Prognostic Significance of miRNA-532 -3p and miRNA-582-5p Gene Expression in a Cohort of Egyptian AML Patients

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Introduction

Acute myeloid leukemia (AML) is a hematologic malignancy characterized by genetic and epigenetic aberration that affect the prognosis and therapeutic outcomes of the patients. MicroRNAs (miRs) have emerged as pivotal regulator of gene expression, influencing cancer pathogenesis, progression, and response to therapy.

Aim

The current study aimed for studying miR-532-3p and mir-582-5p gene expression in a cohort of Egyptian AML patients.

Objectives

To evaluate the prognostic significance of miR-532-3p and miR-582-5p gene expression as a non-invasive molecular biomarker in AML.

Methods

Gene expression of the circulating plasma miR-532-3p, and miR-582-5p in a cohort of 71 denovo newly diagnosed AML patients, as well as, 20 age and gender-matched healthy controls were evaluated using real-time quantitative PCR.

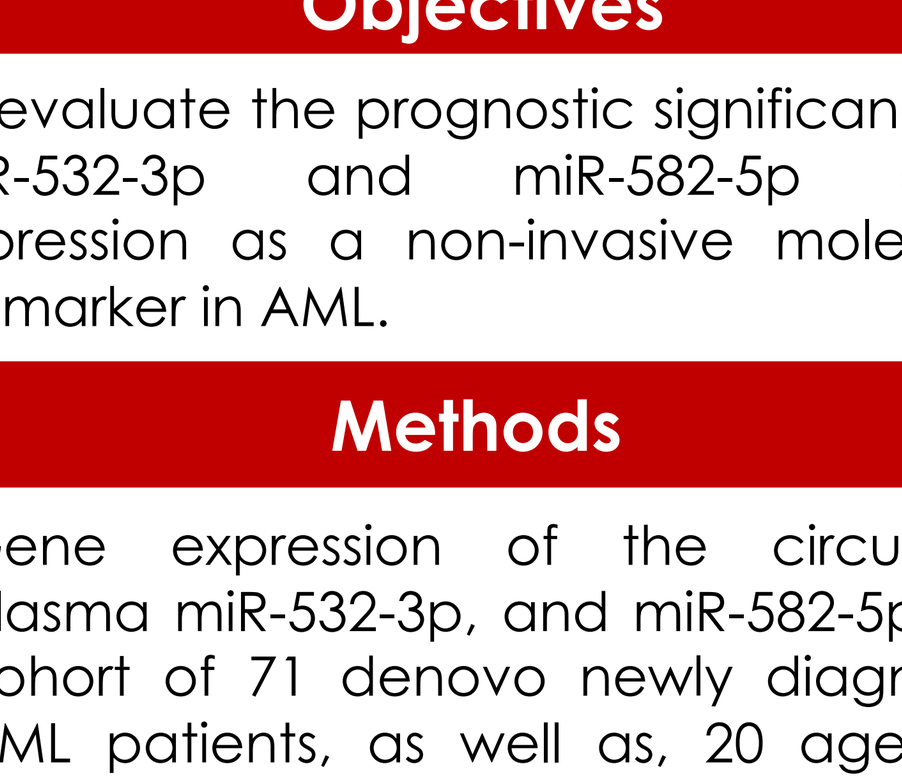


Figure (1): Mir532-3p gene expression in AML cases and controls

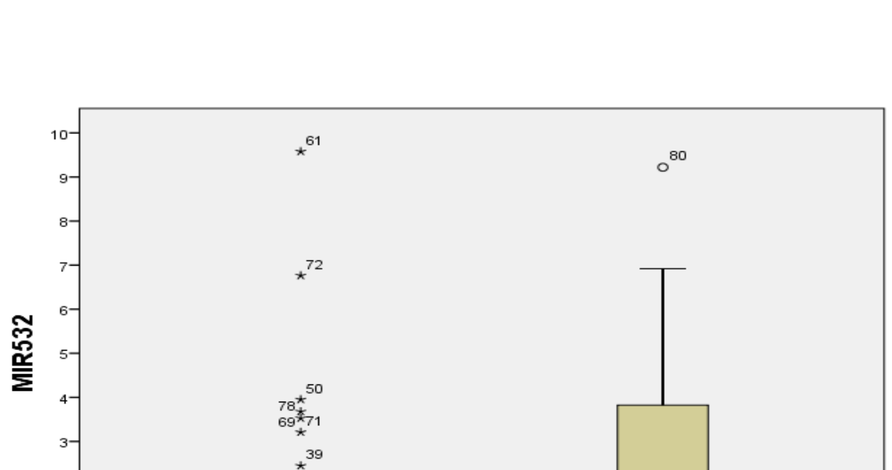


Figure (2): Mir532-3p gene expression in AML cases and controls

Results

MiR-532 -3p expression level was significantly lower in AML patients than controls (P-value <0.001). Though miR-582-5p expression level was lower in AML patients than controls, yet the difference was statistically insignificant (P-value =0.45). There was a statistically significant difference between the high and low miR-532-3p expressers regarding the gender and platelets count (P-value 0.03, and 0.04, respectively). Meanwhile, no statistically significant difference was encountered between high and low miR-532-3p or miR-582-5p expressers as regards age, clinical characteristics, laboratory data, and clinical outcomes, including overall survival (OS) and disease-free survival (DFS) (P-value > 0.05). However, there was a statistically significant positive correlation between miR-582-5p expression level and DFS with a p-value of 0.04. A highly statistically significant positive correlation between miR-532-3p, and miR-582-5p expression levels (p-value 0.001) was demonstrated, in which the increase in miR-582-5p will be associated with the increase in both miR-532-3p and DFS.

Summary

The down regulation of miRNA-582-5p and miRNA-532-3p in AML patients compared to controls, suggesting their antioncogenic role in AML.

Discussion

Furthermore, their plasma gene expression could serve as potential novel non-invasive molecular biomarkers for predicting DFS for further larger multicentric studies.

References

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