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Characterisation of a Heat Shock Protein 70 gene (hsp70) of Wuchereria bancrofti

Wuchereria brancrofti is the primary causativ eagentof lymphatic filariasis. Its life cycle involves migration between a mosquito vector and human host. HSP 70s appear to play an important role in adaptation and survival of the parasite during transmission, when it encounters abrupt changes in temperature and other environmental factors.

W.brancrofti DNAwas digested with selected restiction enzymes Dra I, EcoR V, Pvu II Sca I and Stu I. Genome Walker libraries were constructed by ligating the digested DNA fragments with Genome Walker adapter. Two gene specific nested primers were designed from a conserved region of *Brugia malayi* hsp70gene for initial amplifiction fo the Genome Walker libraries. The amplified fragments were eluted and purified for DNA sequending. Subsequent PCR amplifications of the Genome Walker libraries were carried out with using primers derived from these sequences. All amplified fragments were sequenced to obtain the complete nucleotide sequence of the *W. brancrofti* hsp70gene with the 5'and 3' flanking regions.

The coding region comprises of ten exons which is interrupted by nine introns. The intron sizes range from 82 to 381 nucleotides. Several promoter elements including a putative TATA box, two CCAAT box sequences and four heat shock elements are present in the 5' flanking region. Apolyadenylation signal was present 211 base pairs downstream of the final exon. The G+C content of the coding region is 44.2f% . The coding sequence potentially encodes a protein of 645 amino acids, which has more than 99% homology to the *B. malayi* HSP 70.