ROLE OF LONG NON-CODING RNA MEG3 IN A COHORT CF ACUTE MYELOID LEUKEMIA PATIENTS

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INTRODUCTION

Acute Myeloid Leukemia (AML) is a malignant clonal disorder of hematopoietic cells, characterized by a block of differentiation and arrest of maturation in the myeloid lineage. This leads to the accumulation of myeloid blasts in the bone marrow, causing bone marrow failure. AML is a diverse disease classified by genetic, cytogenetic, and molecular features, with risk factors including genetic predisposition, chemical exposures, and prior chemotherapy or radiation. Its incidence increases with age, and survival rates remain low despite advancements in targeted therapies.

Recent studies highlight the role of long non-coding RNAs (lncRNAs) in AML pathogenesis, particularly MEG3 (Maternally Expressed Gene 3). MEG3, located on chromosome 14q32.3, is a tumor suppressor lncRNA involved in epigenetic regulation, apoptosis, and cell cycle control. Its downregulation has been linked to AML progression and poor prognosis. Understanding MEG3's role in AML may provide insights into disease mechanisms and therapeutic targets, emphasizing the importance of epigenetic regulation in leukemia development.

AIM OF THE WORK

The aim of the present work was to study the expression of lncRNA MEG3 in a cohort of Egyptian newly diagnosed patients with acute myeloid leukemia and its relation with other clinical and laboratory parameters.

SUBJECTS AND METHODS

Subjects: This study included 35 newly diagnosed adult acute myeloid leukemia patients of both sexes admitted to Alexandria Main University Hospital and 35 healthy individuals of matching age and sex as a control group.

Methods:

All subjects underwent full history taking, thorough clinical examination and routine lab investigations including CBC, Bone marrow aspiration, immunophenotyping for establishing diagnosis of the cases, karyotyping was performed whenever feasible for cases, and PCR-based molecular studies (FLT3 and NPM1 mutations). Bone marrow aspirate samples were collected for RNA analysis. Total RNA was extracted using the miRNeasy Mini kit (QIAGEN) and cDNA synthesis was carried out using Revert Aid first strand cDNA synthesis kit (Thermo Fisher Scientific). The expression level of the lncRNA MEG3 was quantified using TaqMan® Universal Master Mix II on the Rotor-Q 3000 RT-PCR system (QIAGEN), following the manufacturer's guidelines. Beta Actin served as the housekeeping gene, and relative expression was analyzed via the comparative Ct method.

RESULTS

Table 1: Comparison between the two studied groups according to lncRNA MEG3 expression

	AML cases (n = 35)	Control (n = 35)	U	P
LncRNA MEG3 expression				
Min. – Max.	0.0002 – 618.2	0.01 – 443.3	326.00*	0.001*
Mean ± SD.	18.82 ± 104.4	27.18 ± 88.71		
Median (IQR)	0.09 (0.01 – 0.45)	1.04 (0.12 – 4.75)		

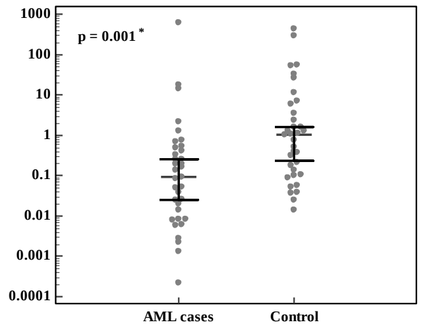

Figure 1: Comparison between the two studied groups according to lncRNA MEG3 expression

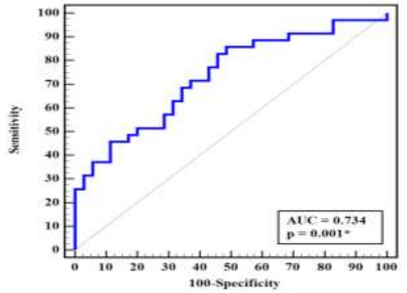

Figure 2: ROC curve for lncRNA MEG3 expression to discriminate AML cases (n = 35) from control (n = 35)

Table 2: Diagnostic performance forLncRNA MEG3expression to discriminate AML cases (n = 35) from control (n = 35)

	AUC	p	95% C.I	Cut off#	Sensitivity	Specificity	PPV	NPV	Accuracy
LncRNA MEG3 expression	0.734	0.001*	0.617 –0.851	≤0.328	71.43	62.86	65.8	68.7	67.15

CONCLUSION

There was a statistically significant difference between LncRNA MEG3 expression among AML patients and control group with a p-value of 0.001. It showed that lncRNA MEG3 was significantly under expressed among newly diagnosed AML patients relative to the control group.

The diagnostic performance of the studied lncRNA MEG3 was analyzed by receiver operating characteristic (ROC) curves and the associated area under the curve (AUC). AUC for LncRNA MEG3 expression was 0.734 and so it showed a good diagnostic power. Thus, lncRNA MEG3 expression is a non-invasive sensitive and specific biomarker for diagnosis of AML.