Gene ontology analysis for differentially expressed genes during neuronal cell death

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Parkinson's disease (PD) is a common neurodegenerative disorder primarily caused by death of dopaminergic neurons in the substantia nigra pars compacta (SN) leading to depleted striatal dopamine (DA) levels. Neurotoxin-based models are important to elucidate the molecular cascade of cell death in DAergic neurons, and 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) has been used to produce PD models in nonhuman primates and mice. 1-Methyl-4-phenyl-pyridium (MPP+), an active metabolite of MPTP, is taken up by DAergic neurons via the dopamine and noradrenaline transporters, resulting in inhibition of complex I of the mitochondrial membrane potential and formation of reactive oxygen species (ROS). Identifying the biological processes involved in MPP+ toxicity could provide a better understanding of the molecular mechanisms in the cell death of PD model. Therefore, differentially expressed genes (DEGs) in MPP+ treated neuronal cells were explored with a commercial whole genome expression array and gene ontology for these DEGs was analyzed with a web-based using the web-based program GOrilla (http://cbl-gorilla.cs.technion.ac.il/).