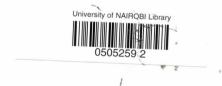
## IDENTIFICATION OF SCHIZONT cDNAs LOCATED ON A SUB-TELOMERIC FRAGMENT OF THE THEILERIA PARVA GENOME

## A THESIS SUBMITTED IN PARTIAL FULFILMENT FOR THE AWARD OF DEGREE OF MASTER OF SCIENCE (M.Sc.) IN BIOCHEMISTRY AT THE UNIVERSITY OF NAIROBI

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## **SUMMARY**

Theileria parva, an intra-cellular protozoan parasite of cattle, causes a lymphoproliferative disease called East Coast fever. The parasite genome is considered to be haploid in both the sporozoite and piroplasm stages of its life cycle while the schizont stages are polyploid. The piroplasm has four chromosomes and hence eight telomeres (reviwed in Morzaria and Young, 1992). The work reported here is based on the finding that *Theileria parva* sub telomeric DNAs contain open reading frames, which potentially secrete proteins (Sohanpal *et al.*, 1995). The main objective of this project was to identify additional schizont cDNAs on different telomeric regions. However, due to problems associated with the purification of large parasite genomic DNAs from gels, the study concentrated on identifying cDNAs located centromere proximal to the subtelomeric DNA on the right arm of chromosome three of the parasite genome.

A 60kb piroplasm genomic DNA, spanning the SfiI site between DNA fragments 17 and 22 was isolated from an arrayed pBeloBAC11 library of the Theileria parva genome and used to probe a total parasite (schizont) RNA blot in order to determine its transcription profile. No homology was however, detected. This was probably due to lack of sensitivity to the mRNA by the probe due to presence of the former in low copy numbers. The 60kb DNA fragment was also used to screen a library of bacteriophage  $\lambda$  clones containing T. parva schizont cDNA. Four positive clones were isolated and these were characterised by partial sequencing and data-base searches. 75% of the schizont cDNAs, representing three different transcripts, were found to express significant homology with genes described in organisms other than Theileria parva, suggesting that the sequence is conserved between species . 50% of the transcripts were found to be homologues of ribosomal genes encoding the S3a protein, 67 kDa laminin binding protein and the 67 kDa laminin receptor, all of which, under certain circumstances, play important roles during transformation of cells (Nelson and Hirumi, 1981; Masse et al., 1990). 25% of the schizont cDNAs, represented by one transcript, expressed a significant homology with the nucleotide sequence from one locus of chromosome III in Caenorhabditis elegans. The remaining 25% of the schizont

cDNAs did not show any significant homology with the sequences in any of the public dormain databases.