confirm PCR results. Descriptive statistics were used for qualitative variables, determining absolute and relative frequencies. For quantitative variables, median values and standard deviations were calculated. ANOVA was applied to assess associations between age groups, according to NCI risk criteria, and clinical data, adopting a p-value ≤ 0.05 as statistically significant. Statistical analyses were performed using RStudio 12.1. **Results:** Regarding sex distribution, 65% of patients were male and 35% female. The median age was 7 years. Median white blood cell count was 19,350/mm^3, median platelet count was 31,000/mm^3, and median hemoglobin level was 8 g/dL. ANOVA revealed no statistically significant differences between NCI age- based risk groups (1–6 years, 6–10 years, and >10 years) and the evaluated hematological parameters. **Discussion:** Studies conducted in Nordic countries, Egypt, China, and Mexico have reported a higher prevalence of females with t(1;19), differing from our findings, which revealed male predominance (ratio 1.86:1). In terms of age, previous reports indicate a median of 5–8 years for patients with the TCF3::PBX1 biomarker, consistent with our observations. Regarding leukocyte count, literature shows a median of approximately 22,000/mm^3 in such patients, aligning with the present study and reinforcing the association of this gene fusion with an unfavorable prognosis during ALL treatment. Conclusion: The TCF3::PBX1 gene fusion activates genes encoding proteins with malignant potential and may also lead to CNS involvement. Further investigation into the leukemogenic mechanisms of this biomarker is warranted. In this cohort, 7% of patients were classified as high-risk according to NCI guidelines due to age >10 years combined with a white blood cell count >50,000/mm^3.

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IMMUNE EVASION IN AML: NK CELL LIGAND ALTERATIONS LINKED TO LEUKEMIC STEM CELL PERSISTENCE

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Introduction: Natural Killer (NK) Cell-Mediated Immune Evasion Plays a Key Role in Clonal Persistence, Refractoriness, and Relapse in Acute Myeloid Leukemia (AML). Growing evidence indicates that alterations in the expression of innate immune recognition ligands by leukemic blasts contribute to the inhibition of NK cell effector responses, thereby favoring disease maintenance. However, the immunophenotypic mechanisms underlying this process remain poorly understood. **Objectives:** In this study, we investigated the expression profile of NK cell ligands on leukemic blasts and their association with clinical outcomes and measurable residual disease (MRD). **Material and methods:** A total of 127 bone marrow samples collected at diagnosis from adult AML patients were analyzed. Samples were processed within 24 hours, lysed using ammonium chloride solution, and stained with monoclonal antibodies targeting CD45, CD34, CD38, CD123, CD112, CD155, and HLA-E. Flow cytometry analysis was performed using a FACSCanto II cytometer (BD Biosciences), applying validated panels for both diagnosis and MRD assessment. At least 500,000 viable events were acquired per sample, and analysis was standardized using internal controls and healthy donor bone marrow samples. Patients were treated according to standard AML therapeutic protocols, including induction with cytarabine and anthracyclines (7+3 regimen), followed by high-dose cytarabine (HiDAC) consolidation, according to clinical and biological eligibility. Leukemic stem cell (LSC)-enriched subpopulations were defined as CD45dim/CD34$^+$/CD38$^-$/CD123$^+$, along with CD34$^-$ blasts. Activating (CD112, CD155) and inhibitory (HLA-E) NK ligands were assessed by both the frequency of positive cells and median fluorescence intensity (MFI). MRD was measured in post-induction samples with a minimum sensitivity of 10^{-4}, and clinical outcomes (remission, relapse, refractoriness, early death) were obtained from electronic medical records, with a minimum follow-up of 12 months. **Results:** Patients with unfavorable clinical outcomes showed, at diagnosis, a significant reduction in CD112 ($p = 0.004$) and CD155 ($p = 0.013$) expression, along with increased HLA-E levels ($p = 0.009$), when compared to patients in remission and healthy controls. MRD positivity after induction was associated with higher HLA-E expression ($p = 0.027$) and a trend toward decreased CD112 ($p = 0.078$) and CD155 ($p = 0.065$), particularly within the CD34$^+$ subpopulation. Among CD34$^+$ blasts, higher HLA-E expression ($p = 0.006$) and lower CD155 levels ($p = 0.021$) were observed compared to CD34$^-$ cells, suggesting enhanced immune evasion capacity in the LSC-enriched fraction. **Discussion and conclusion:** These findings support the hypothesis that phenotypic alterations in NK cell recognition ligands contribute to immune escape and MRD persistence. The consolidation of the inhibitory HLA-E/NKG2A axis as a key mechanism of immune suppression in AML highlights its potential as a therapeutic target. Altogether, our results support the development of immunomodulatory strategies aimed at restoring innate immune surveillance and preventing LSC persistence, with the potential to reduce relapse rates and improve clinical control of AML.

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IMPACTO DE MUTAÇÕES FLT3-ITD E FLT3-TKD NO PROGNÓSTICO E NAS DECISÕES SOBRE USO DE INIBIDORES ALVO

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