indicated intermediate risk, and with wild-type *NPM1*, it indicated unfavorable risk. The 2022 ELN guidelines classify *FLT3-ITD* alone as intermediate risk, regardless of *NPM1* status. Mutated *NPM1* is favorable only when *FLT3-ITD* is absent. Supporting these findings, *FLT3* mutation, regardless of allelic ratio, in the absence of *NPM1*, led to immature SLA and increased GMP-L frequency. This SLA was linked to PD after the 1IR. Immature SLA significantly impacts prognosis with lower survival rates, higher relapse risks, and increased post-induction remission failure. Our findings enhance the understanding of the cell of origin in AML, and further investigation of the SLA-dependent mechanisms that contribute to leukemia resistance are warranted.

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INVESTIGATION OF THE GENETIC ALTERATIONS IN CDKN2A/B AND IL7R IN T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA

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T-cell acute lymphoblastic leukemia (T-ALL) is an aggressive hematopoietic disorder triggered by the acquisition of molecular alterations that affect thymocytes in early stages of its development. Deletions in *CDKN2A/B* are found in ~65-70% of cases. However, their prognostic value is still undefined. Loss of *CDKN2A*, in addition to *IL7R* activation, contributes to the development of B-cell precursor ALL (B-ALL). The activation of *IL7R*, either due to the presence of gain-of-function mutations (~10% of cases) or its upregulation, is a recurrent event in T-ALL associated with disease relapse. Thus, *IL7R* activation is a crucial event in T-ALL initiation, but its transcriptional profile and prognostic role are still unclear. We aimed to investigate the presence of molecular alterations in *CDKN2A/B* and in *IL7R* in samples from pediatric and adult patients diagnosed with T-ALL. Samples from patients with a morphological and immunophenotypic diagnosis of T-ALL between the years 2018-2023 from the INCA Hematology Service and different cancer treatment centers in Brazil were included. The SALSA MLPA P335-C1 kit (MRC Holland), multiplex ligation-dependent probe amplification (MLPA) technique, was used to evaluate the presence of copy number alterations (CNA) in genes related to lymphopoiesis and commonly altered in ALLs, such as *CDKN2A/B*. The presence of mutations/single nucleotide polymorphism (SNP) in *IL7R* was assessed by polymerase chain reaction (PCR) for amplification of exon 6 followed by ABI3500 sanger sequencing. The transcriptional levels of *IL7R* were investigated using real-time quantitative PCR (RT-qPCR). 38 T-ALL samples were included (13 female and 25 male individuals), whose median age was 11.5 years. *CDKN2A/B* deletions were observed in 16 pediatric (44.4%, being 8 monoallelic and 8 biallelic deletions) and 2 adults (5.6%, 1 monoallelic and 1 biallelic deletions). Activating indel mutations in *IL7R*, which affect the juxtamembrane region of the protein, were found in 2 pediatric patients. Both patients had high leukocyte counts ($> 100 \times 10^9$ cells/mL) at diagnosis and presented concomitant *CDKN2A/B* biallelic deletions. Besides, we found that 36.8% of our cohort presented a single nucleotide polymorphism (SNP) rs6897932 in exon 6 of *IL7R*. Among these samples, 12/14 were pediatric and 2/14 adults. In the pediatric subset, 7 samples presented heterozygous (TC) and 5 homozygous variants (TT). Both adult samples had heterozygous genotype (TC). Our data corroborates the literature showing that *CDKN2A/B* genetic alterations are frequently found in T-ALL patients. The analysis of the mutation or SNP on the *IL7R* expression is undergoing. However, the two patients harboring *IL7R* activating mutations did not present transcriptional deregulation in this gene. Since it's still unclear whether the mutations lead to increased gene expression in our series of cases, we aim to explore other transcriptional pathways that might play a role in *IL7R* deregulation scenario in T-ALL. Of note, to the best of our knowledge, this is the first study describing a high frequency of the SNP rs6897932 in T-ALL.

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RHOA KNOCKDOWN AFFECTS P53 SUBCELLULAR LOCALIZATION IN LEUKEMIA CELLS IRRADIATED WITH UVC

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Introduction and aims: Acute myeloid leukemia (AML) is a severe hematological malignancy with low rates of survival. Mutations in the tumor suppressor gene *TP53* are present in around 10% of AML cases and are associated with a worse prognosis. Evidence suggests that the Rho GTPase proteins RhoA and RhoC are involved in the regulation of p53 activity. In this study, we aimed to investigate the relation between RhoA and RhoC expression and p53 expression and subcellular localization in leukemia cells. **Methods:** OCI-AML3 cell line (wild type *TP53*) was transduced with lentiviral particles containing specific shRNA for the silencing of RhoA (shRhoA) or RhoC (shRhoC) or non-specific shRNA (shCTRL). Cells were irradiated with UVC and nucleus (DAPI) and p53 were