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

Modi Syriac¹, Bindu Lakshmanan¹, Priya Manakkulamparambil Narayanan¹, and Uma Radhakrishnan¹

¹College of Veterinary and Animal Sciences Mannuthy

June 5, 2023

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 schistosome 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.

Hosted file

Ramachandran Plot

Plot statistics

- Residues in most favoured regions \([\Phi, \Psi]\) 420 96.1%
- Residues in additionally allowed regions \([-120, \Psi]\) 15 3.4%
- Residues in generously allowed regions \([-150, -120, \Psi]\) 2 0.5%
- Residues in disallowed regions 0 0.0%

- Number of non-glycine and non-proline residues 437 100.0%
- Number of end residues (excl. Gly and Pro) 4
- Number of glycine residues (shown as triangles) 12
- Number of proline residues 3
- Total number of residues 461

Based on an analysis of 118 structures of resolution of at least 2.0 Ångström and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.