عنوان البحث باللغة الإنجليزية

Correlation Between LincR-Gng2-5′and LincREpas1-3′as with The Severity of Multiple Sclerosis in Egyptian Patients.

ABSTRACT

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. Our aim 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 ¼ .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 ± 0.7) than that of RR (1.33 ± 0.3). LincR-Epas1-30 AS was markedly reduced among SP (0.43 ± 0.2) than that of RR (0.66 ± 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- Gng2-5and 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).