

SCP/TAPS proteins of parasitic helminths – future prospects

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Introduction

- SCP/TAPS proteins of parasitic helminths play key roles in fundamental biological processes linked to the invasion of and the establishment in their mammalian host [1].
- Despite the evidence that SCP/TAPS proteins of blood-feeding parasitic nematodes are involved in host-parasite interactions, there is a paucity of information on this protein family for parasitic trematodes of socio-economic importance.

Materials and methods

- Current transcriptomic and/or genomic sequence datasets available the liver flukes *Clonorchis sinensis*, *Opisthorchis viverrini*, *Fasciola hepatica* and *F. gigantica* as well as the blood flukes *Schistosoma mansoni*, *S. japonicum* and *S. haematobium* were mined for the presence of full-length genes and/or transcripts encoding SCP/TAPS proteins [2,3].
- Extensive bioinformatic analyses of inferred amino acid sequences, including identification of conserved protein domains presence/absence of signal peptides, were conducted [4].
- Structure-based sequence alignments were generated, guided by secondary structure elements, and subjected to analysis by Bayesian inference.

Results

- A total of 151 predicted peptides (range 11 – 41 in *F. gigantica* and *S. mansoni*), with high homology to known eukaryotic SCP/TAPS were identified.
- Amino acid sequence alignments, guided by predictions of their secondary structures and sequence similarity, allowed the definition of (at least) four individual groups of trematode SCP/TAPS (Fig. 1 and Fig. 2a-d).
- The abundance of the SCP/TAPS fold and its extension suggest a “vehicle-payload” model for these proteins (Fig. 3).

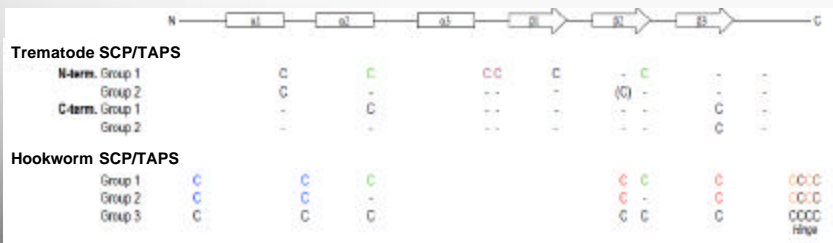


Fig. 1 - Schematic of the topology of the SCP-fold and approximate position of conserved cysteine residues in the primary structure.

Conclusion

- This work guides future structural and functional explorations of key SCP/TAPS molecules associated with diseases caused by flatworms. Future fundamental investigations of these molecules in parasites and the integration of structural and functional data could lead to new approaches for the control of parasitic diseases.

References: [1] Cantacessi C, et al. (2009) *Biotech Adv* 27, 376-388; [2] www.genedb.org; [3] www.gasserlab.org; [4] Cantacessi C, et al. (2010) *Nucleic Acids Res* 38, e171.

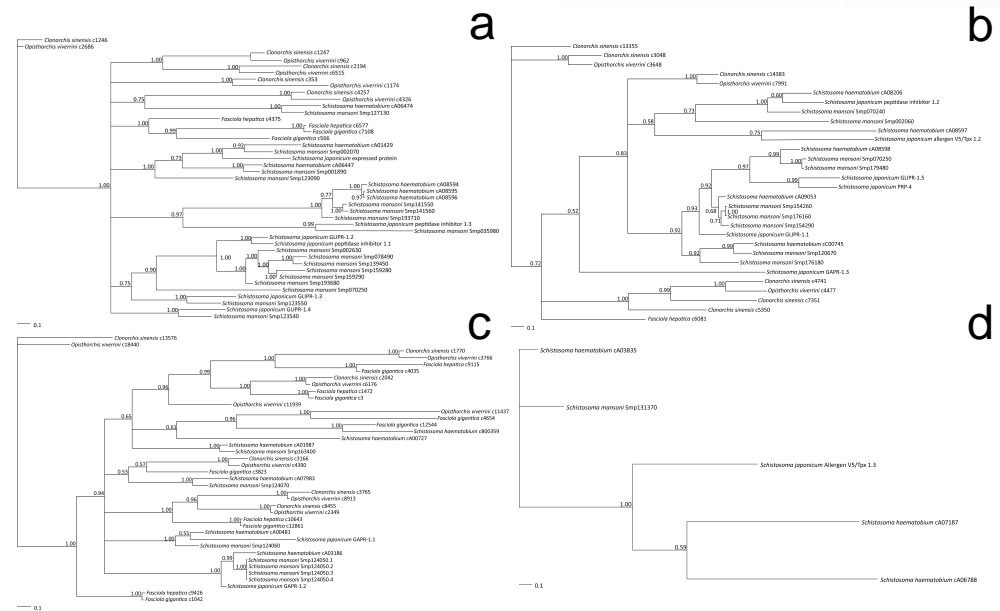


Fig. 2 - The phylogenetic relationships of trematode SCP/TAPS proteins based on Bayesian inference. Group 1 (a); group 2 (b); group 3 (c); group 4 (d).

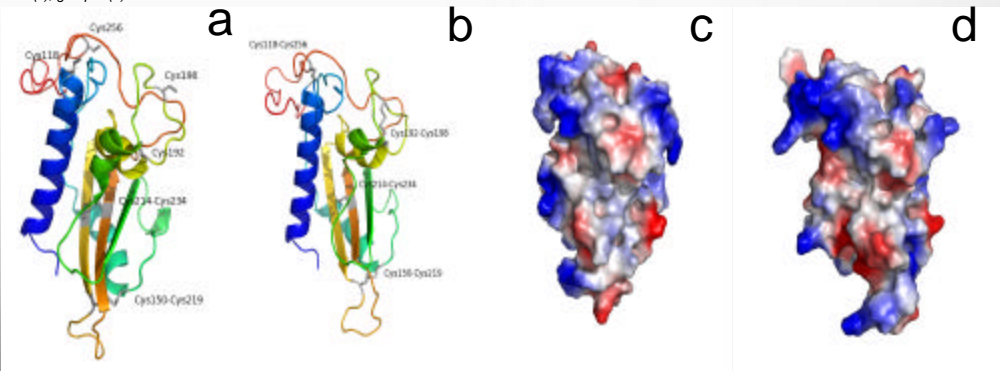


Fig. 3 - Homology models for the molecule c962 from *Opisthorchis viverrini*. The models are rendered in cartoon representation with cysteine side chains shown as bars in grey. The colour mapping ramps from blue (N-terminal end) to red (C-terminal end) (a,b). Surface representation (c,d) of the models.

Acknowledgements: The authors thank Dr Raechel Littman for assistance with the bioinformatic analyses.