Ubiquitin-EP52 fusion protein homologs from *Trypanosoma brucei*

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Screening of a *Trypanosoma brucei* procyclic cDNA library with a *T. brucei* ubiquitin probe identified two clones which encoded ubiquitin-EP52 homologs. The open reading frames of the two clones (Figure 1) predict an identical, 128 amino acid sequence. The amino terminal 76 amino acids are identical to the ubiquitin monomer derived from a *T. brucei* polyubiquitin gene (1). The carboxy terminal 52 amino acids have homologs in other cell types (Figure 2) where they may exist as a discrete polypeptide associated with the small subunit of the ribosome (3). In yeast, the homologs have been implicated in ribosome biogenesis (3).

The two cDNA clones contain two base changes in the coding region and can be further distinguished by sequence divergence in the 3' non-coding region; they therefore represent transcripts from different genes.

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ttgAAG                                     C                                     100
GATAGCACCATGCAGATCTTCGTGAAACCCCTCACTGGTAAACCATTCCTCTTGAGGTTGAGGCCAGCGACACCATTTGAGAACGTAAGGCCA 94
      M Q I F V K T L T G K T I A L E V E A S D T I E N V K A K
                                     A                                     200
AGATTGAGGACAAAGGAGGATCCCTCCGATCAGCAGCGGTTGATTTTGGCCGGAAGCAGTTGGAGGAGGGTCGCACGCTTCCGGACTACACATTCA 194
      I Q D K E G I P P D Q Q R L I F A G K Q L E E G R T L A D Y N I Q
                                     300
GAAGGAGTCGACGCTGCATCTTGTGCTTCGTCTTCGAGGTGGTGTGATGGAGCCAACGCTTGAGGCACTCGCGAAAAATAACAATTGGGAGAAGAAGGTG 294
      K E S T L H L V L R L R G G V M E P T L E A L A K K Y N W E K K V
                                     400
TGCCGCCGCTGCTACGCCGCTGCGCGTACGCGTACGAATTGCCGCAAGAAGGTTGTGGCCACTGCTCCAATTGCGCATGAAGAAGAAGCTGCGTT 394
      C R R C Y A R L P V R A T N C R K K G C G H C S N L R M K K K L R *
                                     A      TGTTAAAGTTTATTTATTTATTTTCGTTT 3'Zn1 474
AATGTACCTATCACTTCATGCTTAGCGGTTATCTGCGGGTTATCTGTGAAACATGCCTCATTTCTTTTTTTTTTCCACCCTGTTCTGTTCTTCTT 494
      TTCG 3'Za 498

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Figure 1. DNA sequence and predicted amino acid sequence of cDNA clones Zn1 and Za. Nucleotide differences in clone Zn1 are shown above the Za sequence. Lower case letters represent the mini-exon sequence found at the 5'-end of kinetoplastid mRNAs. Neither clone contained a poly-A tail.

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A) VMEPTLEALAKKYNWEKKVCRRCYARLPVRATNCRKKGCGHCSNLRMKKKLR
B) .....S.....A.....
C) II..S.K...S...CD.S...KS.....P.....K...TNQ..P...K
D) II..S.RQ..Q...CD.MI..K.....HP..V.....K...TN...P...VK
E) AK.S.VI..R..KCD.MI..K.....HP..V.....MWSL
F) II..S.RQ..Q...CD.MR

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Figure 2. Predicted sequence of the *T. brucei* ubiquitin-EP52 carboxy terminal 52 amino acids A) aligned with similar sequences from B) *T. cruzi* (4); C) yeast (2); D) human (5); E) *Dictyostelium* (6), and F) mouse (7). Dots represent identical amino acids.

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