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Novel Biomolecular information in Rotenone-induced Cellular Model of Parkinson's Disease

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Abstract:

In order to uncover the remarkable pathogenic genes or molecular pathological process in Parkinson's disease(PD), we employed a microarray analysis upon the cellular PD model induced by rotenone. Compared to the control group, 2174 genes were screened out to be expressed differently in the rotenone-induced group by certain criterion. GO analysis and the pathways analysis showed the significant enrichment of genes that were associated with the biological process of cell cycle, apoptotic process, organelle fusion, mitochondrial lesion, endoplasmic reticulum stress and so on. Among these significant DE genes, some were sorted out to be involved in cell cycle and protein processing in endoplasmic reticulum. As the PPI network analysis showed, the interaction relationship of the DEGs involved in the process of protein generation in endoplasmic reticulum(ER) was clearly showed up. As a prediction, we emphasized the genes EDEM1, ATF4, TRAF2 might play central roles in the protein misfolding process during the progression of Parkinson's disease and these new-found genes might be the future research focus and therapeutic targets in PD.

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