Characterization of ARV1 like protein from sheep and goat parasite, *Setaria digitata* and its application in phylogenetic analysis

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Expressed sequence tags (ESTs) is an effective approach to gene discovery of a given organism. In current study, approximately 250 ESTs from sheep and goat parasite *Setaria digitata* were examined and a cDNA clone was identified which code for ARV1 like protein. Here, we report the characterization of this protein using a bioinformatic approach (Authors thank NV Chandrasekharan, JK Casinader, SMT Jayasena and MN Wickramanayake for constructing the *S. digitata* cDNA library). ARV1 like proein of *S. digitata* consist of 217 amino acids and its predicted molecular weight and isoelectric point are 25.33 Kda and 8.91, respectively. BLAST searches were carried out using nucleotide and amino acid sequences and it was possible to identify 21 similar sequences from different molecular taxa, ranging from lower eukarytoes to human. Conserved domain search over the databases at NCBI identified ARV1 domain with potential zinc-binding motifs for *S. digitata* protein. Analysis of ARV1 like protein using, SignalP, TargetP, Psort servers to predicted that this group of protein to be localized in the cell membrane. Analysis with TMHH server elicited two potential regions for transmembrane alpha helixes for *S. digitata* ARV1 like protein and further, the construction of the structure of this protein with Robetta Full Chain Structure server indicted seven potential alpha helical regions, this together with TMHH prediction we hypothesize S. *digitata* ARV1 like protein is to be an alpha helical transmembrane protein. Furthermore, ScanProsite server predicted potential sites for N-glycosylation and N-myristoylation. Furthermore phosphorylation sites for Protein kinase C, Casein kinase II, Tyrosine kinase indicating this protein may be regulated by phosphorylation. Finally, the phylogenetic tree was constructed by neighbour-joining method of Phylip 3.2 using multiple aligned sequences to study the relationship of ARV1 domains of 21 retrieved amino acid sequences and this tree defined distinct clusters for Plants, Fungi, Nematodes, Arthropods and Chordates. The cluster derived from the Chordata, phylogenetically more closely related to Nematodes, to which Arthropod formed a sister cluster. Fungi and Plants also formed sister clusters, but they remained diverge from Chordates, Nematodes and Arthropods. Thus, the topology of ARV1 phylogenetic tree clearly indicated the evolutionary trend of the different taxa by grouping different phyla into different clusters suggesting the versatility of this domain for phylogeneitic analysis.

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