British Neuroscience Association

PARKINSON'S UK
CHANGE ATTITUDES.
FIND A CURE.
JOIN US.

BRAIN | THE GUARANTORS

THE INTERNATIONAL

BNA2023

FESTIVAL OF NEUROSCIENCE

23 - 26 April 2023 | Brighton, UK

Book of abstracts

Poster number: M_PZ4_102 (TP)

Sub-Theme: Parkinson's Disease: Molecular Mechanisms and Novel Therapeutic Approaches in Patient-Derived Models

MicroRNA and gene expression profiles in a Parkinson's disease cell model.

Authors: Paul Moran, University of Hertfordshire; Dr Mahmoud M. Iravani - Department of Clinical, Pharmaceutical and Biological Science University of Hertfordshire; Dr Maria Braoudaki - Department of Clinical, Pharmaceutical and Biological Science University of Hertfordshire

Introduction: Parkinson's disease (PD) is a neurological condition that predominantly effects movement. It is estimated that 1% of the population over 65 will develop PD, rising to 3% by the age of 85. Analysis of MicroRNA (miRNA) may highlight the genetic mechanisms that contribute to pathogenesis of PD. It has been suggested that miRNA regulate up to 60% of protein coding genes and the dysregulation may contribute to the pathogenesis of different disease states within the body. Identification of miRNA expression profiles may allow for the early identification of PD, potentially allowing for earlier medical intervention before the disease onset. The aim of this study was to analyse the expression of miRNAs and the possible interaction of genes in cells of dopaminergic phenotype after they have been subjected to a mitochondrial or proteasomal inhibitor.

Methods: The SH-SY5Y cells were exposed to the mitochondrial neurotoxin MPP+ and proteasome inhibitor MG132 for 24 hours to result in 50% cell death. The cells were extracted using TRIzol and purified using the mirvana kit. Following isolation and purification, reverse transcriptase quantitative polymerase chain reaction was conducted to observe the possible dysregulation of the genes, SNCA, ITPR1 and CACNA1C and the PD associated miRNA: miR-107, and miR-128a, in the absence and the presence of MPP+ or MG132.

Approach for statistical analysis: Paired t-test was used to observe the 2-ΔΔCt for expression variation between wildtype cells and drug exposed cells.

Results and conclusions: The three genes and miR-107 exposed to MPP+ were all significantly down regulated ($p<0.05$), SNCA (90.94%), ITPR1 (56.43%), CACNA1C (79.72%) and miR-107 (74.56%). There was a significant downregulation ($p<0.05$) of SNCA (87.11%) and miRNAs, miR-107 (95.71%) and miR-128a (62.09%) that had exposure to MG132. Interestingly, both MPP+ and MG132 caused a similar level of decreased expression in SNCA, although both drugs have a different mode of action. Based on current findings, the expression data generated indicate that both drugs may cause significant down regulation of specific genes and miRNAs within the cell potentially identifying a contributing factor associated with the pathogenesis of PD.