Characterization of putative nuclear cell envelope like parasitic nematode specific protein from goat and sheep parasite, *Setaria digitata*

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Expressed sequence tags (ESTs) are an effective approach for discovery of new genes in a given organism. In the current study, approximately 250 *Setaria digitata* ESTs were examined and identified a cDNA clone that codes for a protein (UP), which could not be annotated functionally by searching over the publicly available genome, protein, and EST and STS databases. Here, we report the extensive characterization of its ORF using a bioinformatic approach. UP of *S. digitata* (SDUP) consist of 204 amino acids and its predicted molecular weight and isoelectric point were 22.8Kda and 9.94, respectively. BLAST searches using nucleotide and amino acid sequences, and structural features over the various databases, identified a homologous counterpart only from the human parasitic nematode *Wuchereria bancrofti*, for which translated sequence was not available in the SWISSPROT database. However, searching over EST at Parasite Genome Database (PGD), similar sequences were identified from human parasitic [*Onchocerca volvulus* (OV), *W. bancrofti* (WB), *Brugia malayi* (BM) & *Ascaris suum* (AS)] and plant parasitic [*Meloidogyne hapla* (MH)] nematodes. Phylogenetic analysis of UPs of WB & BM and AS & MH grouped into two distinct clusters, SD remains with the latter cluster and OV diverse from the aforementioned groups. Searching EST at PGD revealed BMUP expresses in all the stages. Secondary structure analysis of multiple aligned sequences of homologues using Jpred server indicated UPs are rich in beta-pleated structures and their propensity to form a transmembrane beta barrel was revealed by beta barrel finder programme (BBF). Further, the putative domain characterized in this study is novel and nematode specific. Analysis of UPs using, SingalP, TargetP, PSORT servers predicted this group of proteins is localized in the nucleus. Transmembrane alpha helixes analysis with TMHH server did not elicit any potential regions in UPs. Further analysis by using ScanProsite server for phosphorylation of UPs revealed potential sites for cAMP- and cGMP-dependent protein kinase, Protein kinase C and Casein kinase II. Putative functional analysis using ProtFun 2.1 Server indicated UPs to be a nonenzymatic, cell enveloped, growth factor like protein. Finally, collating all the information derived from bioinformatic analysis, UPs of nematodes are most likely to be expressed in all stages, localized in the nucleus, regulated by phosphorelation, rich in beta-pleated strands, nonenzymatic and nuclear enveloped parasite nematode specific protein.

Acknowledgement: supported by SAREC grant for capacity building in biotechnology.