confere desfecho adverso. Não há opções de tratamento padrão disponíveis para neoplasias hematológicas e tumores sólidos sincrônicos. O manejo desses casos deve ser individualizado, considerando agressividade de cada tumor, risco de progressão e condições clínicas do paciente. No caso relatado, a decisão de priorizar o tratamento da LLA deveu-se ao risco iminente de óbito, com interrupção temporária da terapia do angiossarcoma hepático. Este é o primeiro relato, até onde sabemos, de associação entre angiossarcoma hepático e LLA. O caso ressalta a importância do reconhecimento de tumores sincrônicos e evidencia os desafios terapêuticos impostos, podendo auxiliar na condução de casos futuros.

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ETV6::RUNX1 FUSION IN ACUTE LYMPHOBLASTIC LEUKEMIA: FREQUENCY AND REGIONAL DISTRIBUTION IN THE STATE OF PARÁ

KB Rodrigues [a], YS Santos [a], JCS Oliveira [a], MB Oliveira [a], ÁTM Tavares [a], AV Wanderley [b], LC Pantoja [b], MS Aquino [a], BCM Khayat [a], MM Bernardes [b], AS Khayat [a]

[a] *Universidade Federal do Pará (UFPA), Belém, Brazil*
[b] *Hospital Oncológico Infantil Octávio Lobo (HOIOL), Belém, Brazil*

Introduction: Acute Lymphoblastic Leukemia (ALL) accounts for about 75% of leukemia cases. In Northern Brazil, the state of Pará ranks second in the number of ALL cases. Among the genetic alterations frequently associated with ALL, gene fusions such as ETV6::RUNX1, resulting from the translocation between chromosomes 12 and 21, t(12;21), stand out. This fusion is the most common and is associated with a favorable prognosis, making it crucial for guiding treatment. **Objectives:** This study aims to evaluate the incidence of the *ETV6::RUNX1* fusion in municipalities of Pará and its association with sex and age. **Material and methods:** Data were collected from patients diagnosed with ALL by immunophenotyping at the Octávio Lobo Children's Oncology Hospital, who signed informed consent between 2023 and June 2025. Epidemiological data, such as sex, age, and municipality, were retrieved from medical records. For gene fusion analysis, RNA was extracted from patients and converted into cDNA for the detection of molecular biomarkers by nPCR, using specific primers, with visualization of the products by agarose gel electrophoresis. Data from patients positive for *ETV6::RUNX1* were used in statistical analyses. The chi-square test was performed to assess the frequency of cases by municipality, and the ANOVA test was used to evaluate significant differences in patient age. Other descriptive statistics, such as mode and mean, were also applied, all using RStudio 12.1. **Results:** A total of 56 patients participated in the study, of which 33 children presented the *ETV6::RUNX1* fusion; 9 of these were excluded due to missing data. During the study period, there was no significant predominance between sexes, except in 2024, when approximately 63% were male. The mean age of patients ranged from 6 to 7 years (SD = 4.12). The ANOVA test showed no significant difference in age distribution ($p = 0.791$). In contrast, the chi-square test indicated a statistically significant difference in case distribution by municipality ($p = 0.04585$). Among the municipalities, Belém and Macapá stood out, concentrating 29.17% and 16.67% of cases, respectively. Furthermore, the Belém Metropolitan Region accounted for one-third of all positive cases. **Discussion and conclusion:** The mean age of patients is consistent with the literature, despite the standard deviation of 4.12 years, indicating considerable variation around the mean. The ANOVA test presented a value above the significance level (0.05), indicating no statistical difference. Conversely, the chi-square test showed a p-value below the significance level, indicating a significant difference in case distribution, highlighting the concentration in Belém and Macapá. This finding may reflect greater access to molecular diagnosis and the oncology reference network in these cities. It is concluded that this study highlights the relevance of the *ETV6::RUNX1* fusion as a biomarker in ALL due to its high incidence. The analysis revealed significant differences in the distribution of cases, and the representation of the Metropolitan Region of Belém suggests the influence of access to diagnosis and the oncology network, as well as the concentration of cases in Belém and Macapá. These results reinforce the need for molecular and epidemiological mapping to expand diagnosis in municipalities outside the metropolitan area, making it more accessible. For this purpose, multicenter studies with broader regional coverage are necessary to deepen the understanding of the fusion's distribution in the Northern region.

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ALTERAÇÕES GENÉTICAS, IMPACTO PROGNÓSTICO E ABORDAGENS TERAPÊUTICAS NA PROGRESSÃO DA LEUCEMIA MIELOIDE CRÔNICA PARA LEUCEMIA MIELOIDE AGUDA: REVISÃO NARRATIVA

EA Dutra [a], DEL Laborda [a], ADD Martinez [a], JF Paes [a,b]

[a] *Faculdade Metropolitana de Manaus (FAMETRO), Manaus, AM, Brasil*
[b] *Pós-Graduação em Imunologia Básica e Aplicada (PPGIBA), Universidade Federal do Amazonas (UFAM), Manaus, AM, Brasil*

Introdução: A Leucemia Mieloide Aguda (LMA) representa uma das neoplasias hematológicas mais complexas e agressivas, caracterizada pela proliferação descontrolada de células progenitoras mieloides na medula óssea, podendo ser advinda de uma desregulação hematopoiética primária ou a partir da evolução de uma outra neoplasia hematológica, como a leucemia mieloide crônica (LMC). Esta doença possui uma patogênese molecular heterogênea, onde mutações genéticas desempenham papéis fundamentais no