Perturbed pathways in neurotoxin treated human neuroblastoma SH-EP cells

도진환†, 김나연
동양대학교
(jinhwando@dyu.ac.kr†)

Neuronal cell death by treatment of neurotoxin may be associated with perturbation of pathways within cell. An R package SPIA [1] accounts for system-level dependencies and interactions, as well as identify perturbations and modifications at the pathway by overcoming the limitation of the most currently available approaches such as over-representation analysis and functional class scoring, which consider only the set of genes on any given pathway and ignore their position in those pathways. In this study, pathways that were significantly perturbed in MPP+ -treated human neuroblastoma SH-EP cells were identified by using SPIA with genome-wide gene expression data after MPP+ treatment. The mitogen-activated protein kinase (MAPK) signaling pathway and protein processing in the endoplasmic reticulum (ER) pathway showed significant perturbation. Perturbation of these pathways resulted in the common outcome of upregulation of DNA-damage-inducible transcript 3 (DDIT3). This study suggests that upregulation of DDIT3 might play a key role in MPP+ -induced neuronal cell death.