



## Research 8:

# Correlation between LincR-Gng2-5'and LincR-Epas1-3'AS with the Severity of Multiple Sclerosis in Egyptian patients

Olfat G. Shaker<sup>1</sup>, Rehab M.Golam<sup>2</sup>, Shymaa Ayoub<sup>2</sup>, Lamiaa I. Daker<sup>3</sup>, Mohamed K. Abd elguaad<sup>4</sup>, Eman S. Said<sup>5</sup>, Mahmoud A.F. Khalil<sup>6\*</sup>

<sup>1</sup>)Department of Medical Biochemistry and Molecular Biology Faculty of Medicine, Cairo University, Egypt

<sup>2</sup>)Department of Medical Biochemistry and Molecular Biology , Faculty of Medicine, Fayoum University, Fayoum, 63514, Egypt.

<sup>3</sup>)Department of Neurology, Faculty of Medicine, Fayoum University, Fayoum, 63514, Egypt.

<sup>4</sup>)Department of Medical Physiology, Faculty of Medicine, Fayoum University, Fayoum, 63514, Egypt.

<sup>5</sup>)Department of Clinical Pharmacology , Faculty of Medicine, Fayoum University, Fayoum, 63514, Egypt.

<sup>6</sup>)Department of Microbiology and Immunology, Faculty of Pharmacy, Fayoum University, Fayoum, 63514, Egypt.

**Introduction:** Multiple sclerosis (MS) is an immune-mediated disorder. Long noncoding RNAs (lncRNAs, LncR, Linc RNA) have role in many autoimmune and inflammatory disorders, including MS. LincR-Gng2-5 AS locus in T helper 1 cell (TH1) and LincR-Epas1-3AS in T helper 2 cell (TH2) cell were located in a genomic region rich in genes code for proteins with immune regulatory function. The aim of this study was to evaluate the LincR-Gng2-50 and LincR-Epas1-30 AS fold change in blood of MS patients versus healthy controls and correlate it with disease severity, assessed based on Expanded Disability Status Scale (EDSS). **Material and Methods:** Sixty MS patients 42 relapsing remitting (RR, RRMS), 18 Secondary progressive (SP, SPMS) and sixty controls (age-matched and sex-matched) were studied. Blood of patients and control group undergone the investigation of LincR-Gng2-50 and LincR-Epas1-30 AS fold change by real-time PCR. Fold change  $>2$  and  $p < .05$  represent significant result. Results: LincR-Gng2-50 was significantly upregulated in MS patients with mean fold change (2.559) and ( $p = .03$ ). Meanwhile, LincR-Epas1-30 AS levels were significantly downregulated with mean fold change (0.5964) and ( $p < .004$ ). Patients with SP showed a significantly higher level of LincR-Gng2-5-fold change ( $3.71 \pm 0.7$ ) than that of RR ( $1.33 \pm 0.3$ ). LincR-Epas1-30

القائم بأعمال عميد الكلية

أ.د/ عاصم العيسوي

رئيس القسم

أ.د/ حنان عبدالمنعم



AS was markedly reduced among SP ( $0.43 \pm 0.2$ ) than that of RR ( $0.66 \pm 0.1$ ) but with no significant difference. As regards disease severity (EDSS); there was a significant positive correlation with LincR-Gng2-5 and negative correlation with LincR-Epas1-30 AS. LincR- Gng2-5 and LincR-Epas1-30 AS, both are dysregulated in MS patient suggesting a role in disease pathogenesis. Conclusion: LincR-Gng2-5 AS and LincR-Epas1-30 AS fold change are correlated to MS severity (EDSS).

**Key words**

Multiple sclerosis, long non coding RNA, LincR-Gng2-5' and LincR-Epas1-3'AS

تاريخ النشر: December 2019

القائم بأعمال عميد الكلية

أ.د/ عاصم العيسوي

رئيس القسم

أ.د/ حنان عبدالمنعم