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miR-185 and SEPT5 Genes May Contribute to Parkinson's Disease Pathophysiology

Arman Rahimmi

Department of Molecular Medicine, Kurdistan University of Medical Sciences, Sanandaj, Iran

There are still unknown mechanisms involved in the development of Parkinson's disease (PD), which elucidating them can assist in developing efficient therapies. Recently, studies showed that genes located on the human chromosomal location 22q11.2 might be involved in the development of PD. Therefore, the present study was designed to evaluate the role of two genes located on the chromosomal location (miR-185 and SEPT5), which were the most probable candidates based on our bibliography. In vivo and in vitro models of PD were developed using male Wistar rats and SHSY-5Y cell line, respectively. The expression levels of miR- 185, SEPT5, LRRK2, and PARK2 genes were measured at a mRNA level in dopaminergic areas of rats' brains and SHSY-5Y cells using the SYBR Green Real-Time PCR Method. Additionally, the effect of inhibition on the genes or their products on cell viability and gene expression pattern in SHSY-5Y cells was investigated. The level of miR-185 gene expression was significantly decreased in the substantia nigra (SN) and striatum (ST) of the rotenone-treated group (control group) compared to the healthy normal group ($P < 0:05$). In addition, there was a significant difference in the expression of SEPT5 gene ($P < 0:05$) in the substantia nigra between two studied groups. The results of an in vitro study showed no significant change in the expression of the genes; however, the inhibition on miR-185 gene expression led to the increase in LRRK2 gene expression in SHSY-5Y cells. The inhibition on LRRK2 protein also decreased the cellular toxicity effect of rotenone on SHSY-5Y cells. The results suggested the protective role of miR-185 gene in preventing the development of PD.

Keywords: Parkinson's disease, MiRNA-185, SEPT5, Rotenone, Animal model

a.rahimmi@yahoo.com