**البحث الأول**: بحث **فردي** غير مشتق من رسالة ولم يسبق تقييمه **منشور دولي**.

**عنوان البحث باللغة الانجليزية:**

**Correlation 1 between LincRGng2-5′and LincREpas1- 3′as with the severity of multiple sclerosis in Egyptian patients**

**عنوان البحث باللغة العربية:**

**العلاقة بين LincR-Gng2-5′ و LincR Epas1-3′as مع شدة التصلب المتعدد في المرضى المصريين**

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## 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-Epas1-3, AS fold change are correlated to MS severity (EDSS)