

Cloning, Sequencing and Characterisation of Filarial Parasite Specific Genes

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The causative agent of lymphatic filariasis in Sri Lanka, *Wuchereria bancrofti*, is not amenable to culture. Therefore, we used the cattle filarial parasite, *Setaria digitata*, as a model organism to study filarial parasite specific genes. Eight cDNA clones were selected following screening of a cDNA library constructed in Zap Express system. DNA was extracted from the eight clones designated cDNAsd-1 to cDNAsd-8, insert sizes were estimated and sequenced using automated MegaBACE 1000 sequencer. Sequences obtained were analysed using bioinformatics tools. Southern blot analysis revealed that all eight cDNA clones were derived from the genome of *S. digitata*. Amino acid sequence of cDNAsd-1 aligned with *Brugia malayi* glucose phosphate isomerase enzyme with 78% homology. The sequence of cDNAsd-4 aligned with the *B. malayi* chr 9, Wayne State University 20, partial mRNA sequence with 82% homology. The ORF of cDNAsd-4 sequence encodes a 195 amino acid protein. Both the ORF (nucleotide-protein blast) and the amino acid sequence (protein-protein blast) aligned with the *B. malayi* chr 9 protein. The predicted protein is non secretory with a molecular weight of 22,419.76 Da and a theoretical isoelectric point of 6.41. It also has a conserved domain common to CDC super family of proteins. The sequence of cDNAsd-3 revealed an ORF coding for a novel protein having 86 amino acids, a molecular weight of 9,948.79 Da and an isoelectric point of 9.58. This is neither a mitochondrial nor a secretory protein, but is a transmembrane protein which might be located on the cytoplasmic side. cDNAsd-5 clone of 1021 bp partially aligned with the sequence of the partial mRNA of *B. malayi* RNA promoter binding protein (1968 bp) with a homology of 73%.

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