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Research Article

SEQUENCE ANALYSIS OF AKT1 PROTEIN FROM *Homo sapiens*

KHARAT A.S.[1] AND GULWE A.B.*[2]

[1]Dr. Babasaheb Ambedkar Marathwada University, Subcampus Osmanabad, India
[2]Swami Ramanand Teerth Marathwada University Nanded, Sub Centre Latur India
*Corresponding Author: Email-ashishgulwe@gmail.com

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Abstract- The aim of the present study is to identify the origin, evolutionary distance and conserved domain analysis of the divergent phylogenetic lineage of AKT1 protein from *Homo sapiens*. The prediction of structure and function of protein by multiple sequences analysis and observed the conserved pattern of amino acid residues and to construct the phylogenetic tree for organizing evolutionary history.

Keywords- AKT1, Multiple sequence alignment, Conserve domain, Phylogenetic analysis.

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Introduction

Akt1 is a key signaling protein in the cellular pathways that lead to skeletal muscle hypertrophy, and general tissue growth. This ability to induce protein synthesis pathways. In a mouse model with complete deletion of Akt1 manifests growth retardation and increased spontaneous apoptosis in tissues such as the testes and thymus. Since it can block apoptosis, and thereby promote cell survival, Akt1 has been implicated as a major factor in many types of cancer [1,2]. Akt1 was originally identified as the oncogene in the transforming retrovirus, AKT8. Akt is an important signaling molecule in the Insulin signaling pathway. It is required to induce glucose transport. In a mouse which is null for Akt1 but normal for Akt2, glucose homeostasis is unperturbed, but the animals are smaller, consistent with a role for Akt1 in growth. In contrast, mice which do not have Akt2, but have normal Akt1, have a mild growth deficiency and display a diabetic phenotype (insulin resistance), again consistent with the idea that Akt2 is more specific for the insulin receptor signaling pathway. This protein isoforms are over expressed in a variety of human tumors, and, at the genomic level, are amplified in gastric adenocarcinomas (Akt1), ovarian (Akt2), pancreatic (Akt2) and breast (Akt2) cancer. The role of Akt3 is less clear, though it appears to be predominantly expressed in the brain. It has been reported that mice lacking Akt3 have small brains [3,4].

Materials and Methods

Sources and sequence information of AKT1

AKT1 has taken from *Homo sapiens*, in which targeted protein data were used to observe molecular resemble of related protein by phylogenetic analysis. AKT1 comprised of 480 amino acids residue were retrieve from the from www.ncbi.nlm.nih.gov, UniProt databases are initially the most important [5].

AKT1_HUMAN RecName: Full=RAC-alpha serine/threonine-protein kinase
MSDVAIVKEGWLHKRGEYIKTWRPRYFLLKNDGTFIGYKERPQDVDQREAPLNN
FSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREEWTTAIQTVADG
LKKQEEEEMDFRSGSPSDNSGAEEMEVSLAKPKHRVTMNEFEYLKLLGKGTFG
KVILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQ
THDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVVY
RDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYG
RAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPEAKSLLS
GLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQHVYEKKLSPPFKPQVTSETDT
RYFDEEFTAQMITITPPDQDDSMECVDSERRPHFPQFSYSASGTA

Multiple sequence alignment of AKT1

Multiple sequence alignment [MSA] is conducted by COBALT, which aligns AKT1 sequences of similar protein using a combination of distance matrix and approximate parsimony methods. Identity setting used for only columns with one residue type will be colored in red [6].

Construction of a phylogenetic tree AKT1 protein

Phylogenetic analyses were performed by fast minimum evolution algorithm and Neighbor Joining algorithms to allow the reconstruction phylogenetic tree of the molecular evolutionary history of various aligned sequences that are useful to align highly evolved gene families clearing evolutionary relationships such as multiple acting proteins [7]. Trees were obtained by the methods fast minimum evolution algorithm and Neighbor Joining algorithms. Evolutionary distance is studied by Grishin (protein) model [8] and distance between two sequences modeled as expected fraction of amino acid substitutions per site given the fraction of mismatched amino acids in the aligned region and can be computed for a fraction of mismatched amino acids larger than 0.75 [9, 15].

Results and Discussion

Evolutionary distance

This study, AKT1 protein from *Homo sapiens is* summarized to study the evolutionary distance. The identification of the origin of protein, multiple sequences analysis, observing the conserved amino acid residues and reconstruct the phylogenetic tree specify the evolutionary history, relationship of protein with different species [Table-1]. Rectangle tree shows a rectangular shaped rooted tree, where the root is placed on the longest edge. Fast minimum evolution algorithm produces un-rooted trees such as the ones shown as radial or force in the tabs below. The rooted trees are created by placing a root in the

middle of the longest edge. The slanted tree shows similar to a rectangle, but with a triangular tree shape [Fig-1-2]. Neighbor Joining algorithms produce un-rooted trees such as the ones shown as radial or circular [Fig-1,2] in the tabs below. The rooted trees are created by placing a root in the middle of the longest edge.

Table-1 *Sequences producing significant alignments*

Description	Accession	Max score	Total score	Query cover	E value	Ident
RAC-alpha serine/threonine-protein kinase [*Homo sapiens*]	NP_005154.2	1004	1004	100%	0	100%
v-akt murine thymoma viral oncogene-like 1 [*synthetic construct*]	AAX36962.1	1002	1002	100%	0	99%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Cebuscapucinus imitator*]	XP_017360887.1	1000	1000	100%	0	99%
RAC-alpha serine/threonine-protein kinase *[Macacamulatta*]	NP_001248554.1	1000	1000	100%	0	99%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Saimiri boliviensis boliviensis*]	XP_003933397.1	998	998	100%	0	99%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Rhinopithecus roxellana*]	XP_010375239.1	998	998	100%	0	99%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Propithecus coquereli*]	XP_012502543.1	996	996	100%	0	99%
PREDICTED: RAC-alpha serine/threonine-protein kinase isoform X1 [*Microcebus murinus*]	XP_012601844.1	994	994	100%	0	99%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Mesocricetus auratus*]	XP_005068362.1	991	991	100%	0	99%
RAC-alpha serine/threonine-protein kinase isoform 1 [Mus musculus]	NP_033782.1	989	989	100%	0	98%
PREDICTED: RAC-alpha serine/threonine-protein kinase isoform X1 [*Peromyscus maniculatus bairdii*]	XP_006988064.1	989	989	100%	0	98%
AKT [*Meriones unguiculatus*]	ANU06111.1	988	988	100%	0	98%
RAC-alpha serine/threonine-protein kinase [Rattusnorvegicus]	NP_150233.1	988	988	100%	0	98%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Cavia porcellus*]	XP_003463160.1	988	988	100%	0	98%
PREDICTED: RAC-alpha serine/threonine-protein kinase [*Jaculus jaculus*]	XP_004665705.1	987	987	100%	0	98%

Fig-1 Multiple sequence alignment by COBALT of AKT1 protein from *Homo sapiens*. The Conservation Setting can be used to select a threshold for determining, which columns are colored in red.

MSA(Multiple sequence alignment)

Multiple sequence alignment analysis shows columns with no gaps are colour in blue or red. The red colour indicates highly conserved regions and blue indicates less conserved ones. The Conservation analysis can be used to select a threshold for determining which columns are colours in red [Fig-1]. Multiple sequence alignment identify conserved motifs and to predict functional role in the variable sites as well as conserved sites show the sequence divergence profile of these proteins, which demonstrate the sequence enrichment strategy of these sequences for adaptation to different physiological systems. Here we observed that from all sequences of neurotoxin proteins that Cys (c), Thr (T), Asn (N) (Hydrophilic amino acid) Phe (F), Gly (G), Ala (A), Pro (P) (hydrophobic amino acid), Lys (K), Arg (R), Positive charged, Asp (D), Negative charged which is conserved in all peptides having a common ancestor. That all of these peptides share eight highly conserved cysteines which were involved in the formation of β-strands are almost conserved. Multiple sequence alignment is carried out by COBALT of AKT1 protein from *Homo sapiens*.

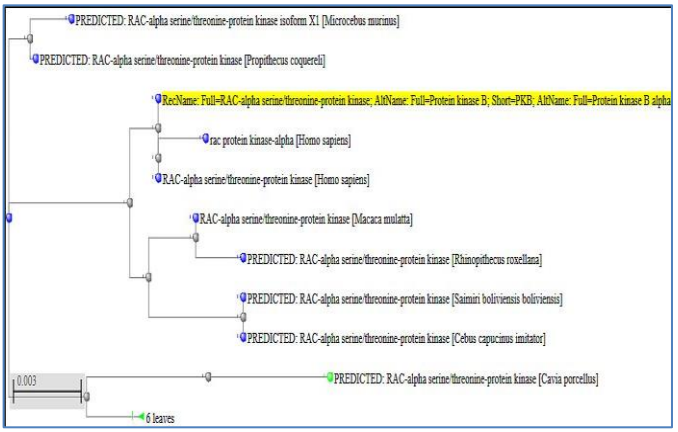

Fig-2 Rectangle tree - Neighbor joining algorithms-model-Phylogenetic study of AKT1 protein from *Homo sapiens* with the help of rendering tree. Radial tree is unrooted tree

Conclusion

AKT1 protein of *Homo sapiens* are summarized the identical regions. Using multiple sequences analysis and phylogenetic tree we observe the conserved residues to specify the evolutionary history and analyzing sequence structure relationship of AKT1. Efficient utilization of Polar, nonpolar, positively and negatively charged amino acids and their distribution in protein sequence make them to be more antigenic. Comparative analyses specify that the protein demonstrates how proteins are generated within the nature's testing ground for tailor-made biologic needs. Evolutionary studies of AKT1 sequence of *Homo sapiens found* the common ancestor. In future, this study will encourage to engineering to design a synthetic peptide vaccine in the high positive effective role.

Abbreviations

MSA- Multiple sequence alignment
COBALT: constraint-based alignment tool for multiple protein sequences
UniProt: The Universal Protein Resource
NCBI: National Center for Biotechnology Information

BLAST: Basic Local Alignment Search Tool

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