

Diagnostic and Prognostic Significance of miRNA-511 and miRNA-16 Expression in Adult B-Acute Lymphoblastic Leukemia Patients

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Background

Acute lymphoblastic leukemia (ALL) is a neoplastic disease that results from multistep somatic mutations in a single lymphoid progenitor cell. MicroRNAs (miRNAs) are critical regulators of gene expression, tumor suppression and oncogenesis

Objective

To evaluate miRNA-511 and miRNA-16 expression in Egyptian adult B ALL.

PATIENTS & METHODS

37 newly diagnosed adult B-ALL patients admitted to Alexandria Main University Hospital in 2019. Investigations included CBC, bone marrow aspiration, immunophenotyping, BCR-ABL testing, Karyotyping, MiRNA extraction using miRNeasy Mini, RQ-PCR combines cDNA synthesis from RNA templates using miScript II RT Kit followed by real time PCR for miR-511 and MiR-16 expression.

RESULTS

Mean age of ALL patients was 30.65±10.39 years with male to female ratio 1.4:1. Cytogenetic

findings showed only 3 patients had favorable risk and the rest were either intermediate risk (19) or high risk (15). Among the high risk group, there were 11 patients with Philadelphia (BCR-ABL 190) positive. Regarding the expression of MiRNAs, most patients showed overexpression of both miR-16 and miR-511. MiR-511 was overexpressed in 81.1% (30) patients; among these patients 43.3% (13) had adverse cytogenetic findings. MiR-16 was overexpressed in 70.3 % (26) patients; half of them (13) had adverse cytogenetic findings. ROC curves showed diagnostic significance in B-ALL for miR-16 with sensitivity of 75.7% and specificity of 80% and for miR-511 was sensitivity 89.2% and specificity 90%, (p<0.05).). Among the studied group 9 (24%) patients developed COVID 19 viral infection and of those 3 (33%) patients died forming (21%) of all deaths. The three patients were either refractory or relapsed and treated mostly as palliative cases.

As shown in table 2 the association between the risk stratification and Micro RNA 16 and 511 expression together with BCR ABL-1 transcripts.

Table 1: Association between the risk stratification and the expression of Micro RNA 16, 511 and BCR ABL

Micro RNA 511	Risk stratification						Monte Carlo test (p-value)
	Favorable (n=3)		Intermediate (n=19)		Adverse (n=15)		
	n	%	n	%	n	%	
Under expression (n=2)	0	0.0	1	5.3	1	6.7	$\chi^2_{MC} = 2.250$ P = 0.729
Normal (n=5)	0	0.0	4	21.1	1	6.7	
Over expression (n=30)	3	100.0	14	73.7	13	86.8	
Micro RNA 16							
Under expression (n=5)	0	0.0	5	26.3	0	0.0	$\chi^2_{MC} = 6.351$ P = 0.174
Normal (n=6)	1	33.3	3	15.8	2	13.3	
Over expression (n=26)	2	66.7	11	57.9	13	86.7	
BCR ABL 190							
Negative (n=26)	3	100.0	19	100.0	4	26.7	$\chi^2_{MC} = 22.959$ P = <0.001*
Positive (n=11)	0	0.0	0	0.0	11	73.3	
Cytogenetics							
Normal	0	0.0	16	84.2	1	6.7	$\chi^2_{MC} = 23.070$ P = <0.001*
Abnormal	3	100.0	3	15.8	14	93.3	

*significance p<0.05]

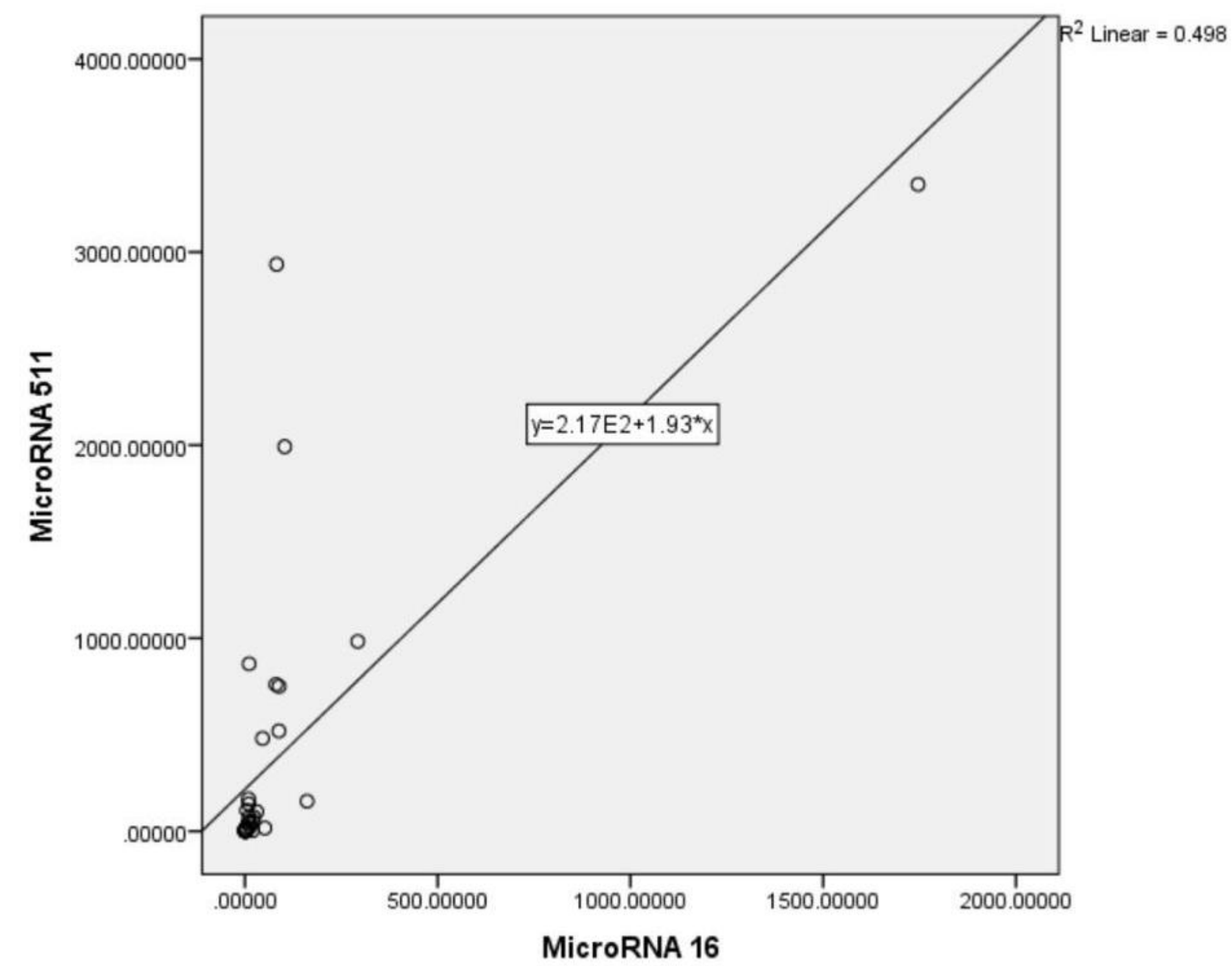


Figure 1: Scatter plot showing Spearman's correlation between Micro RNA 16 and 511
Correlation coefficient (r)= 0.829, P=<0.001*

On the other hand figure 1 shows a scatter plot with Spearman's correlation between MicroRNA 16 and 511 and confirms the strong positive correlation between the two Micro RNAs

Conclusion

Conclusion: MiR-16 and miR-511 were significantly overexpressed in adult B ALL. They have role in diagnosis, but weak role in patients prognosis.

References

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Disclosure

There is nothing to disclose.