A- 34: Sequence analysis of a *hsp*70 gene from the filarial parasite *Setaria digitata*

S M T Jayasena, N V Chandrasekharan , E H Karunanayake
(*Dept of Biochemistry and Molecular Biology, Faculty of Medicine, University of Colombo, Colombo 8*)

The isolation of a *Setaria digitata hsp* 70 genomic clone designated LESH 1 and the partial sequencing of a subcloned fragment has been previously reported.

LESH 1 was further digested with the selected restriction enzymes, *Bam*H I, *Eco*R I and *Sal* I, and the resulting fragments were subeloned into pUC or pBluescript vectors. Four subclones were sequenced completely and 3 additional subclones were partially sequenced. Sequence analysis revealed that LESH 1 contained sequences from 2 *hsp*70 genes (designated *hsp70-1* and *hsp70-2*) arranged in direct tandem.

Hsp70-2 was completely sequenced and contained 1935 bp of coding sequences potentially encoding a protein of 645 amino acids. The gene contained 9 short introns varying in length from 78-195 bp. The presence of introns in a *hsp70* gene is indicative of a constitutive pattern of expression. The upstream region of *hsp70-2* gene contained several putative promoter elements including a transcription initiation site, a TATA box, 2 CAAT box sequences and 3 heat shock elements which are comprised of consecutive inverted repeating units of the 5 bp sequence, nGAAn. Analysis of the 3' untranslated region (318 bp) did not reveal any potential polyadenylation signals. The *hsp70-2* gene of *S. digitata* was characteristically AT-rich. The G+C content of the coding sequences and introns were 44.6% and 35.2% respectively.

This work was supported by the SAREC grant for Capacity Building in Biotechnology.