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Comparative Analysis of the Migraine Pathway in Human and *C. elegans*

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Abstract: Migraine is an episodic pain disorder whose path physiology is related to deficiency of serotonin signaling and abnormal function of the P/Q-type calcium channel CACNA1A. Because the relationship of the CACNA1A channel to serotonin signaling is unknown and potentially therapeutic interest used genetic analysis of the *Caenorhabditis elegans* ortholog of this calcium channel. UNC-2 helps to identify candidate downstream effectors of the human channel. Analyze the Ca++ channel pathway (responsible for migraine) in Human. Identification of the genes involved in this pathway and does the complete analysis of the protein synthesized by the selected gene. Find out the domains and motifs in human for the protein and their positions. Now for the comparative analysis of the migraine pathway in human and *C. elegans*, searching of *C. elegans* genome for homologous genes present in Ca++ channel pathway in Human and perform the alignment of nucleotide as well as protein sequences for human and *C. elegans*. Identify the domain and motifs in *C. elegans* for comparative studies.

Key words: Episodic, KEGG, migraine, neurodegenerative disorders

INTRODUCTION

Neurodegenerative and psychiatric disorders account for more hospitalizations and long-term care than nearly all other disorders combined. Neurodegenerative disorders are among the most devastating illnesses in western society. Age is a risk factor, and that means the problem will only grow worse, as the number of people over the age of 65 is expected to double by 2025 (John, 2002).

The population of the United States is aging, and an ever-increasing number of Americans afflicted with neurodegenerative diseases. Because the pathogenesis of many of these diseases remains unknown, the environmental factors may also play a causal role (Rebecca *et al*., 2005). The study of metabolic pathways is becoming increasingly important to exploit an integrated, systems-level approach for optimizing a desired cellular property or phenotype (Matteo *et al*., 2007).

Age is the most important risk factor for Alzheimer's disease, a progressive, neurodegenerative disease characterized by amyloid plaques and neurofibrillary tangles in the brain (Laino, 2007). Prion diseases belong to group of progressive conditions that affect the nervous system in humans and animals. In people, prion diseases impair brain function, causing memory changes, personality changes, a decline in intellectual function (dementia) and problems with movement that worsen over time (Cooper, 2003).

Dentatorubral-pallidoluysian atrophy (DRPLA) is an autosomal dominant spinocerebellar degeneration caused by an expansion of a CAG repeat encoding a polyglutamine tract in the atrophin-1 protein (Kanazawa, 1999). Parkinson's disease is a chronic, progressive disorder of the central nervous system that belongs to a group of conditions called motor system disorders..

Amyotrophic lateral sclerosis is a form of motor neuron disease. ALS is a progressive, fatal, neurodegenerative disease caused by the degeneration of motor neurons, the nerve cells in the central nervous system that control voluntary muscle movement. Huntington disease (HD) is a neurodegenerative disease that affects approximately 1 in 10,000 individuals of European decent and is characterized by progressive motor impairment and dementia (The Huntington's Disease Collaborative Research Group, 1993).

All these NDs are correlated with each other through some common proteins/genes. By study it found that few of these proteins are responsible for other NDs like Alexander disease and Pick's disease. The common pathway present in Kyoto Encyclopedia of Genes and Genomes (KEGG, 2008) for Neurodegenerative Disorders contains all above-mentioned NDs except Alexander disease and Pick's disease. A common pathway is constructed for Neurodegenerative Disorders including these two (Alexander and Pick's) diseases in PATHWAY STUDIO 4.0.

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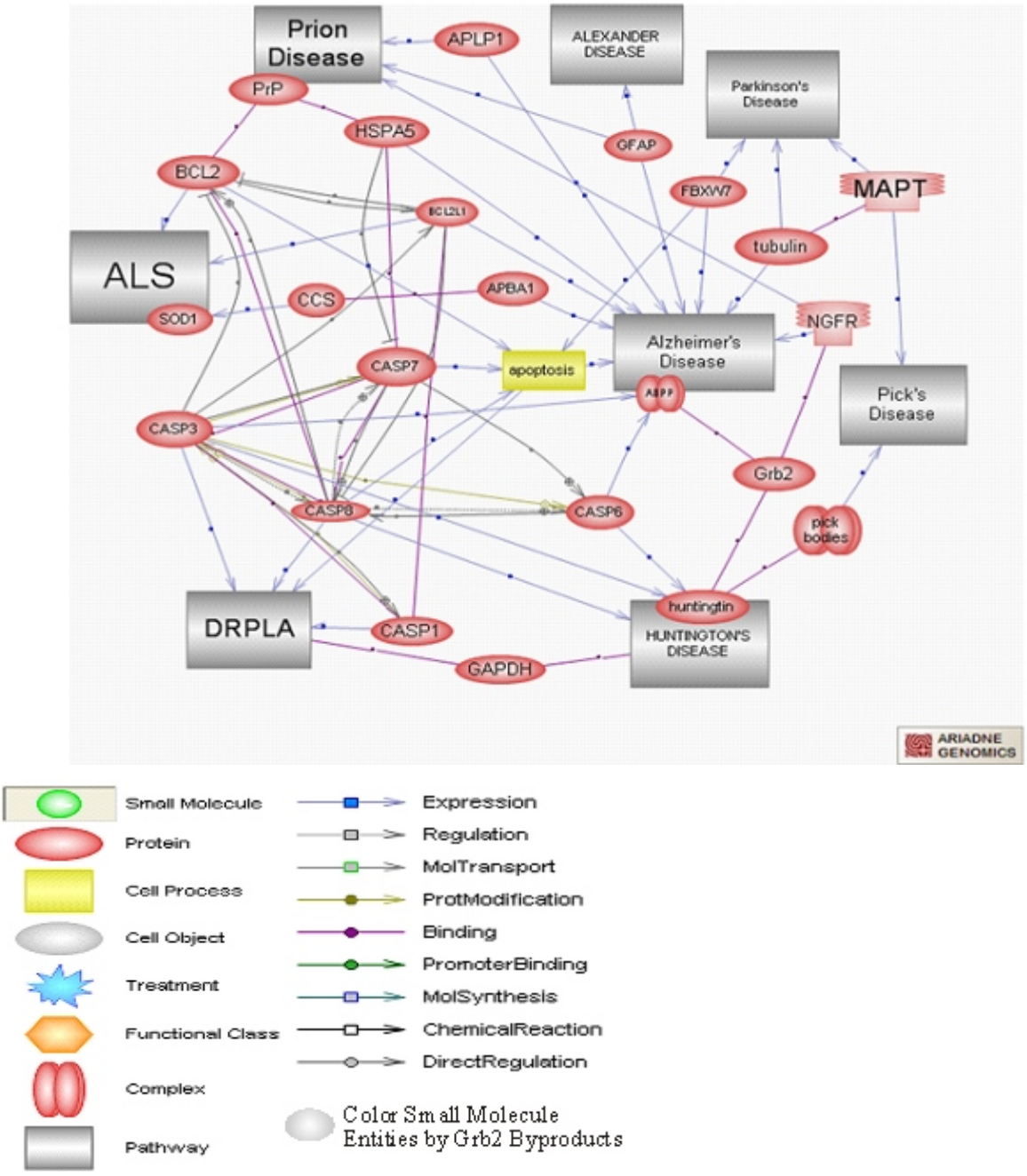

Fig. 1: Common pathway for neurodegenerative disorders

MATERIALS AND METHODS

An approach is taken to design a new pathway in PATHWAY STUDIO 4.0 including all six pre available NDs (KEGG, 2008) and two other diseases (Alexander disease and Pick's disease). We studied the individual pathways and common ND pathway during the March-April, 2008 at "The Bioinformatica Solutions Lucknow (India)" and it was identified that there are following proteins which are interlinked with more than one diseases-NGFR, APLP1, GFAP, BCL2, HSPA5, MAPT, FBXW7, CASP8, CASP3, CASP6, CASP7, CASP1, GRB2, GAPD, APBA1, BCL2L1.

Following steps are used to build the final comparative pathway for above mentioned neurodegenerative disorders:

- Downloading Database
- Importing Protein List
- Build Pathway
- Edit Pathway
- Save Pathway

After downloading the database the common proteins are imported using import wizard and finally the build pathway function makes the pathway automatically which can be edited or modified as per requirement in Pathway Studio 4.0

The software is supplied with the ResNet database, generated by the MedScan automated text-mining tool from the entire PubMed and other public sources. The software can also work with a number of public and commercial databases such as KEGG, BIND, GO, and the PathArt database of curated signaling and disease pathways.

Using the Pathway Studio databases one can conveniently organize and effectively manage a large amount of biological data. Database objects can be organized into arbitrary number of folders and subfolders.

RESULTS AND DISCUSSION

With the help of PATHWAY STUDIO the common pathway for showing the relations among the mentioned NDs and the proteins related with them is made and finally this compartive pathway is shown (Fig. 1). The pathway available previously shows the interactions among the neurodegenerative disorders except Alexander and Pick disease, which are added in this common pathway. The GFAP and MAPT (protein) are very important in this pathway because they add two more disease in pre available pathway and makes the new pathway. GFAP(glial fibrillary acidic protein) is the responsible protein for the Alexander disease. The mutation in this pritein is is the main factor of Alexander disease. This protein is also foud for the Prion Disease and Alzheimer's Disease.

MAPT (Microtubule-associated protein tau) is very important factor in case of Alzheimer's disease and Parkinson's disease because this is a microtubule associative protein and bind with tubulin. This is common factor in these both diseases. It is also identified that MAPT is responsible for Pick Disease also.

In this common pathway there are many proteins which are interlinked with more than one disease. So it can be identified that the possibility of a drug for more than one disease. A unique and common drug can be designed for more than one diseases.

CONCLUSION

This pathway is important and useful in many sense like there may be identified a common and suitable drug for more than one NDs because there are many proteins, which are common in three mentioned diseases. In this pathway there are eight NDs and the pre available pathway for NDs has only six diseases (KEGG, 2008), two extra diseases (Alexander disease and Pick disease) are added in this pathway.

REFERENCES

Cooper, D.N., 2003. Nature Encyclopedia of the Human Genome. Nature Pub. Group, New York, London, pp: 64-67, 712-720.

John, B., 2002. Neurodegeneration in a Nutshell, Bio-IT World.

Kanazawa, I., 1999. Molecular pathology of dentatorubral-pallidoluysian atrophy. Philos. Trans. R. Soc. Lond. B Biol. Sci., 354(1386): 1069-1074.

Laino, C., 2007. The hunt for genes and cures. Neurol. Now, 3(2): 20-27.

Matteo, B., F. Renato and L. Pietro, 2007. Current trends in the bioinformatics sequence analysis of metabolic pathways in prokaryotes. Brief. Bioinform., 9(1): 34-45.

Rebecca, C.B., H.L. Alan and R.S. Babasaheb, 2005. Neurodegenerative diseases: An overview of environmental risk factors. Environ. Health Perspect., 113(9): 1250-1256.

The Huntington's Disease Collaborative Research Group, 1993. A novel gene containing a trinucleotide repeat that is expanded and unstable on huntington's disease chromosomes. Cell, 72: 971-983.

KEGG, (Kyoto Encyclopedia of Genes and Genomes), 2008. Retrieved from: http://www.genome.jp/kegg/ (Accessed: 13 April 2008).