

Bioinformatics Analysis of α -Synuclein

Damu Wei, Canquan Mao

School of Life Science and Engineering of Southwest Jiaotong University,
Sichuan Chengdu 610031

Abstract—Authors of papers to the bioinformatics approach to analyse the nucleotide and amino acid sequence of alpha synuclein nucleotide and amino acid, including as the character of physical and hydrophobicity, secondary structure prediction domains, prediction of the conserved domains and phylogenetic analysis. The results showed the α -synuclein encode a deduced 1462 amino acid, had a predicted molecular weight of 156.91 kD, and the protein which hadn't peptide, transmembrane domain and 205 phosphorylation sites is alkaline and instability. Helix secondary structure mainly composed of α helix, β turn, extended strand and random crimped. Phylogenetic analysis showed that α -synuclein of human had a very high homology with mammals, and bonobos and sumatran species of orangutans in the most close relatives. These studies built a theoretical foundation for the further research on the structure and function of α -synuclein.

Keywords— α -synuclein; Parkinson Disease; Bioinformatics.

I. INSTRUCTION

Alpha-synuclein is a widely distributed protein of the central nervous system presynaptic membrane upon the small molecules soluble proteins, which are mainly distributed in presynaptic endings of nerve cells in hippocampus and cortex area to express more abundant, myelin contact area and the neocortex of incomplete expression is most obvious, and the motion area and primary sensory contact area, before fully myelinated primary motor and express the weakest primary sensory area and myelin sheath of neurons in brain tissue that develops complete area, alpha-synuclein express the less [2]. At the same time, in bonobos, sumatran orangutan, white-cheeked gibbons and cynomolgus monkeys, people found genes encoding for alpha-synuclein, with for alpha-synuclein rich expression in brain tissue, and is uncommon in other organizations, that it is the product of evolution. In addition, alpha-synuclein is a synaptic proteins of unknown function, is a major part of the small Louis body (LBS) - gathered neuronal cytoplasm protein inclusion, with idiopathic Parkinson's disease (PD) and familial characteristics sign [3].

II. MATERIALS AND METHODS

A. Materials

From NCBI, Searching alpha synuclein, choose number 60392197 amino acid sequence and the following sequence: XP_005274609.1; XP_003819634.1; XP_008971238.1; XP_002831517.1; XP_003261212.1; XP_009232952.1; XP_001091195.1; XP_007989513.1; XP_005593254.1; EH

H60771.1; XP_003917565.1. A total of 12 amino acid sequence to download

B. Methods

The alpha synuclein use online software: ProtParam analysis of physical and chemical properties (<http://web.expasy.org/protparam/>); Phosphorylation sites with NetPhos 2.0 Server (<http://www.cbs.dtu.dk/services/NetPhos/>) and hydrophobic/hydrophilic protein sequence analysis with ProtScale (<http://web.expasy.org/protscale/>); Signal peptide analysis with SignalP 4.1 Server (<http://www.cbs.dtu.dk/services/SignalP/>) and transmembrane domain structure prediction using TMHMM Server v. 2.0 (<http://www.cbs.dtu.dk/services/TMHMM-2.0/>); Secondary structure prediction, by SOPM (https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_sopma.html) and USES the NCBI web site online software Conserved Domains predict conservative structure domain; System evolutionary Tree using Mega5.0 software in the Maximum Likelihood Tree method [4].

III. RESULT

A. The physical and chemical properties

Using ProtParam software analysis the physical and chemical properties of the alpha synuclein sequence of amino acids numbered 60392197, the results are as follows, the gene encoding 1462 amino acids, the protein of the relative molecular weight of 165.91; The theoretical isoelectric point is 5.61, is acidic protein, unstable coefficient is 46.13, of unstable protein.

B. Phosphorylation sites and hydrophobicity analysis

Through NetPhos2.0 Server for alpha synuclein phosphorylation site analysis, the result is shown in figure 1, use online software ProtScale analysis of alpha synuclein hydrophobic as shown in figure 2.

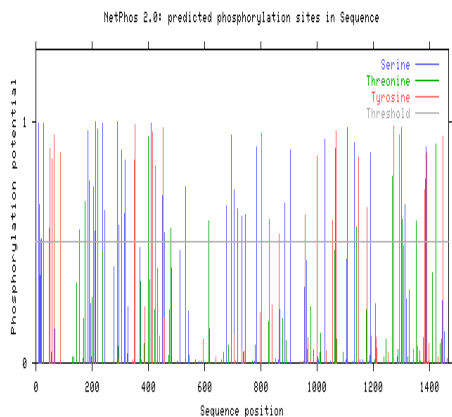


Figure 1. alpha synuclein phosphorylation site analysis

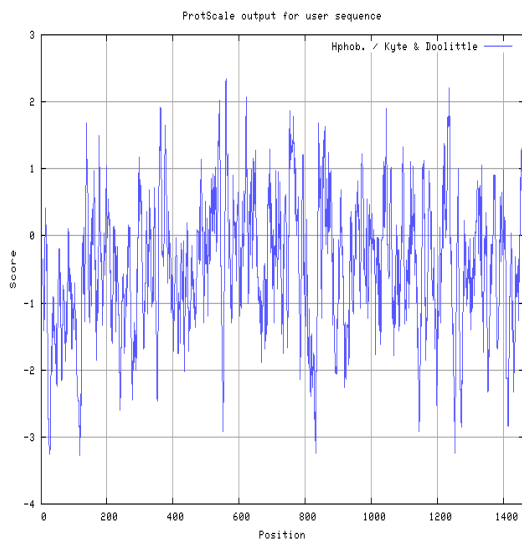


Figure 2. alpha synuclein Hydrophobicity analysis

C. Protein signal peptide and across a membrane structure analysis

Through online tools SignalP4.1 analysis of signal peptide alpha synuclein Server, as shown in figure 3, use online software TMHMM Server v. 2.0 analysis of alpha synuclein across a membrane structure, as shown in figure 4.

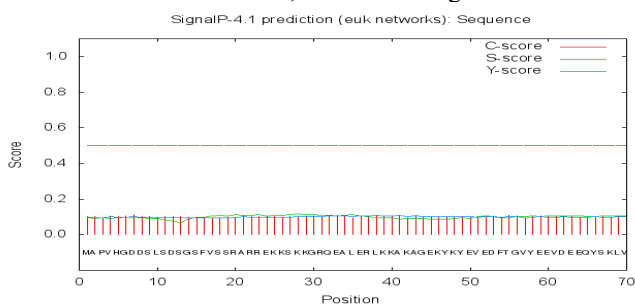


Figure 3. alpha synuclein signal peptide protein analysis

As shown in figure 3, should not have a signal peptide protein prediction, the protein is not a secreted protein, it is synthesized from free ribosomes, into the cytoplasmic protein sol, participate in the mitochondria, nucleus, peroxidase and other chemical reactions.

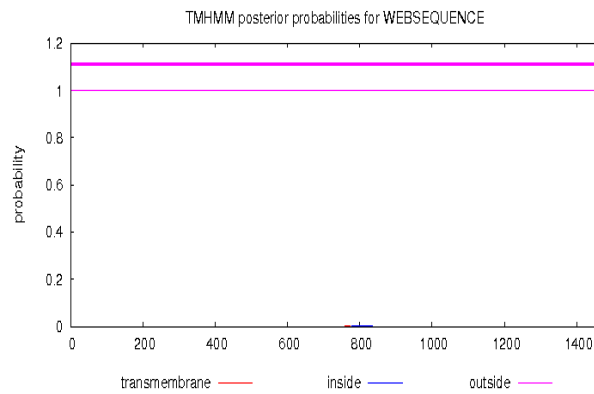


Figure 4. alpha synuclein proteins across the membrane structure of domain analysis

As shown in figure 4, TMHMM of alpha synuclein proteins across the membrane structure analysis forecast, according to some across membrane area, located at 800 or so.

D. Protein secondary structure and conservative structure domain analysis

Using SOMPA software analysis of alpha synuclein secondary structure, as shown in figure 5, through the Conserved Domains to predict alpha synuclein conservative structure, as shown in figure 6.

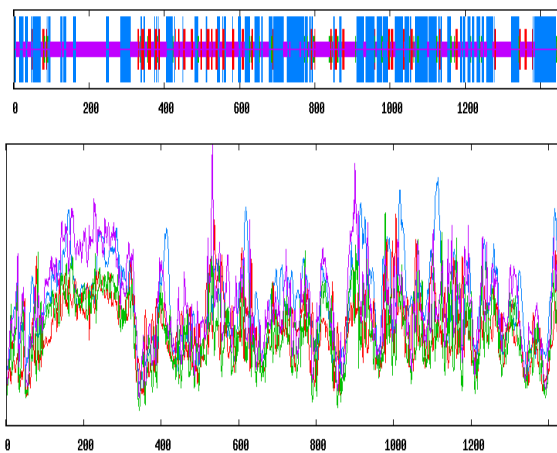


Figure 5. alpha synuclein protein secondary structure prediction

The results showed that the protein secondary structure mainly have alpha helix (41.04%), beta corner (3.83%), extended chain (10.12%) and random curl (45.01%).

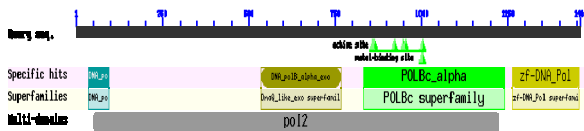


Figure 6. alpha synuclein conservative domain structure prediction

Figure 6 shows, alpha synuclein encoding protein contains three conservative domain structure, DnaQ_like_exo superfamily, POLBc superfamily and zf - DNA_Pol superfamily.

E. Analysis of the evolution

Using Blastp programs in NCBI, alpha synuclein protein amino acid homology analysis, the results are shown in figure 7.

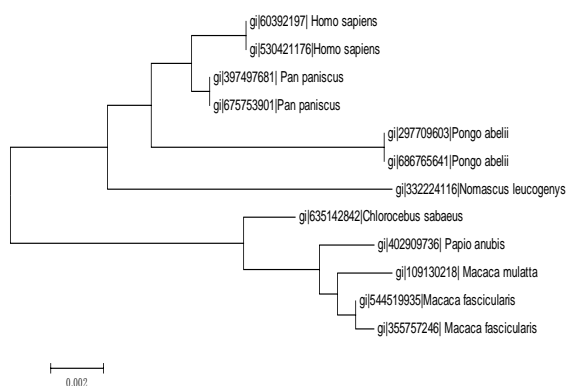


Figure 7. based on maximum likelihood method (M - L) alpha synuclein protein system in the tree

As shown in figure 7, find the 7 species from the NCBI 12 alpha synuclein sequence alignment and protein sequences using MEGA5, ML method, constructs the evolutionary tree, as shown in figure 7, according to the results of alpha synuclein first divided into two, Homo sapiens, Pan paniscus, Pongo abelii and Nomascus leucogenys for a class, Macaca mulatta, Chlorocebus sabaeus and Papio anubis for category, the first YaZhi is divided into Nomascus leucogenys and Homo sapiens, Pan paniscus and Pongo abelii, then Homo sapiens and Pan paniscus affinity recently.

IV. DISCUSSION

Now, China's aging population problem will be more and more serious, and the incidence of Parkinson's disease will be increased, then the study of age-related diseases such as Parkinson's disease is very meaningful. China's national bureau of statistics in January 2013, according to data from China's total population of 1.3 billion people, including those aged more than 60 years accounted for 14.9%, in 2030 is expected to reach 25% of the total population. At the same time, the end of 2012, the Chinese people over age 65 proportion is 9.4%. China's existing ageing population has exceeded 160 million, and an annual rate of nearly 8 million increase [5]. And alpha synuclein occupy a key role in Parkinson's disease, in recent years, along with the de-

velopment of genome research, bioinformatics method is applied more and more get the attention of researchers, and has been applied to the actual research. By bioinformatics method to find the alpha synuclein protein has carried on the preliminary bioinformatics analysis, results show that the genetic encoding 1462 amino acids, the molecular weight of 165.91 KD, unstable acidic protein. There is no signal peptide and partly across a membrane structure, a total of 205 phosphorylation sites; Secondary structure is mainly composed of alpha helix, beta Angle, extending chain and random curl, it is generally believed that in the secondary structure of alpha helix, beta fold more stable than random curl, to maintain relatively stable in the spatial structure of protein molecules play an important role, at the same time there may be three conservative in conservative domain analysis area, indicated that the protein is a conservative protein, it for research. Phylogenetic tree analysis showed that Homo sapiens alpha synuclein and Pan paniscus and Pongo abelii are more affinity. Above these bioinformatics research, for further research of alpha synuclein gene structure and function of the provided the necessary theoretical basis.

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