SCHISTOSOMA MANSONI ENCODES A STRUCTURAL UBC9 TRANSCRIPT AND A PSEUDOGENE THROUGH ITS DEVELOPMENT

Gomes MS[1], Cabral FJ[2], Macedo EA[2], Brigato OM[2], Baba EH[1], Rodrigues V[2] and Guerra-Sá R[1]. (1) NUPEB-UFOP, Ouro Preto MG. (2) FMRP-USP, Ribeirão Preto - SP.

Schistosomes are parasitic blood flukes, which causes the chronic debilitating disease schistosomiasis, affecting hundreds of millions people worldwide. To date little is known about the roles of posttranslational pathways in the development of *S. mansoni*. SUMO, the small ubiquitin modifier, is covalently attached to a broad spectrum of substrates and is well known that Ubc9 is the main protein, which conjugates SUMO to its targeted substrates through E2 catalytic activity. Based on searches on FAPESP databank, RT-PCR and genomic PCR our results suggest that *S. mansoni* presents a structural Ubc9 gene, which encodes a functional protein and an Ubc9 pseudogene with a disrupted ORF. The alignment of cDNA and genomic sequences for both genes has shown that SmUbc9 as well as ?SmUbc9 is interrupted by small introns spliced by one non-canonical splicing rule AT-AC. In addition mRNA expression of SmUbc9 and ?SmUbc9 genes was also evaluated in the developmental stages of the parasite. Whereas structural Ubc9 is expressed in all studied stages, ?Ubc9 is expressed only in adult worms. Furthermore Western blot using human anti-ubc9 has detected a protein of 20kDa. Taken together our results suggest that *S. mansoni* presents a structural Ubc9 and a pseudogene playing a role on its development.

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