IN SILICO ANALYSIS AND PHYLOGENY OF VERTEBRATE RHODOPSIN

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Abstract: Phylogenetics & Evolutionary Biology is the field that deals with the study of evolutionary relations among groups of organisms and the computational simulation techniques for the study of biological, behavioural, and social systems. A phylogeny or evolutionary tree represents the evolutionary relationships among a set of organisms or groups of organisms. To analyze the protein rhodopsin, the amino acid sequence of human rhodopsin was retrieved from NCBI site and was used for analysis in PepTool 2.0. From the results of present *in silico* protein analysis and phylogenetic study of vertebrate rhodopsin it can be concluded that the amino acid sequences among different vertebrate species show slight to moderate differences without affecting its function of light absorption during the phenomenon of vision.

Keywords: phylogeny, evolutionary relationships, rhodopsin, amino acid sequence differences, effect on vision.

1. Introduction

The area within the eye that detects light and colour is the called the Retina. The two types of detection cell present, rods and cones, process information coming through the Lens and send it down the optic nerve to the brain. Rod cells detect the degree of lightness entering the eye and their sensitivity is dependent on the amount of Rhodopsin present, which is itself generated within the cells. Rhodopsin, also known as visual purple, is a biological pigment in photoreceptor cells of the retina that is responsible for the first events in the perception of light. Rhodopsin of the rods most strongly absorbs green-blue light and, therefore, appears reddish-purple, which is why it is also called "visual purple". It is responsible for monochromatic vision in the dark. Several closely related opsins exist that differ only in a few amino acids and in the wavelengths of light that they absorb most strongly. A phylogenentic tree, represents the evolutionary relationships among a set of organisms.

2. Review of literature

Mario X. et al., 2003 studied the evolutionary history of type 1 rhodopsins. Type 1 (archaeal) rhodopsins and related Rhodopsin-like proteins had been described in a few halophile archaea, c-proteobacteria, a single cyanobacterium, some fungi, and a green alga. These close relationships suggest that at least one horizontal gene transfer event involving rhodopsin genes occurred between prokaryotes and eukaryotes.

Belinda and Campbell, 2000, studied the phylogenetic reconstruction of vertebrate Rhodopsin. Two spurious nodes were found in phylogenetic analyses of vertebrate rhodopsin sequences in comparison with well established vertebrate relationships. These spurious reconstructions were well supported in bootstrap analyses and occurred independently of the method of phylogenetic analysis used. Use of this data set of vertebrate rhodopsin sequences allowed us to exploit establish vertebrate relationships, as well as the considerable amount known about the molecular evolution of this gene, to identify important factors contributing to the spurious reconstructions.

Kumar and Dwivedi, 2013, studied the evolutionary analysis and motif discovery in Rhodopsin from vertebrates. In their investigation, total twenty different protein sequences of rhodopsin from different organisms of vertebrates were obtained from GenPept database and only 347 characters of each sequence were considered for motif discovery, motif family analysis and phylogenetic analysis.

3. Research Methodology

To analyse the protein rhodopsin the amino acid sequence of human rhodopsin was retrieved from NCBI site and was used for analysis in PepTool 2.0

Method for Obtaining Protein Sequences in FASTA Format: - Google window of internet explorer was opened. Wrote NCBI, pressed enter, NCBI home page was displayed. On home page, wrote protein name, got list of animals in display box. Clicked on name of animal, sequences of protein were displayed. Copied required information of animals. Then clicked on FASTA. Amino acid sequence of a protein in FASTA format was displayed. Copied the sequence and pasted into MS word. Copied as many as larger number of sequences as possible.

Method for Phylogenetic Tree Reconstruction: -

The amino acid sequences downloaded from the NCBI site were subjected to alignment and for the construction of phylogenetic tree using MEGA 5.03. A phylogenetic tree was saved and analysed.

4. Observation and result

PHYLOGENY OF RHODOPSIN: -

4.1. Sequences Alignment:-

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4.2. <u>Phylogenetic Tree:</u> -

<u>Phylogenetic Tree:</u>

The multiple sequence alignment file was used for the phylogenetic analysis by MEGA 5.03. From the multiple sequence alignment of rhodopsin, it is clear that the sequences analyzed in 23 vertebrates share the strong similarity among themselves.

The phylogenetic analysis was carried out by using distance method and clustering by UPGMA (Unweighted Pair Group Method with Arithmetic Mean), A dendogram of rhodopsin drawn by using MEGA 5.03 reveals the formation of an outgroup comprising of *Sus scrofa, Cavia porcellus, Bos Taur*us and *Canis lupus familaris* sequence. The sequences of *Gallus gallus* and *Taeniopygia guttta*, and *Anolis carolinensis* and *Ophiophagus Hannah* does shows the considerable similarity with others. The remaining fifteen sequences of rhodopsin from different animals form four groups. The first group comprises of *Rattus norvegicus, Mus musculus, Felis catus, Cricetulus*., the second group comprise of *Oryctolagus cuniculus, Homo sapiens, Macaca faciularis*., the third group comprise of *Rana catesbeiana, Xenopus laevis, Xenopus (Silurana) tropicalis.*, and the fourth group comprise of *Sargocentron diadema, Neoniphon sammara, plecoglossus altivelis, Cyprinus carpio, Poecillia reticulata*. The dendogram based upon the protein sequences of rhodopsin demonstrate the presence of four clusters among the 23 different animals.

4.3 Conclusion

From the results and discussion of present *in silico* protein analysis and phylogenetic study of vertebrate rhodopsin it can be concluded that the amino acid sequences among different vertebrate species show slight to moderate differences without affecting its function of light absorption during the phenomenon of vision.

Acknowledgement

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