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Molecule of the month: miRNA and Parkinson's disease protein PARK2

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Parkinson's disease is generally associated with aging, i.e. elderly individuals. We are gaining many deep insights into neuropathogenesis in Parkinson's disease and there are many publications on this topic; we briefly mention a few as they relate to the increasingly studied miRNAs. Parkinson's disease results from protein inclusions or Lewy bodies and destruction of (mid-brain) *substantia nigra pars compacta* neurons that are dopaminergic. A novel approach to investigate molecular processes in human diseases as well as in normal control and function is through the study of miRNAs. miRNAs are increasingly associated with many diseases and in Parkinson's disease **[1, 2].**

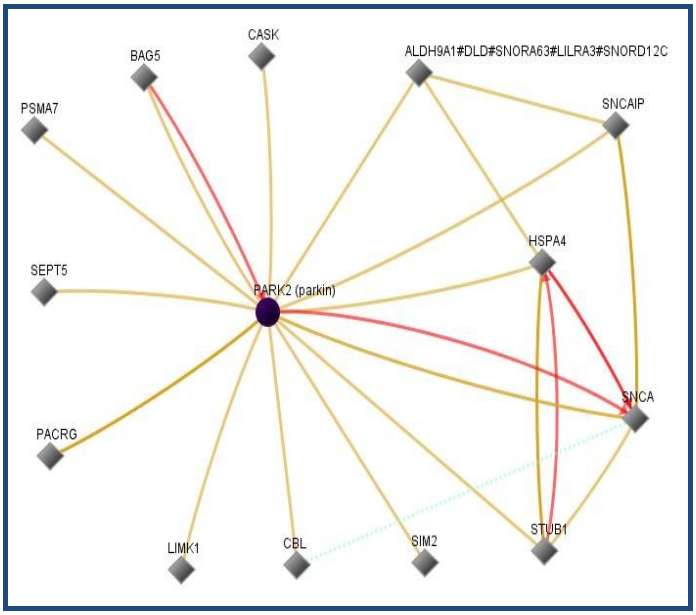

Figure 1: Network of input protein (Park2) with immediate interactive proteins. In this figure, line-colors and various interactions with other genes are red Down-regulation, green Up-regulation, beige Regulation, purple Co-expression, brown Physical Interaction, turquoise dotted Predicted Protein Interaction, and mauve dotted Predicted TFactor Regulation (GenePro SA Biosciences, http://www.sabiosciences.com/).

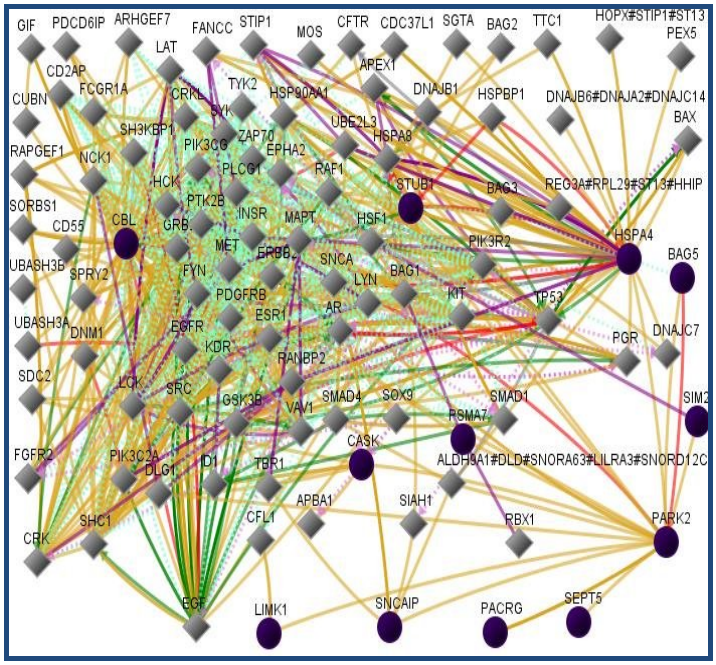

Figure 2: Network of input proteins from figure 1 (Park2, CASK, SNCAIP, HSPA4, STUB1, SIM2, CBL, LIMK1, PACRG, SEPT5, PSMA7, BAG5) and showing additional neighbors of these proteins (up to 100 total). In this figure, line-colors and various interactions with other genes are red Down-regulation, green Up-regulation, beige Regulation, purple Co-expression, brown Physical Interaction, turquoise dotted Predicted Protein Interaction, and mauve dotted Predicted TFactor Regulation (5-GenePro SA Biosciences, http://www.sabiosciences.com/).

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Additional studies used a bioinformatics and computational approach to the analysis of gene expression using the Gene Expression Omnibus database at NIH **[3]**. They then predicated Parkinson's disease associated transcription factors, miRNAs, and identified 11 genes that include a new transcription factor, N-Myc down-regulated gene 1 (NDRG1) and junction plakoglobin (JUP).In Parkinson's disease, NDRG1 is regulated by miRNA-133 **[4].**

miRNA profile analysis indicated miR-34b and miR-34c decreased expression. These changes were found in the *substantia nigra*, frontal cortex, cerebellum, and *amygdala*. In aneuroblastoma cell culture line, depletion of miR-34b or miR-34c resulted in cell death. In addition, depletion of these miRNAs resulted in decreased expression of Parkin or parkinson protein 2 (Park2) and parkinson protein 7 (DJ1). These cellular changes appear to result in mitochondrial dysfunction in Parkinson's disease **[2].**

Figure 1 shows an interactive network diagram of input neighbors to Park2 (parkin) and **Figure 2** shows an interactive network diagram of input proteins from figure 1 (Park2, CASK, SNCAIP, HSPA4, STUB1, SIM2, CBL, LIMK1, PACRG, SEPT5, PSMA7, and BAG5). It is left as a puzzle for the interested reader to identify the various genes and their functions in the figures **[5-7].**

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