POSTER - RNA AND TRANSCRIPTOMICS

ARGINASE I PATHWAY-ASSOCIATED MICRORNAS AS PROGNOSTIC BIOMARKERS IN ACUTE MYELOID LEUKEMIA (AML)

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Acute myeloid leukemia (AML) is a hematologic malignancy that presents significant reductions in normal blood cells due to the accumulation of leukemic blasts in the bone marrow, blood, and other tissues. The low 5-year survival rate and the risk of relapse are among the main reasons for poor outcomes due to the biological diversity of the patient and intratumoral heterogeneity. Metabolic and cellular reprogramming are hallmarks of neoplastic initiation and progression in AML. L-arginine metabolism regulates the suppressive activity of AML blasts, which express and release arginase. Increased arginase enzymatic activity in the plasma of AML patients suppresses T-cell proliferation and increases the ability of blasts to create an immunosuppressive microenvironment. Increased arginase I expression and enzymatic activity in AML patients may be related to the expansion of myeloid blasts and immunosuppression of the immune response. MicroRNAs (miRNA), responsible for controlling post-transcriptional gene expression, give us the relevance of their potential mechanisms in the relationship of their expression in aggressive variables and clinical prognosis, increasing the importance of their role in

tumorigenesis as oncogenes or suppressors. The aim of the research was identify miRNAs differentially expressed in serum, blood and plasma samples as new biomarkers that regulate Arginase I activity in AML patients for application in prognosis. The search for dysregulated miRNAs for AML was performed using public databases, prioritizing studies between the years 2015 and 2025 that utilized samples from AML patients. In the later stages of the study, specialized software will be used to assign Gene ontology (GO) terms to miRNAs using a reverse annotation strategy and to analyze the network interactions between miRNA-TF-miRNA or TF-miRNA-TF. Within the context of the Arginase pathway in AML, potential biomarkers will be identified through the analysis of these interaction networks. Therefore, for the partial results were found a total of 126 articles were retrieved from the PubMed database using the keywords: “miRNAs”, “acute myeloid leukemia”, “serum”, “peripheral blood” and “plasma” focusing on the studies published between 2015 to 2025 that compared AML patients with control subjects. Patient ages ranged from 3 to 87 years. The most frequently used method to measure expression levels was qRT-PCR using the Applied Biosystems 7500 Fast platform (Applied Biosystems, CA, USA). Induction chemotherapy was the most commonly reported treatment among the studies. The majority of studies were conducted in China. From these, 28 dysregulated miRNAs were identified in serum samples, 17 downregulated and 11 upregulated. In peripheral blood samples, 19 miRNAs were identified, with 11 upregulated and 8 downregulated. For plasma samples, we have 31 miRNAs with 15 downregulated and 16 upregulated. In this analysis, using an integrated reverse-transcriptomics-based bioinformatics approach, we aim to identify key transcription factors that may contribute to the development of pathway-specific biomarkers within the Arginase I axis in acute myeloid leukemia (AML).

Palavras-chave: micrornas; acute myeloid leukemia (aml); arginase i.