

Research Article

MicroRNA Hsa-484 expression in Multiple sclerosis patients and its relation to radiological features



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Abstract

Background: Multiple sclerosis (MS) is an autoimmune disease that causes inflammatory demyelination in the central nervous system (CNS). The pathogenesis of MS involves interaction between a lot of factors including genetic, epigenetic and environmental factors. Many studies have focused on the role of micro-Ribonucleic acids in the pathogenesis of MS including miRNA 145 and miRNA 484. **Objectives:** The aim of this study is to evaluate the relation between the expression of micro-Ribonucleic acid 484 and the radiological features of MS patients. **Patients and Methods:** Plasma samples of 31 MS patients were analyzed using real time polymerase chain reaction technique to measure the relative expression of micro-Ribonucleic acid 484 in addition to MRI of those patients were analyzed for the number of T2 lesions in the brain and the spinal cord. **Results:** There was an insignificant positive correlation between miRNA expression and MRI T2 lesion number. **Conclusion:** miRNA -484 expression in MS patients is not significantly correlated with radiological features.

Key words: MicroRNAs, Gene expression, Multiple sclerosis.

Introduction

Multiple sclerosis (MS) is an autoimmune disease that causes inflammatory demyelination in the central nervous system (CNS). It is the leading nontraumatic cause of neurological disability in young people.^[1] The most commonly affected sites of the CNS are periventricular white matter, brain stem, cerebellum, optic nerve and spinal cord.^[2]

The main clinical characteristics of MS include relapsing remittent course of neurological symptoms, they are multiple disseminated in site and time along course of the disease.^[3]

The pathogenesis of MS involves interaction between genetic, epigenetic and environmental factors.^[4]

Current studies on pathophysiological changes that occur in MS have reported T-cell-mediated inflammatory responses that promotes the release of proinflammatory cytokines by immune cells, abnormalities in blood-cerebrospinal fluid (CSF) barrier permeability, macrophage activation, and the resulting progressive demyelination, also there is an increase in proinflammatory miRNAs and other pathogenic biomarkers.^[5]

Definite diagnosis of MS depends on clinical assessments including neurological examination, cerebrospinal fluid (CSF) analysis, brain and spinal magnetic resonance imaging (MRI) and electrophysiological tests.^[6]

Many studies have focused on the role of miRNAs in pathogenesis of MS.^{[7], [8]} MiRNAs are endogenous non-coding RNA that have regulatory functions. MiRNAs are formed of 21–25 nucleotides and are able to regulate mRNA expression mainly at the posttranscriptional level.^[8]

Several studies have shown that miRNAs have an important role in early development and regulation of the immune system.^[9]

Studies searching for microRNA 484 expression in MS patients showed that there was significant upregulation of its expression in MS patients vs control group.^{[10], [11]}

Aim of the study

The aim of the study to evaluate miRNA 484 expression in MS patients and correlation with MRI T2 lesion load.

Methods

The study included 31 MS patients with no other neurological or autoimmune comorbidities.

Patients are diagnosed to have MS using Mc Donald criteria 2017.

Brain and spinal cord T2 lesions were analyzed by 1.5 tesla MRI device.

Brain T2 lesion number is categorized to three groups: lesion number from 0- 5, from 5-10, more than 10 lesions respectively.

plasma samples of MS patients were analyzed for miRNA-484 expression by real time quantitative polymerase chain reaction (PCR) after miRNA extraction using miRNeasy supplied by Qiagen.

Statistical analysis

The collected data was analyzed using Statistical Package for Social Science (SPSS 20).

A 2-sided probability (*P*) value was used for all statistical analyses and a *P* value of <0.05 was considered statistically significant.

Correlation between miRNA expression and MRI T2 lesion no in brain and spinal cord using Kruskal Wallis test.

Results

It was found that microRNA expression increases with the increase of T2 brain and spine lesion number, however this is statistically insignificant. (*P*-value = 0.89), (*P*-value = 0.62) respectively (table 1), (table 2), (figure 1)

Table 1: miRNA-484 expression among the three T2 brain lesions group.

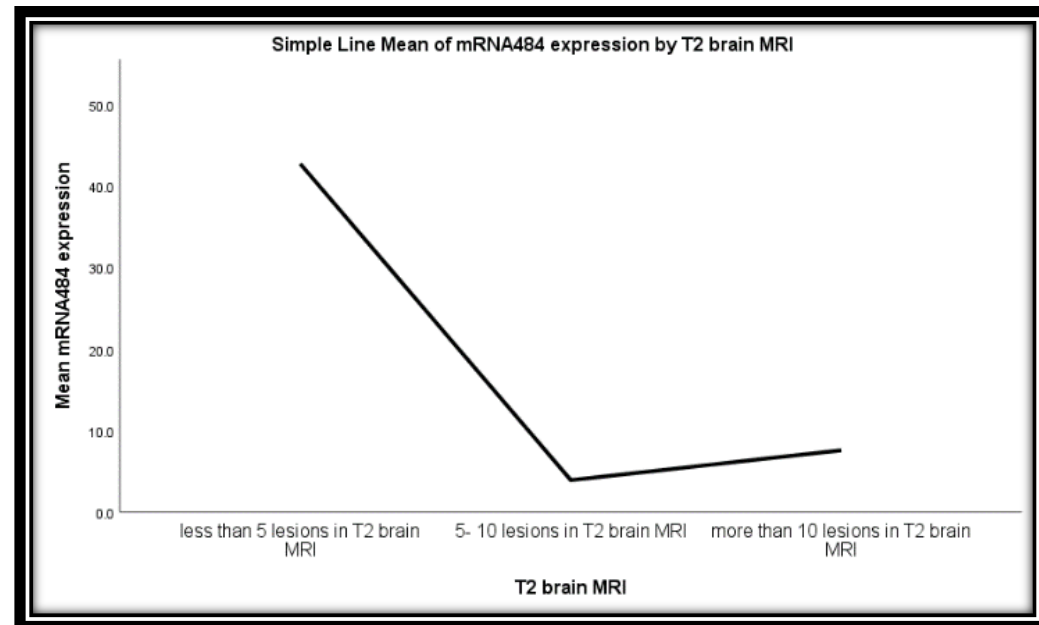
	T2 lesions number						X ² *	P value
	Less than 5		5-10		More than 10			
	Median	IQR	Median	IQR	Median	IQR		
miRNA 484	1.65	.80-6.20	2.50	.30-6.20	4.05	1.25-5.20	0.23	0.89

*Kruskal Wallis test

Table 2: miRNA-484 expression and its relation to the number of spine MRI T2 lesions.

	T2 Spine lesion number								X ² *	P value		
	0		1		2		3					
	Median	IQR	Median	IQR	Median	IQR	Median	IQR				
miRNA 484	.60	.30-.90	3.55	.60-7.70	2.50	.20-5.50	3.10	2.10-4.10	1.78	0.62		

*Kruskal Wallis test

**Fig. (1): linear chart shows miRNA-484 expression among the three T2 brain lesions group.**

Discussion

Magnetic resonance imaging analysis of lesions help in defining the pathobiology reflected by biomarkers. Since miRNAs regulate several cellular pathways included in pathogenesis of MS, it is hypothesized that different miRNAs expressions may show relations with specific MRI measures of brain and spinal cord lesions.

Several studies searched for the relation between miRNAs expression and MRI lesions.

Regev et al., found that four miRNAs showed significant protective correlations

with T1:T2 lesion volume, with the others included hsa.miR.486.5p and hsa.miR.92a.3p showed significant pathogenic correlations with T1:T2 and hsa.miR.375 showed significant pathogenic correlations with brain atrophy.^[12] Also, they found significant pathogenic relation between hsa.miRNA.484 and whole brain volume as well as central gray matter volume.

Conclusion

After studying the relation between miRNA-484 expression in a group of 31 MS patients and the no of T2 lesions in the brain and spinal cord, it was found that

there was upregulation of miRNA-484 expression with increased lesion number however this was insignificant.

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