Identification of a heat shock-like antigen in *P.falciparum*, related to the heat shock protein 90 family

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Previous reports have shown that squirrel monkeys vaccinated with a protein fraction of 75Kd prepared from culture forms of the Palo Alto FUP strain of *P.falciparum*, showed a high degree of protection which correlated with the presence of antibodies essentially against parasite polypeptides of 90Kd and 72Kd (1,2). The 72 Kd polypeptide was identified as a member of the *P.falciparum* heat shock 70 family (3-6). Two other related proteins of the heat shock 70 family have also been identified (7-8). Using a polyclonal immune sera against the 90Kd region from *P.falciparum*, several cDNA clones were isolated from an expression library constructed in the pUC9 vector. Interestingly, the deduced amino-acid sequence of clone C27 shows significant homology with proteins from the heat shock 90 family (50-56%)(9-10) and lower homology with the Glucose regulated protein GRP94 of mammalian cells (42%)(11). This antigen thus represent the fourth Hsp-like protein expressed by *P.falciparum*.

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P.falciparum: KDFDGGKCLKCTKEGLDIHHSEEAKKDFETLKAEEYGLCKVIKDVHLHKKV
T.cruzi      : ...ED..FA.L....VHFEET..E..QR.EE.TA..R...AM....GD..
Human       : .E....S.VSV.....ELPED..E..KM.ES..KF.N...LM.EI.D...

P.falciparum: EKVVVGQRITDSPCVLVTSEFGWSANMERIMKAQALRDNMSMTSYMLSKKI
T.cruzi      : .....SE.LAT...I.....H..Q..RN.....S..SA..M...T
Human       : ...TISN.LVS...CI...TY..T.....TMG..MA..H

P.falciparum: MEINARHPIISALKQKADADKSDKTVKYLWLLFDTSLLTSGFALEEPTT
T.cruzi      : ....PA...VKE..RRVE..EN..A..D.VY.....A.....T.DD..S
Human       : L...PD...VET.R...E...N..A..D.VV...E.A..S...S..D.Q.

P.falciparum: FSKRIHRMIKLGLSIDEEENNDID-----LPPLEETVDATDSKMEEVD
T.cruzi      : YAE.....L.D.D.GNEEAEPAAAV---PA-.P.AG.S.-..Q..
Human       : H.N..Y.....G...D.VAAEPPNAAVPDEI....GDE...-R.....
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Fig.1 Homologies between the *P.falciparum* C27 cDNA clone, hsp 85 from *T.cruzi* (9) and human Hsp 90 (10). The identical amino-acids are represented by dots, the sequences have been aligned for maximum homologies.

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