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Poster Abstract

Comparative 'omics' identification of coproantigens for diagnosis of *Strongyloides stercoralis* infection

Background

Strongyloides stercoralis is a soil transmitted helminth with potential to cause fatal hyperinfection if not successfully treated. It is therefore important both to diagnose strongyloidiasis and to confirm cure after treatment. Diagnosis currently requires *Strongyloides*-specific methods that vary in sensitivity and are slow to give a result or unable to determine cure. An ideal alternative would be an antigen detection rapid diagnostic test (RDT) for application at point-of-care and capable of confirming cure.

Methods

We analysed open access transcriptomic, genomic and proteomic data and searched published literature on *S. stercoralis* and *S. ratti*, a parasite of rodents, to identify proteins that are likely to be *Strongyloides*-specific, antigenic and detectable in stool. Proteins expressed in the gut-dwelling life stages of the nematode were compared, using phylogenetic trees, with homologues from 14 other helminth species and humans. *Strongyloides*-specific protein regions were then mapped onto 3D models and analysed for predicted epitopes. The excretory/secretory (E/S) proteome of *S. ratti* was used to identify *S. stercoralis* E/S homologues. Genomes of 3 *Strongyloides* species were mapped to the *S. ratti* reference in order to reveal variants in genes of interest. Datasets were cross-referred to build evidence for strong candidate antigens.

Results

Transcriptomic data revealed 328 proteins differentially expressed in gut-dwelling versus non-gut dwelling life stages of *S. stercoralis*. Over 50 *S. stercoralis* proteins from seven protein families contained species-specific sequences as revealed by phylogenetic comparison with outgroups and by sequence alignments. In total, 125 epitope regions were predicted in proteins expressed by gut-stage *S. stercoralis*. *Strongyloides* unique, predicted epitope peptides of selected proteins were 3D mapped to the surface of the molecules and revealed adjacent amino acid residues that may form conformational diagnostic epitopes.

Conclusion

The comparative 'omics' approach used here for the first time for *Strongyloides* has identified numerous candidate antigens that should be investigated as targets for a *S. stercoralis* coproantigen assay. Furthermore, online analytical tools and the increasing wealth of open access data on multiple helminth and other parasites means that this approach can be applied more widely to diagnostics discovery and development.