IN SILICO PREDICTION OF MIR-619-5P, MIR-1285-5P, AND MIR-4298 INTERACTIONS WITH HUMAN MRNA GENES ASSOCIATED WITH PARKINSON'S DISEASE

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Background: Parkinson's disease (PD) is a progressive neurodegenerative disorder marked by dopaminergic neuronal loss, mitochondrial dysfunction, and abnormal protein aggregation [1,2]. Circulating microRNAs (miRNAs) are emerging as minimally invasive biomarkers and potential regulators of disease-related pathways [3]. Computational prediction tools enable the identification of miRNA–mRNA interactions, providing insights into post-transcriptional regulation in PD [3,4].

Materials and methods: The nucleotide sequences of 2567 human miRNAs were downloaded from miRBase (http://mirbase.org). The nucleotide sequences of human mRNA genes associated with PD were obtained from GenBank (http://www.ncbi.nlm.nih.gov). The analyzed gene set included: ATP13A2, FBXO7, GBA, HLA-DRB5, LRRK2, MAPT, PARK2, PARK7, PINK1, SMPD1, SNCA, UCHL1, and VPS35. Potential binding sites between miRNAs and mRNAs were identified using the MirTarget program. This tool predicts miRNA–mRNA interactions based on nucleotide complementarity across the whole mRNA sequence, including the 5′UTR, CDS, and 3′UTR. For each predicted interaction, the binding position, binding region, free energy (ΔG, kJ/mol), interaction score, and binding length were recorded.

Results: The in silico analysis revealed multiple high-affinity miRNA–mRNA interactions across the PD-related gene set. PARK2 was targeted by miR-619-5p (3′UTR, −121 kJ/mole, ΔG/ΔGm, 100%) and miR-1285-5p (3′UTR, ΔG = −104 kJ/mole, ΔG/ΔGm, 92%), suggesting potential suppression of Parkin-mediated mitophagy. Moreover, MAPT showed strong predicted binding with miR-4298 (3′UTR, ΔG = −112 kJ/mole, ΔG/ΔGm, 89%), indicating possible post- transcriptional regulation of Tau protein expression.

Conclusion: Based on these results, the identified miRNA–gene associations are recommended for further validation as potential biomarkers for PD, and their expression patterns should be experimentally confirmed in plasma or serum samples from PD patients and healthy controls using qPCR to evaluate diagnostic potential and relevance to PD pathogenesis.

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Keywords: microRNA, mRNA, Parkinson's disease, bioinformatics prediction

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