SUMOylation pathway components in Schistosoma mansoni: differential expression and demonstration of a sumo-conjugation system during cercariae to adult worm differentiation.

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Schistosoma mansoni during its developmental processes suffers complex structural reorganization of the tegument and several metabolic transformations. It is suggestive that signaling pathways may play a role giving molecular signals to define the route which the parasite must carry on. Thus, post-translational proteins modification, such as sumoylation, modify their target substrates during the parasite life cycle, regulating the transcription of important molecules, altering theirs sub-localization and controlling the stability of some proteins. Based in searches through transcriptome databases of *S. mansoni* we found seven genes of sumoylation pathway: two SUMO genes (SmSMT3B and SmSMT3C), one conjugation enzyme (SmUBC9), two E3 ligases (SmRBP2 and SmPIAS) and two sumo-specific proteases (SmSenp1 and SmSenp7). Expression of sumo pathway genes were performed by qPCR from cercariae, adult worms, and cultured schistosomula from 3,5 hours to 3 days. These data showed that the levels of SmUBC9 transcripts were not modified during the evolutive stages. The levels of SmRBP2, SmPIAS, SmSENP1 and SmSENP7 were down or up regulation depending of parasite stage. The SUMO conjugation systems were investigated using specific antibody to SmSMT3B/C. The results showed that there are specifc sumoylated proteins in cercaria to schistossomula developmental and demonstrated that SUMO and many SUMO conjugated are concentrated in the nucleus. This is also strongly suggested by our finding that S. mansoni contains a functional sumo conjugation system. Determining the exact contribution of sumoylation pathway during *S. mansoni* development will be an important area for further study.

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