

Objectives: Acute lymphoblastic leukemia (ALL) is a heterogeneous disease characterized by altered clonal proliferation of lymphoid progenitor cells and their accumulation in the bone marrow (BM) and other organs. Precursor B-cell ALL (B-ALL) is the most common immunological subtype of ALL and the most frequent cancer in children. According to the World Health Organization, any disease classification must be periodically reviewed and updated, thus, there is a constant need for the characterization of new molecular biomarkers for diagnostic and prognostic purposes. This study aimed to compare microRNA (miRNA) expression profiles between bone marrow and peripheral blood samples and evaluate potential diagnostic biomarkers for childhood B-ALL. **Materials and methods:** Peripheral blood and bone marrow samples were collected from children with B-ALL admitted to the Onco-Hematology Service of the Joana de Gusmão Children's Hospital (HIJG), Florianópolis, Santa Catarina, as well as healthy controls. The samples were subjected to miRNA microarray analysis followed by RT-qPCR validation. **Results:** Microarray analysis revealed no differences in miRNA expression between peripheral blood and bone marrow samples from the same B-ALL patients. Comparison of peripheral blood profiles between B-ALL and control subjects revealed 13 differentially expressed miRNAs, and among these, five were selected as potential biomarkers for RT-qPCR validation based on their respective expression status. Additionally, nine miRNAs were included in the RT-qPCR validation based on literature findings. RT-qPCR analysis did not show significant differences between bone marrow and peripheral blood samples for 12 of the 14 miRNAs tested. Furthermore, it was found that one miRNA was downregulated and 10 were upregulated in B-ALL patients. Enriched pathway analysis of these differentially expressed miRNAs identified genes with important regulatory roles associated with cell cycle, proliferation, and apoptosis. **Discussion:** miRNA profile signatures have a high potential for cancer diagnosis, including that of childhood acute leukemia. In this study, we demonstrate important similarities between miRNA profile signatures of peripheral blood and bone marrow samples of children with B-ALL. Also, we demonstrated that some miRNAs are differentially expressed in leukemia patients when compared with healthy controls. Importantly, receiver operating characteristic analysis showed that all miRNAs significantly altered in B-ALL had high performance and could be used to distinguish patients from healthy subjects. **Conclusion:** Together, these data suggest an equivalence between peripheral blood and bone marrow miRNA expression profiles and demonstrate the potential of some miRNAs as B-ALL biomarkers.

<https://doi.org/10.1016/j.htct.2024.09.571>

IMPACT OF THE COVID-19 PANDEMIC ON CHEMOTHERAPY/RADIOTHERAPY BURDEN FOR PATIENTS WITH ACUTE MYELOID LEUKEMIA IN BRAZIL, 2017-2023

ICG Moura, V Goularte, L Galhardo, MC Evangelista, R Pereira

IQVIA Sollutions do Brasil, Brazil

Objectives: To assess the chemotherapy (CT) and radiotherapy (RT) burden among Brazilian patients with Acute Myeloid Leukemia (AML) from 2017 to 2023. **Materials and methods:** This retrospective evaluation utilized data from the High Complexity Procedures Authorization (APAC) in Brazil, covering the period from January 2017 to the end of September 2023. Included patients were 18 years or older, with AML diagnosed according to the Therapeutic Diagnostic Guidelines of the Ministry of Health. Statistical analysis included descriptive indicators evaluated per patient per year (PPPY), along with corresponding 95% confidence intervals (CI). The comparison of PPPY before and after the pandemic was conducted using the z-test. All analyses were performed using Python 3.6.9. **Results:** A total of 12,466 patients were included in the study. PPPY rates were significantly higher in the post-pandemic period (14.77 [95% CI 14.76; 14.78] pre-pandemic vs. 16.26 [95% CI 16.24; 16.28] post-pandemic, $p < 0.001$). When comparing pre- and post-pandemic periods within Brazilian regions, no significant change in PPPY was observed for the Southeast, Midwest, and North. However, both the Northeast and South regions showed an increase in PPPY (Northeast: 14.41 [95% CI 14.38; 14.43] pre-pandemic vs. 17.01 [95% CI 15.00; 19.00] post-pandemic, $p < 0.001$; South: 15.10 [95% CI 14.77; 15.43] pre-pandemic vs. 16.89 [95% CI 16.49; 17.29], $p < 0.001$). **Discussion:** The post-pandemic increase in PPPY for RT/CT in AML patients can be attributed to several factors. Firstly, the pandemic led to a higher overall demand for healthcare, potentially resulting in increased RT/CT sessions. Additionally, oncology patients were considered a high-risk group during the pandemic, and treatment plans may have been adjusted due to changes in healthcare demands and quarantine guidelines, leading to increased treatment frequency after the pandemic. Notably, while the Southeast region of Brazil showed no significant changes, the Northeast and South regions experienced a general increase. One hypothesis is that the more robust healthcare infrastructure in the Southeast allowed for alternative solutions to prevent interruptions or excessive spacing between planned RT/CT sessions. **Conclusion:** Restricted access to healthcare systems during the pandemic and potential disease progression in AML patients inadequately monitored during the COVID-19 period are hypotheses explaining the increased post-pandemic demand for CT/RT. The Southeast region appears less affected by this phenomenon, while the impact is pronounced in the Northeast and South. Further studies are needed to better understand the pandemic's effect on healthcare resource utilization among AML patients.

<https://doi.org/10.1016/j.htct.2024.09.572>

INTRAGENIC ANTIMICROBIAL PEPTIDE HS02 INCREASES THE EXPRESSION OF COMPONENTS INVOLVED IN PYROPTOSIS AND EXERTS ANTINEOPLASTIC EFFECTS IN HUMAN LEUKEMIA CELL LINES

IS Mota ^a, M Cardoso ^b, J Bueno ^a, IGM Silva ^a, J Gonçalves ^b, SN Bao ^a, BAD Neto ^a, G Brand ^a, JR Corrêa ^a, JRSA Leite ^a, F Saldanha-Araujo ^a

^a Universidade de Brasília (UnB), Brasília, Brazil

^b University of Lisbon, Lisbon, Portugal

The anticancer potential of some antimicrobial peptides has been reported. Hs02 is a recently characterized Intragenic Antimicrobial Peptide (IAP), which was able to exhibit potent antimicrobial and anti-inflammatory action. In this study, we evaluate for the first time the antineoplastic potential of IAP Hs02 using cell lines representing the main types of leukemia as cancer models. Interestingly, this peptide decreased the viability of several leukemic cell lines, without compromising the viability of PBMCs. In the HL-60 line, treatment with Hs02 controlled cell division, leading to cell arrest in the G1 phase of the cell cycle. More importantly, HL-60 cells treated with Hs02 undergo cell death, with the formation of pores in the plasma membrane and the release of LDH. Accordingly, Hs02 treatment stimulated the expression of components involved in pyroptosis, such as NLRP1, CASP-1, GSDME, and IL-1 β . Taken together, our data characterize the antineoplastic potential of Hs02 and open an opportunity for both evaluating the peptide's antineoplastic potential in other cancer models and using this molecule as a template for new peptides with therapeutic potential against cancer.

<https://doi.org/10.1016/j.htct.2024.09.573>

IMPACTO CLÍNICO DA EXPRESSÃO DO GENE ID1 NA LEUCEMIA PROMIELOCÍTICA AGUDA

BV Alcântara ^a, LCA Koury ^b, RAM Melo ^c,
ABF Gloria ^d, EC Nunes ^e,
LL Figueiredo-Pontes ^b, F Traina ^b, BKL Duarte ^f,
EM Rego ^g, AR Lucena-Araujo ^a

^a Universidade Federal de Pernambuco (UFPE),
Recife, PE, Brasil

^b Universidade de São Paulo (USP), Ribeirão Preto,
SP, Brasil

^c Universidade de Pernambuco (UPE), Recife, PE,
Brasil

^d Universidade Federal de Minas Gerais (UFMG),
Belo Horizonte, MG, Brasil

^e Universidade Federal do Paraná (UFPR), Curitiba,
PR, Brasil

^f Universidade Estadual de Campinas (UNICAMP),
Campinas, SP, Brasil

^g Universidade de São Paulo (USP), São Paulo, SP,
Brasil

O inibidor de ligação ao DNA 1 (ID1) tem sido frequentemente associado com o início e progressão de diversos tumores humanos devido às suas funções reguladoras em vias de proliferação e diferenciação celular. Na leucemia mieloide aguda (LMA), um crescente número de evidências sugere que a alta expressão desse gene pode afetar tanto a leucemogênese quanto o prognóstico dos pacientes. No entanto, pouco se sabe sobre o papel do ID1 na leucemia promielocítica aguda (LPA), uma doença que, embora tenha um prognóstico favorável, ainda apresenta um número significativo de recaídas em pacientes tratados com ácido all-trans

retinoico (ATRA) e quimioterapia. **Objetivos, materiais e métodos:** Utilizando a reação em cadeia da polimerase em tempo real (qPCR), investigamos a expressão aberrante do gene ID1 em 226 amostras de medula óssea de pacientes adultos com LPA tratados com ATRA e quimioterapia, incluídos no estudo IC-APL (*International Consortium on Acute Promyelocytic Leukemia*) e associamos esses achados com os principais desfechos clínicos da doença. **Resultados:** No geral, 186 (82%) dos 226 pacientes alcançaram remissão hematológica completa (RC). O tempo médio para atingir a RC foi de 39 dias (intervalo: 12-389 dias). 22 pacientes tiveram morte precoce ocasionada por hemorragia (n = 16), seguida por infecção (n = 5) e síndrome de diferenciação (resistência ao ATRA, n = 1). Pacientes com alta expressão de ID1 tiveram menor taxa de remissão completa (73%) em comparação com aqueles com baixa expressão de ID1 (85%) (p = 0,046). O tempo médio de acompanhamento entre os sobreviventes foi de 39 meses (intervalo de confiança [IC] de 95%: 36-43 meses), com SG (sobrevivência global) estimada em 5 anos de 74% (IC 95%: 68-80%) e sobrevivência livre de doença estimada em 5 anos de 84% (IC 95%: 78-90%). Além disso, os pacientes com alta expressão desse gene tiveram uma menor SG (41%, IC 95%: 28-54%), quando comparados aos pacientes de baixa expressão (83%, IC 95%: 76-89%) (p < 0,001). De forma semelhante, pacientes de alto risco (ou seja, aqueles com contagem de leucócitos > 10 × 10⁹/L) com alta expressão de ID1 apresentaram uma taxa de SG significativamente menor (23%, IC 95%: 8-42) do que aqueles com baixa expressão de ID1 (62%, IC 95%: 45-75) (p = 0,0047). **Discussão:** Corroborando nossos achados, a literatura relata maiores níveis de expressão de ID1 associados a desfechos clínicos mais desfavoráveis em outras neoplasias humanas, incluindo LMA (não-LPA). Recentemente, nosso grupo demonstrou que a superexpressão do ID1 foi um fator preditor para uma menor SG. **Conclusão:** Assim, concluímos que a expressão aberrante do ID1 pode subestratificar pacientes de alto risco, identificando aqueles com maiores chances de recaída, pelo menos quando o tratamento é à base de ATRA e quimioterapia. Ademais, como já proposto por nosso grupo e outros, esses resultados podem ser úteis para refinar a estratificação do risco de recaída de acordo com o perfil molecular do paciente, possibilitando intervenções precoces, independentemente da contagem de leucócitos.

<https://doi.org/10.1016/j.htct.2024.09.574>

ANÁLISE TEMPORAL DE 2013 A 2023 ACERCA DOS NOVOS CASOS DE LEUCEMIA MIELOIDE TRATADOS COM RADIOTERAPIA NO BRASIL.

MLP Pereira ^a, JA Souza ^a, LGSR Fernandes ^a,
IJL Ferreira ^a, HS Bellettini ^b

^a Universidade Nove de Julho (UNINOVE), São
Paulo, SP, Brasil

^b Universidade Federal de Santa Catarina (UFSC),
Florianópolis, SC, Brasil

Introdução: A leucemia mieloide é uma doença maligna caracterizada pela proliferação anormal das células mieloides.