individuals aged 0 to 17 years, of both sexes. RNA was extracted from the samples using TRIzol Reagent® and converted into cDNA using High-Capacity cDNA Reverse Transcription® kit. Gene expression was evaluated via RT-qPCR, using the TaqMan® probe system for KIAA0125 and reference genes ACTB (Hs01060665_g1) and ABL1 (Hs01060665_g1). Then, the mean cycle threshold (Ct), Δ Ct, and fold change (FC) were calculated. Normality was assessed using the Shapiro–Wilk and D’Agostino–Pearson tests, and Student’s t-test or Welch test were used to evaluate differences in global expression

levels between patients and healthy controls. Statistical significance was set at $p \leq 0.05$, and analyses were conducted using PSPP v2.0.0 and Endogene Analyzer software.

Results: The mean ΔCt in the control group was 3.94 ± 1.23 cycles, lower than ALL (6.83 ± 3.10) and AML (8.10 ± 2.93) patients. Further analysis of ALL subtypes revealed that the mean ΔCt for B-ALL (6.75 ± 3.16) was higher than that of T-ALL (5.42 ± 2.81). Such variations became even more evident when evaluating FC between groups, with the mean being higher for AML (0.06 ± 1.30) than for ALL (0.15 ± 5.20). Additionally, B-ALL (0.14 ± 5.59) cases presented a lower mean value than T-ALL (0.35 ± 0.69). When comparing the differential global expression of KIAA0125 among AML, ALL and control groups, a statistically significant reduction in gene expression was observed in both AML ($p = 0.0025$) and ALL ($p = 6.056e-05$) groups. As demonstrated in previous analyses, a statistically significant difference was found when comparing expression levels between controls and B-ALL ($p = 5.418e-05$) and T-ALL ($p = 0.0142$) groups.

Conclusion: Thus, our results suggest that KIAA0125 expression is significantly suppressed in the analyzed pediatric acute leukemia cases, indicating that this lncRNA is a promising biomarker candidate for the disease.

Keywords: Acute Leukemia; KIAA0125; Biomarker