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**The Thesis Submitted for the Degree of M.Sc (in the field of Genetic)**

# Evaluation of alterations in LncRNA PAN3-AS1 transcription level in the peripheral blood samples of MS patients and its relationship with disease severity

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Winter 2023

# Abstract

**Multiple sclerosis (MS) is an autoimmune and nerodegeranaive diseases associated inflammation and destruction of myelin sheath in the CNS. No single and/or specific cause has been identified for this disease yet. But genetic and environmental factors both play a role in MS development and can impose exacerbation or relapsing effects in MS pathogenic process.Long non-coding RNAs (LNCRNAs) also been identified as important keys in biological and epigenetic processes, tIn addition to their diverse functional roles, their presence in body liquids and their ease of access for further investigations opens up new windows regarding their possible activities in pathogenesis, and make them an appropriate candidate to be served as diagnostic factors. In this research long non-coding *PAN3-AS1* was selected according to microarray data analyses regarding the investigation and the effective role of its expression level in the MS, Then the expression level of this lncRNA was analysed in patients compared to healthy people, using the qRT PCR technique. The blood of MS sample of 48 patients in two phases of SPMS and RRMS with severity and disability (EDSS) of 1 to 6 and age range of 31 to 61 years were drained. 48 sample of normal healthy individuals were taken as control group. According to the results of microarray analysis, which showed a significant decreasing expression in this disease compared to healthy people, the same result was also observed in our study It can be concluded that the present findings reveal the potential role of PAN3-AS1 as a biomarker for MS. *PAN3-AS1* expression level did not show any significant correlation with age and severity of the disease.**