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CONSTRUCTION AND ANALYSIS OF PARKINSON DISEASE PROTEIN NETWORK

Shobha Shouche and Sachin Rahangdale
Govt. Madhav Science College, Ujjain (M.P.)
shobha.shouche@gmail.com

Abstract
Neurological Disorders are diseases of the central and peripheral nervous system. These disorders Parkinson's disease of the nervous system. Parkinson's disease (PD) belongs to a group of conditions called motor system disorders, which are the result of the loss of dopamine-producing brain cells. Biological network is a network that applies to the biological system. These networks are widely used in many branches of biology as convenient representation of patterns of interaction between appropriate biological elements. Proteins-protein interaction (PPIs) in a cell form protein interaction networks (PINs) where proteins are nodes and their interaction are edges. In the present work to investigate network properties of proteins in disease protein-protein interaction network framework.
Keywords- appropriate, interaction, framework, network, disorders.

Introduction

Parkinson's disease (PD) belongs to a group of conditions called motor system disorders, which are the result of the loss of dopamine-producing brain cells. The four primary symptoms of PD are tremor, or trembling in hands, arms, legs, jaw, and face; rigidity, or stiffness of the limbs and trunk; bradykinesia, or slowness of movement; and postural instability, or impaired balance and coordination. As these symptoms become more pronounced, patients may have difficulty walking, talking, or completing other simple tasks. PD usually affects people over the age of 60. Early symptoms of PD are subtle and occur gradually. In some people the disease progresses more quickly than in others. As the disease progresses, the shaking, or tremor, which affects the majority of people with PD may begin to interfere with daily activities. Other symptoms may include depression and other emotional changes; difficulty in swallowing, chewing, and speaking; urinary problems or constipation; skin problems; and sleep disruptions. There are currently no blood or laboratory tests that have been proven to help in diagnosing sporadic PD. Therefore the diagnosis is based on medical history and a neurological examination. The disease can be difficult to diagnose accurately. Doctors may sometimes request brain scans or laboratory tests in order to rule out other diseases

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Material and Methodology:

Literature survey:
Literature mining was carried out to collect miRs in **Parkinson** using Literature databases such as PubMed, Sirus etc., and search engines such as Google, Google Scholar etc. miR2Disease [1] was also used to gather **Parkinson** specific miRs information.

Annotation of selected miRs:
We identified experimentally validated miR targets using miRNA target database. Using miRNA target database mirWalk **[3]**, miRecords **[4],** miReg **[5] and** miRTarBase **[2].** We collected target of the selected miRNAs. These targets were further analyzed into DAVID **[6]** and TOPPGENE **[7]** for functional annotation and gene list enrichment and candidate gene prioritization.

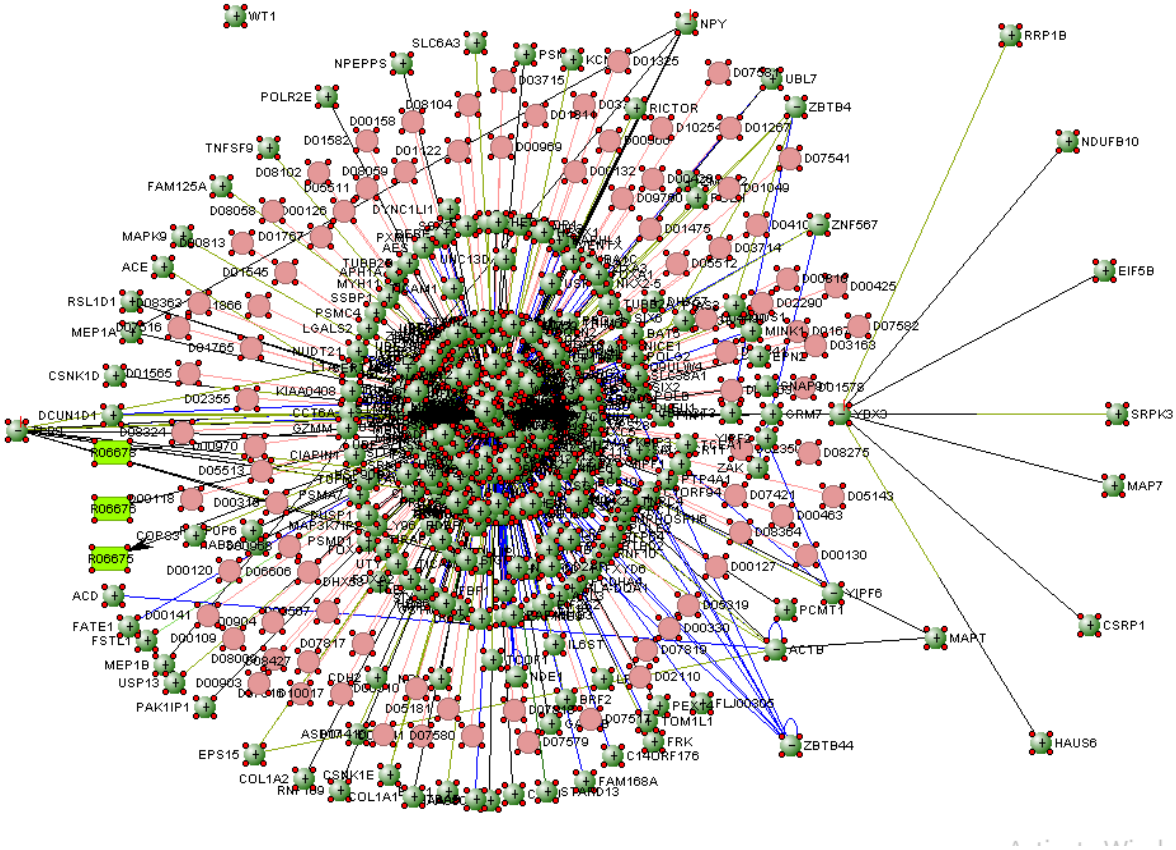

Figure -1: Parkinson Disease specific TFs/miRs interaction Network.

miRNAs Targets Interaction network:

We made an interaction network using target proteins of miRNA with the help of Osprey v1.2.0 **[8]** powered by human using Grid database and Visant **[9].** It predicts interaction network and mapped pathway of target proteins.

Result

We collected 5 miRNAs for Parkinson Disease using literature mining such as PubMed, miR2disease database.Using miRNA target database mirWalk , miRecords **,** miReg and miRTarBase. We identified 298 targets for Parkinson Disease. We made an interaction network using target proteins of miRs with the help of Visant. **Conclusion**

Protein-protein interaction network are a powerful tool to study biological processes in living cells. In this review we present the process of PPIN studies from abstract to more default representative recent studies have used structural information on PPIN to also understand the molecular mechanism of binding protein selection. In the optimization of targeted studies to design novel chemical components for medicinal treatment.

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