Molecular characterisation and in silico analysis of the gene encoding 14-3-3 tegumental protein of Schistosoma spindale

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Abstract

Background Schistosoma spindale is a highly prevalent and pathogenic snail borne trematode of ruminants in the Indian subcontinent. The zoonotic significance of this parasite is associated with cercarial dermatitis in man. Human schistosome infection is infamous for its high morbidity and mortality rates and, animal schistosomosis adversely affects the livestock sector in endemic areas. Several protein candidates of schistosomes have been characterised to exploit the diagnostic and vaccine potential for the control of infection in man and animals, amongst which tegumental proteins have been found quite promising. However, such proteins of Indian schistsosome species have not been yet studied systematically. *Objectives* In this study, molecular characterisation of 14-3-3 tegumental protein encoding gene of *S. spindale* and *in silico* analysis of the predicted protein structure were done to assess its immunogenicity. *Methods* Kerala isolates of adult *S. spindale* worms were collected from mesentery samples, Total RNA was isolated and cDNA was synthesised from it. The synthesised cDNA was used as a template for the PCR amplification of the Ss14-3-3 gene and the confirmed amplicons were then column purified and bidirectionally sequenced using Sanger's di-deoxynucleotide chain termination method. The sequences obtained were merged and subjected to further analysis using bioinformatic tools. *Results* A 759 bp amplicon of 14-3-3 tegumental protein encoding gene of *S. spindale* was translated into a protein sequence having 252 amino acids. The Ss14-3-3 nucleotide sequence showed the highest similarity of 94.99 per cent with *S. bovis* 14-3-3 zeta isoform mRNA. However, Ss14-3-3 protein sequence had the highest similarity with the 14-3-3 putative protein of *S. mansoni* (99.21 per cent). With the help of bioinformatic tools, it was concluded that the secondary and tertiary structures of this protein were stable and three potential B cell epitopes exists within the translated protein sequence. The protein was shown to possess structural stability and immunogenicity which makes it a potential immunogenic candidate against schistosomosis. *Conclusions* A 14-3-3 tegumental protein encoding gene of *S. spindale* was characterized for the first time. Sequence data was generated and *in silico* analysis revealed structural stability and possible immunogenicity. The study would serve as a platform to unravel the characteristics of tegumental proteins of animal schistosomes to be used in diagnostics and vaccines. However, further wet lab experiments including expression studies are necessary to validate these findings.

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