EXPRESSION OF INTEGRIN ALPHA 7 IN NEWLY DIAGNOSED ACUTE MYELOID LEUKEMIA PATIENTS

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Introduction

Acute myeloid leukemia (AML) is a clonal hematopoietic stem cell malignancy in which immature hematopoietic cells proliferate and accumulate in the bone marrow, peripheral blood and other tissues. Some patients may have the emergence of abnormal myeloid clones in the bone marrow, termed clonal hematopoiesis, years before diagnosis.

It accounts for 25% of all types of leukemia being the most common leukemia in adults, and is ranked as the sixth highest cause of death because of cancer in males worldwide. AML has greater predominance in the elderly compared to the overall population.

Integrin alpha7 (ITGA7), a member of the extracellular matrix binding proteins and one of the integrin family of adhesion molecules, is located on chromosome 12p13 and consists of over 27 exons spanning a region of about 22.5 kb. It participates in various cellular processes and has been recognized as a tumour promoter in a number of solid carcinomas.

Aim of the Work

To explore Integrin alpha 7 gene expression in de novo acute myeloid leukemia patients and its relation to disease characteristics and response to induction chemotherapy.

Subjects and Methods

This study was conducted on 80 subjects that were classified into:

- 40 de novo adult acute myeloid leukemia patients with exclusion of acute promyelocytic leukemia, recruited from the Hematology Department, Medical Research Institute, and Hematology unit, Internal Medicine department, Alexandria Main University Hospital.
- 40 healthy age and sex matched candidates as a control group.

This study was performed in the period from April 2022 to May 2023.

All patients in our present study were subjected to full history taking, clinical examination, complete blood count (CBC) with blood film examination, bone marrow examination and WHO classification at diagnosis.

Real time quantitative polymerase chain reaction (RT-qPCR) assay to detect the Integrin Alpha7 mRNA relative gene expression in peripheral blood from newly diagnosed AML patients and normal controls.

Results

Table 1: ITGA-7 gene expression among AML cases and controls

ITGA-7 gene	Cases (n = 40)	Control (n = 40)	U	p
Min. – Max.	0.20 – 11.36	0.27 – 1.80	270.00*	<0.001*
Mean ± SD.	2.67 ± 2.51	0.82 ± 0.46		
Median (IQR)	2.0 (0.99 – 3.22)	0.77 (0.41 – 1.05)		

Table 2: ITGA-7 gene expression according to response to induction chemotherapy in cases group (n = 26)

Response to induction chemotherapy	No.	ITGA-7 gene		Test of Sig	p
		Mean ± SD.	Median (Min. – Max.)		
CR + PR	16	1.42 ± 0.63	1.23 (0.43 – 2.42)	U= 22.50*	0.001*
Refractory	10	3.31 ± 1.63	3.22 (1.48 – 5.84)		

Conclusion

The present study highlighted the role of ITGA7 in denovo AML patients:

ITGA7 expression in AML patient group showed statistically significant differences with those of the control group. Patients with a higher ITGA7 gene expression level were significantly less likely to attain complete remission after standard induction chemotherapy than those with a lower ITGA7 expression level. ITGA7 high expression correlated with shorter overall survival. In the future, ITGA7 might be adopted as a biomarker for AML.