disparities affect patients with myelodysplastic syndromes (MDS). **Objectives:** This study aims to characterize and compare the diagnostic and therapeutic profiles of MDS patients treated within the public and private systems in a Brazilian cancer center. **Material and methods:** We performed a retrospective cohort study of patients diagnosed with MDS between 2014 and 2024 at a tertiary cancer center in Brazil. Patients were categorized by healthcare system. Variables analyzed included time from symptom onset to diagnosis, MDS subtype, cytogenetic and mutational profiles, treatment modalities, and duration of follow-up. **Results:** Among the 96 patients included, 32 (33%) were treated in the public system and 64 (67%) in the private sector, a 2:1 ratio. The overall median age at diagnosis was 70 years. The highest level of education among SUS patients was high school, while within the private group, 50% of patients were college graduates. The median time from cytopenia investigation to diagnosis was 165 days in the SUS group versus 30 days in the private group. None of the SUS patients underwent an NGS molecular panel for more appropriate risk stratification, compared to 35 (54%) of the private sector who did. Of the total number of patients, 53 (55%) were classified as having therapy-related MDS due to a history of oncological treatment with radiotherapy and/or chemotherapy (26 from SUS and 27 from private). The most common mutations in the private sector patient panels were SF3B1 (22%), ASXL1 (14%), RUNX1 (14%), TP53 (11.4%), U2AF1 (11.4%), and TET2 (11.4%). In the M-IPSS risk assessment, 6 (17%) were classified as very low risk, 2 (5%) as low risk, 3 (8.5%) as low-intermediate risk, 5 (14.2%) as high-intermediate risk, 6 (17%) as high risk, 5 (14.2%) as very high risk, and 29 (45%) were at unknown risk. In the R-IPSS analysis, the public sector group showed: 8 (25%) patients as very low risk, 8 (25%) as low risk, 2 (6%) as intermediate risk, 8 (25%) as high risk, 4 (12.5%) as very high risk, and 2 (6%) as unknown. Regarding treatment, 20 (62%) SUS patients received first-line treatment with erythropoietin, and only 2 underwent consolidation with allogeneic transplant. In the private sector group, the median number of lines of treatment was 1 (maximum: 3), with treatments ranging from erythropoietin (31%), azacitidine (20%), a combination of venetoclax and hypomethylating agent (7%), luspatercept (3%), to lenalidomide (1.5%). Sixteen (25%) private sector patients underwent consolidation with allogeneic transplant. During the entire follow-up (median of 15 months), 24 patients presented transformation to Acute Myeloid Leukemia (8 from the SUS and 16 from the private sector). **Discussion and conclusion:** This study highlights significant disparities in the diagnosis and therapeutic management of MDS patients between Brazil's public and private healthcare systems. Although the underlying disease biology appeared similar, reduced access to timely diagnosis, molecular testing, and advanced therapies in the public system may contribute to poorer outcomes. Our findings provide real-world evidence from a developing country context.

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## IMPACT OF INNATE IMMUNITY-RELATED GENE ON THE SURVIVAL OF PATIENTS WITH MYELODYSPLASTIC NEOPLASMS

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**Introduction:** Myelodysplastic neoplasms (MDS) are clonal disorders characterized by cytopenias, bone marrow dysplasia, and a risk of progression to acute myeloid leukemia related to myelodysplasia (AML-RM). The accumulation of driver mutations in hematopoietic stem cells (HSCs) leads to clonal expansion and ineffective hematopoiesis. Activation of innate immune pathways, particularly through Toll-like receptors (TLRs), is increasingly recognized as a key contributor to disease progression, fostering inflammation, apoptosis, and abnormal cell proliferation. Dysregulated TLR signaling and chronic inflammation disrupt bone marrow homeostasis and are frequently associated with chromosomal abnormalities and poor prognosis. **Objectives:** This study aimed to evaluate overall survival in relation to the expression of key genes involved in immune and inflammatory signaling. **Material and methods:** Data from 48 patients with either MDS or AML-RM were collected and stored in the RedCap database. RNA was extracted from bone marrow and the following genes had their expression analyzed through RT-PCR: NFKB, TRAF6, MYd88, IRAK1, IRAK2 and IRAK4. 2^−ΔCT was used for this assessment, in which patients were divided into three groups based on the expression level of each gene: low expression, intermediate expression, and high expression. Furthermore, K-means clustering was applied to the 2^−ΔCT values in order to split patients into meaningful groups based on their gene expression. The elbow method was used to determine the ideal number of clusters. Kaplan-Meier estimates were used to plot survival curves, with the log-rank test being used for comparisons. **Results:** After splitting the patients by gene expression, no gene emerged as a moderator of survival ($p = 0.92, 0.63, 0.54, 0.89, 0.36$, and $0.64$, respectively for NFKB, TRAF6, MYd88, IRAK1, IRAK2 and IRAK4). Through the elbow method, the ideal number of gene expression clusters was two, defining two clusters that only differed significantly by their expression of IRAK4 ($p = 0.03$, 8 patients in the IRAK4-high cluster). Although the IRAK4-high cluster had lower median survival (1.8 months vs 4 months for the IRAK4-low cluster), no significant differences emerged ($p = 0.32$). **Discussion and conclusion:** Our findings suggest that the isolated expression of innate immune signaling genes does not independently predict survival in patients with MDS or AML-RM. These results underscore the multifactorial nature of MDS

pathogenesis, where gene expression patterns may interact with other biological and clinical variables. Notably, the potential relevance of IRAK4 warrants further investigation in larger cohorts to clarify its prognostic value and biological significance in disease progression.

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## IMPACTO PROGNÓSTICO DAS MUTAÇÕES ASXL1 EM NEOPLASIAS MIELOIDES: REVISÃO SISTEMÁTICA E METANÁLISE

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**Introdução:** As neoplasias mieloides são caracterizadas por hematopoiese clonal e citopenias persistentes. Esse grupo de doenças da medula óssea inclui as síndromes mielodisplásicas (SMD), cuja presença de mutações no gene ASXL1 têm sido associadas a desfechos desfavoráveis, incluindo pior sobrevida global (OS). Embora estudos apontem para esse desfecho, há variação na magnitude dos resultados, o que justifica a necessidade de estimar precisamente esse risco. **Objetivos:** Avaliar, por meio de metanálise, o impacto da mutação ASXL1 na OS de pacientes com SMD, LMA associada a SMD e leucemia mielomonocítica crônica (LMMC). **Material e métodos:** Foi realizada metanálise conforme as diretrizes do PRISMA. Incluíram-se estudos observacionais que relataram hazard ratios (HR) para OS comparando pacientes com e sem mutação ASXL1. A busca foi conduzida na base PubMed, excluindo revisões sistemáticas e metanálises. Os dados foram analisados no R (versão 4.5.1) com o pacote metafor. O efeito combinado foi estimado por modelo de efeitos aleatórios com ajuste de Hartung-Knapp. A heterogeneidade foi avaliada pelo teste Q de Cochran e pelo índice $I^2$, e o potencial viés de publicação, por funnel plot. **Discussão e conclusão:** Cinco estudos preencheram os critérios de inclusão, envolvendo coortes com SMD, AML/MDS e LMMC. Os HR individuais variaram de 1,64 a 4,30. A análise combinada demonstrou que a mutação ASXL1 esteve associada a pior OS (HR = 1,94; IC 95%: 1,45–2,61; $p < 0,001$), correspondendo a um aumento de 94% no risco de morte. Não foi observada heterogeneidade significativa ($I^2 = 0\%$, $p = 0,5682$). O funnel plot mostrou distribuição simétrica. O estudo com maior peso foi o de Pratcorona et al. (2013), seguido por Cui et al. (2015). A metanálise confirma o efeito adverso da mutação ASXL1 na sobrevida de pacientes com SMD e doenças correlatas. A ausência de heterogeneidade ($I^2 = 0\%$) reforça a consistência dos achados, e a magnitude do risco observado é clinicamente relevante. Esses resultados alinham-se a evidências prévias que indicam que ASXL1 atua como marcador prognóstico independente, possivelmente relacionado a mecanismos de instabilidade epigenética e maior resistência terapêutica. Apesar da robustez estatística, algumas limitações devem ser consideradas. O número restrito de estudos e a ausência de análises padronizadas de variáveis de confusão podem influenciar a precisão da estimativa. Do ponto de vista clínico, os achados reforçam a importância da genotipagem no diagnóstico e estratificação de risco das neoplasias mielodisplásicas e doenças relacionadas, permitindo a personalização da conduta terapêutica. Estudos prospectivos multicêntricos, com ajustes multivariados robustos e estratificação por subtipo, são necessários para consolidar o papel prognóstico da mutação ASXL1 e explorar potenciais interações com outros marcadores moleculares. A mutação ASXL1 associa-se a pior prognóstico em SMD e síndromes relacionadas, aumentando significativamente o risco de morte. Esses resultados sustentam sua inclusão em modelos prognósticos e no planejamento terapêutico individualizado.

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## IMPORTÂNCIA DO ESTUDO CITOGENÉTICO NA AVALIAÇÃO DIAGNÓSTICA E PROGNÓSTICA DE PACIENTES COM SÍNDROME MIELODISPLÁSICA E SUA RELAÇÃO COM A EVOLUÇÃO PARA LEUCEMIA MIELOIDE AGUDA

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**Introdução:** A síndrome mielodisplásica (SMD) é uma doença clonal de células tronco hematopoéticas caracterizada por uma hematopoese ineficaz, levando à displasia e citopenia na medula óssea e sangue periférico. A incidência da SMD é maior em pacientes idosos e o risco de progressão para leucemia mieloide aguda (LMA) é variável. Anormalidades cromossômicas estão presentes em cerca de 50% dos casos e possuem grande significado para o diagnóstico, prognóstico e tratamento dos pacientes com SMD, além de estarem relacionadas com a transformação para LMA. Devido a heterogeneidade da doença, a SMD é dividida em subgrupos dependendo das características clínicas encontrados no diagnóstico. Além disso, o Sistema Internacional de Escala Prognóstica (IPSS-R) classifica estes pacientes em uma escala de progressão de risco utilizando como critérios os dados clínicos, morfológicos e citogenéticos. **Objetivos:** O objetivo deste estudo foi avaliar o perfil cariotípico dos pacientes com SMD no HEMORIO e