

## Abstract

Previous molecular genetic studies on the African trypanosome have focused on only a few genes and gene products, the majority of which are concerned with surface antigenic variation; consequently, an insignificant number of the genes of this organism have been characterized to date. In order to: (1) identify new genes and analyze their expression profile, (2) generate expressed sequence tags (ESTs) for derivation of a physical map of the trypanosome genome, and (3) make available the partial sequence information and the corresponding clones for general biomedical research on the parasite, we have performed single-pass sequencing of random, directionally cloned cDNAs from a bloodstream form *Trypanosoma brucei rhodesiense* library. Analysis of 2128 such ESTs sequenced so far in this study showed significant similarities [BLASTX  $P(n)$ -value  $<10^{-4}$ , and a match  $>10$  amino acid residues] with proteins whose genes have been described in diverse organisms including man, rodents, kinetoplastids, yeasts and plants. A number of the ESTs encode homologues of proteins involved in various functions including signal reception and transduction, cell division, gene regulation, DNA repair and replication, general metabolism, and structural integrity. Although some of these genes may have been expected to be present in the African trypanosomes, the majority of them had not previously been described in these organisms. A large proportion, 768 individual ESTs (36%, representing 385 different transcripts), had a significant homology with genes described in organisms other than the African trypanosomes; however, 15% of the ESTs were from genes already described in trypanosomes. Among the ESTs analysed were 462 distinct known genes, only 77 of which have been described in *T. brucei*. Approximately 52% of the ESTs did not show any significant homology with the sequences in any of the public domain databases.