1 Characterisation of a *Teladorsagia circumcincta* glutathione transferase

2

3

4

5 Saleh Umair^{a*}, Charlotte L.G. Bouchet^a, Qing Deng^a, Nikola Palevich^a, Heather V.
6 Simpson^b

7

8

9

10 ^aAgResearch Ltd, Private Bag 11-008, Palmerston North, New Zealand

11 ^bInstitute of Veterinary, Animal and Biomedical Sciences, Massey University, Private
12 Bag 11-222, Palmerston North, New Zealand

13

14

15

16

17

18

19

20

21 * Corresponding author

22 Saleh Umair, AgResearch Ltd, Hopkirk Research Institute, Grasslands Research
23 Centre, Tennent Drive, Private Bag 11008, Palmerston North 4442, New Zealand.

24 E-mail: saleh.umair@agresearch.co.nz

25

ABSTRACT

A 615 bp full length cDNA encoding a *Teladorsagia circumcincta* glutathione transferase (*TcGST*) was cloned, expressed in *Escherichia coli* and the recombinant protein purified and its kinetic properties determined. The predicted protein consisted of 205 amino acids and was present as a single band of about 24 kDa on SDS-PAGE. Multiple alignments of the protein sequence of *TcGST* with homologues from other helminths showed that the highest identity of 53-68% with haem-binding nematode proteins designated as members of the nu class of GSTs. Substrate binding sites and conserved regions were identified and were generally conserved. The predicted 3-dimensional structures of *TcGST* and *HcGST* revealed highly open binding cavities typical of this class of GST, considered to allow greater accessibility to diverse ligands compared with other classes of GST. At 25 °C, the optimum pH for *TcGST* activity was pH 7, the $V_{\max}$ was 1535 ± 33 nmoles.min⁻¹.mg⁻¹ protein and the apparent K_m for the substrate 1-chloro-2,4-dinitrobenzene (CDNB) was 0.22 ± 0.01 mM (mean $\pm$ SD, n = 2). Antibodies in both serum and saliva from field-immune, but not nematode-naïve, sheep, recognised recombinant *TcGST* in enzyme-linked immunosorbent assays. The recognition of the recombinant protein by antibodies generated by exposure of sheep to the native enzyme indicates similar antigenicity of the two proteins. These findings could aid in the design of novel drugs and vaccine antigens for economically important parasites of livestock.

Keywords: *Teladorsagia circumcincta*; Glutathione transferase; GST; Cloning; Expression; ELISA; Kinetic properties

1. Introduction

Glutathione transferases (GSTs) (E.C. 2.5.1.18) are a large superfamily of enzymes, which have the principal function of protecting cells against oxidative stress, toxic, carcinogenic and mutagenic effects of endogenous substances and xenobiotics (Hayes and Pulford, 1995). The detoxification reactions involve the catalysis by GSTs of the conjugation of many electrophilic substances to the thiol group of the tripeptide glutathione (L- γ -glutamyl-L-cysteinylglycine) (Sheehan et al., 2001; Hayes et al., 2005; Deponte, 2013), followed by removal of the conjugated chemicals from the cells by transporters (Cole and Deeley, 2006). Additional functions of particular classes of GSTs include binding to hydrophobic molecules, modifying immune functions and participating in cellular metabolism and signalling (Brophy and Barrett, 1990; Board and Menon, 2013).

GSTs are universally present in bacteria and eukaryotes, in which multiple classes of the enzyme are expressed, although some classes have restricted distributions. The superfamily includes distantly related families of cytosolic GSTs (alpha, mu, omega, pi, sigma, theta and zeta), as well as mitochondrial/microsomal enzymes (kappa GSTs) and membrane-bound glutathione and eicosanoid metabolising enzymes (Hayes and Pulford, 1995; Sheehan et al., 2001; Hayes et al., 2005; Board and Menon, 2013). Proteins in the same cytosolic GST class have sequence identity of at least 40%, contrasting with less than 25% between classes (Oakley, 2011). The cytosolic enzymes are mainly responsible for detoxification, with the different classes showing a range of substrate affinities (Deponte, 2013). Other specific activities include immune modulation by the theta class of GSTs, which are MIF (macrophage migration inhibitory factor) protein homologues (Blocki et al., 1993), and the sigma

76 GSTs, which have both pro- and anti- inflammatory functions in mammals and an
77 immunomodulatory role in helminths (Flanagan and Smythe, 2011). The mitochondrial
78 kappa GSTs are involved in energy and lipid metabolism (Petit et al., 2009; Morel and
79 Aninat, 2011).

80 Many helminths express multiple GSTs, homologues of most classes of
81 enzymes; these have been characterised using genomic and proteomic approaches
82 (Brophy and Pritchard, 1994; Sheehan et al., 2001; Markov et al., 2015; Bae et al.,
83 2016; Matoušová et al., 2016). Genome-wide sequencing is possible for some
84 helminths and has allowed analysis of gene homology across the phylum (Campbell et
85 al., 2001) and revealed the large number of genes encode for GSTs, e.g. around 50
86 different GST proteins in *Caenorhabditis elegans* (Markov et al., 2015). Detoxification
87 of anthelmintic drugs by the numerous cytosolic GSTs is protective of internal parasites
88 (Matoušová et al., 2016). MIF proteins (theta GSTs) have been identified in numerous
89 species of helminth (Sparkes et al., 2017) and these proteins can modulate host immune
90 responses to promote parasite survival (Matoušová et al., 2016). A family of haem-
91 binding proteins, which also bind haematin, in the ruminant nematode *Haemonchus*
92 *contortus* (van Rossum et al., 2004) and hookworms of the genera *Necator* and
93 *Ancylostoma* (Zhan et al., 2005; Goud et al., 2012) have been assigned to the nu family,
94 which may be a nematode-specific class, or possibly a subfamily of the sigma class
95 (Markov et al., 2015).

96 Development of vaccines against parasitic helminths is an alternative control
97 strategy to counter widespread anthelmintic resistance. Recombinant GST vaccines
98 have provoked high levels of immune response and protection against cestode
99 (Preyavichyapugdee et al., 2008) and hookworm infections (Zhan et al., 2005),
100 suggesting GSTs could also be used in vaccines against other parasites. In the present

study, the cDNA encoding a *Teladorsagia circumcincta* glutathione transferase (TcGST) was cloned, expressed in *Escherichia coli* and the recombinant protein was produced and purified. TcGST was verified as a GST protein by determining its kinetic properties in catalysing the conjugation of CDNB (1-chloro-2,4-dinitrobenzene) to the thiol group of L-glutathione. Enzyme-linked immunosorbent assays (ELISAs) were performed to determine if the recombinant protein was recognised by saliva and serum from sheep previously exposed to nematode parasites in the field.

2. Materials and methods

All chemicals were purchased from the Sigma Chemical Co. (Mo, USA) unless stated otherwise. Use of experimental animals for culturing and harvesting adult worms for RNA extraction has been approved by the AgResearch Grasslands Animal Ethics Committee (protocol #13052).

2.1. Parasites

Pure cultures of *T. circumcincta* were maintained in the laboratory by regular passage through sheep. Adult worms were recovered from the abomasa of infected sheep as described previously (Umair et al., 2013). Briefly, abomasal contents were mixed 2:1 with 3% agar and the solidified agar blocks incubated at 37°C in a saline bath. Clumps of parasites were collected from the saline soon after emergence and frozen in Eppendorff tubes at -80°C for molecular biology procedures.

2.2. RNA isolation and synthesis of cDNA

Adult *T. circumcincta* (50-100 µl packed volume) in 1 ml Trizol (Life Technologies) were ground to a fine powder in a mortar under liquid N₂ and total RNA extracted according to the manufacturer's instructions. The quality and concentration of the RNA was assessed, and first strand was synthesised from 1µg using the iScript Select cDNA Synthesis Kit (Bio-Rad) and a 1:1 mixture of Oligo (dT)₂₀ and random primers. A full-length *T. circumcincta* GST sequence TDC00922-1 (AgResearch's Internal database) was amplified from cDNA in a PCR containing the oligonucleotide primers *TcGST-FL-F* (5'- ATCGCATATGGTTCACACTACAGACTGCTT -3') and *TcGST-FL-R* (5'- CGATGCGGCCGCGAATGGTGTGTTC -3') and cloned into the expression vector AY2.4 (Knight et al., 2004), using the restriction enzymes NdeI and NotI (inserted into the forward and reverse primers, underlined in primer sequences, respectively) to allow the production of N-terminal His-tagged recombinant protein. The expression clone was sequenced to confirm the sequence identity.

Alignments were performed using the Muscle alignment option in Geneious Prime (Biomatters Ltd) with the Blosum 62 similarity matrix used to determine 100% similarity to a *H. contortus* amino acid sequence and other helminth GSTs. A second alignment against the Protein Data Bank (PDB) was carried out using the Position-Specific Iterative Basic Local Alignment Search Tool (PSI-BLAST) (Altschul et al. 1997).

2.3. Protein modelling and structural analysis of *TcGST*

PSI-BLAST was used to compare the *TcGST* and *HcGST* protein sequences with deposited structures in the PDB. A structural model of *TcGST* was constructed by submitting the amino acid sequence obtained to the I-TASSER server (Yang et al., 2015). For comparison, the amino acid sequence of the *H. contortus* GST (locus tag

HCON_NP_LOC15789), located on chromosome 2 (GenBank accession number [CP035801](#), BioProject accession number [PRJNA517503](#)) from the *H. contortus* NZ_Hco_NP genome v1.0 (Palevich et al., 2019a,b), was modelled and described as *H. contortus* GST. The structural model with highest C- and TM-score was further validated using Procheck (Laskowski et al., 1996) and ProSA-web (Wiederstein and Sippl, 2007). TM-score is a metric for measuring the similarity of two protein structures, or a global fold similarity between the generated model and the structure it was based on. Scores higher than 0.5 assumes the parent structure and modelled protein share the same fold while below 0.17 suggests a random nature to the produced model (Zhang and Skolnick, 2004). C-score is a confidence score for estimating the quality of predicted models by I-TASSER. It is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is typically in the range of -5 to 2, where a C-score of higher value signifies a model with a high confidence and vice-versa. The substrate binding domain was identified and active site residues were deduced and pictured using the PyMol molecular graphics system version 1.0 (Schrodinger).

2.4. Expression of *T. circumcincta* recombinant TcGST in *E. coli*

E. coli strain BL21 (DE3) were transformed with *E. coli* AY2.4 TcGST and grown in 10 ml Luria Broth (LB) supplemented with 100 µg/ml ampicillin for 16 h at 37 °C and 250 rpm. The culture was diluted 20-fold in LB with 100 µg/ml ampicillin and grown to OD₆₀₀ 0.6-0.8 at 37 °C and 250 rpm. L-arabinose was added to a final concentration of 0.2% and the culture grown for an additional 3 h at 37 °C and 250 rpm. Bacteria were harvested by centrifugation at 5,000 g for 10 min at 4 °C. The pellet was weighed and the bacteria resuspended (10 g/ml) in equilibration buffer (20 mM sodium biphosphate, 0.5 M NaCl, 20 mM imidazole, pH 7.4). Protease inhibitors were added

to the suspension, which was then passed through the chamber of a MP110 Microfluidizer® (Microfluidics, USA) seven times consecutively under ice at 20,000 psi to ensure the full lysis of *E.coli*, as recommended by the manufacturer. The crude lysate was centrifuged at 15,000 g for 20 min at 4 °C to remove cell debris and the supernatant filtered through a 0.22 µm filter prior to purification.

2.5. Purification of recombinant TcGST

Purified recombinant polyhistidine protein was obtained by fast protein liquid chromatography (FPLC) under native conditions, using a Ni-NTA column (Qiagen), coupled to the Biologic DUO-FLOW BIO-RAD chromatography system (Bio-Rad, USA). Sodium biphosphate buffer was used as an equilibration buffer, sodium biphosphate containing 20 mM imidazole as the wash buffer, and sodium biphosphate containing 500 mM imidazole as elution buffer. The protein was dialysed overnight following the elution and the concentration was determined by the Nanodrop A280 nm assay, using the extinction coefficient 32890 M⁻¹cm⁻¹ and molecular weight 23.5 KDa.

2.6. Gel electrophoresis

SDS-PAGE was performed using NuPAGE Novex 4-12% Bis-Tris gels according to the instructions of the manufacturer (Life Technologies). Gels were stained with Coomassie Blue (Life Technologies). A western blot was performed on the purified protein, using a monoclonal anti-polyhistidine-peroxidase antibody. Blots were incubated overnight in 1:2000 antibody in buffer (4% skim milk powder in tris-buffered saline and 0.1% Tween-20) at room temperature and developed to detect His-tagged recombinant protein.

2.7. *TcGST* activity (*E.C. 2.5.1.18*)

TcGST enzyme activity was measured at 25 °C by monitoring the conjugation of 1-chloro-2,4-dinitrobenzene (CDNB) to the thiol group of L-glutathione. The reaction product absorbs at 340 nm and the rate of increase in the absorption is directly proportional to *TcGST* activity. The final reaction mixture (1 ml) contained assay buffer, enzyme mix, enzyme developer, recombinant protein (50 µg) and the substrate CDNB.

(1) The optimum pH was determined over a pH range 6 to 9 with a substrate concentration of 5 mM glutathione and 1 mM CDNB. Subsequent assays were carried out at pH 7.

(2) The apparent K_m for CDNB was determined in reaction mixtures containing 0-5 mM CDNB and 5 mM L-glutathione at pH 7.

2.8 *ELISA*

Pooled serum and saliva samples collected from parasite-naïve and parasite-exposed sheep were tested by ELISA for the presence of antibodies that react with recombinant *TcGST*. Serum and saliva samples were collected from 18 male 6-7 months-old Romney lambs previously exposed to multiple species of parasite, including *H. contortus* and *T. circumcincta*. These lambs had developed immunity against *T. circumcincta* infection. 5 µg/ml *TcGST* were immobilised onto ELISA plates (Maxisorp, Thermofisher Scientific), free binding sites were blocked with Superblock (Thermofisher Scientific) followed by incubation for 2 h at room temperature with serial dilutions of serum (200- to 6400-fold) or saliva (20- to 160-fold) in ELISA buffer for 2 h at room temperature. Bound serum immunoglobulins were detected by incubation for 2 h at 37 °C with 1:4000 diluted rabbit anti-sheep IgG-

HRP and colour development with 3,3',5,5'-tetramethylbenzidine (TMB). Salivary IgA was similarly detected with rabbit anti-sheep IgA-HRP.

2.9. Data analysis

Replicate data are presented as mean $\pm$ SD. Graph Prism v5 was used to plot kinetic data and estimate K_m and V_{max} .

3. Results

3.1. TcGST gene sequence

The 615 bp full length *T. circumcincta* cDNA sequence, amplified from adult *T. circumcincta* cDNA, has been deposited in Genbank as Accession No. NX452942. Multiple alignments of the predicted TcGST protein of 205 amino acids were made with helminth homologues, using Alignment Geneious 8 (Fig. 1). There was 53-68% identity with proteins from *Ancylostoma ceylanicum*, *Ancylostoma duodenale*, *H. contortus*, *Heligmosomoides polygyrus*, *Necator americanus*, *Oesophagostomum dentatum*, *Nippostrongylus brasiliensis*, *Ancylostoma caninum*, *C. elegans* and *Caenorhabditis briggsae*. Identity was 26% or less with GST homologues from 9 other helminths. Substrate binding sites and conserved regions in other homologues were identified during protein modelling and are shown in Fig. 1.

In the second alignment of the amino-acid sequence of TcGST using PSI-BLAST, the protein sequence of TcGST had the highest similarity (64.4%) to the HcGST (HCON_NP_LOC15789) of *H. contortus* NZ_Hco_NP (Palevich et al., 2019a). This search also resulted in the assignment of a putative function to two of the top blast hits annotated as hypothetical protein (locus tag EYC01088 of *A. ceylanicum*) or

proteins of unknown function (locus tag VDO85500 of *H. polygyrus*) with 68% and 63% identity respectively, based on the invertebrate non redundant (NR) database.

3.2. GST structure

The predicted 3D structures of *TcGST* and *HcGST*, and the binding and catalytic sites over a wide range of ligands are shown in Fig. 2. The protein structures for *TcGST* and *HcGST* were the superimposed best structural models corresponding to the monomer of [2ON5](#) (Asojo et al., 2007), associated with *Na-GST-2* from the human hookworm *N. americanus*. The binding site and catalytic and active site residues that fall within 4 Å of the substrate (Tyr-8, Arg-14, Trp-39, Lys-43, Gly-49, Gln-50, Leu-51, Pro-52, Gln-63, Ser-64 and His-65) were similar in *TcGST* and *HcGST* (Fig. 2D). Both *TcGST* and *HcGST* had a TM Score of 0.90 ± 0.06 , a root-mean-square deviation (RMSD) value of 2.8 ± 2.0 Å and normalized z-scores were less than 6.05. The main difference between the two structures was that *TcGST* had a C-score of 1.33, whereas *HcGST* had a C-score of 1.32.

3.3. Recombinant protein expression

Maximal production of functional recombinant GST was obtained in the *E. coli* strain BL21 (DE3) when expression was induced with 0.2% L-arabinose for 3 h at 37 °C. The purified N-terminal His recombinant *TcGST* protein appeared as a single band of about 24 kDa on SDS-PAGE (Fig. 3A). The presence of a His-tagged recombinant protein was confirmed by Western blotting (Fig. 3B).

3.4. Enzyme activity

The optimum pH for recombinant *TcGST* activity at 25 °C was pH 7 (Fig. 4). The apparent K_m for CDNB was 0.22 ± 0.01 mM and the V_{max} 1535 ± 33 nmoles min⁻¹ mg⁻¹ protein (mean $\pm$ SD, n = 2) (Fig. 4). The Hill coefficient was calculated to be 1.70.

3.5. Host recognition

Recombinant *TcGST* was recognised in an ELISA by antibodies in both serum and saliva collected from adult sheep exposed to nematodes in the field (Fig. 5). No antibody was detected when serum or saliva from parasite-naïve animals was used.

4. Discussion

This study showed the close structural relationship between a *T. circumcincta* GST (*TcGST*) and homologues from *H. contortus* and several animal parasitic nematodes and free-living species. This 615 bp full length cDNA sequence encoding *TcGST* was amplified from adult *T. circumcincta* cDNA, cloned and expressed in *E. coli* and the 205 amino acid *TcGST* protein was verified as a detoxifying enzyme capable of conjugating the substrate CDNB with L-glutathione. The protein was recognised by antibodies in both serum and saliva from field-immune sheep, but not nematode-naïve animals.

The GST superfamily is a large one, consisting of distantly related families of cytosolic and mitochondrial/microsomal enzymes, as well as membrane-bound glutathione and eicosanoid metabolising enzymes (Hayes and Pulford, 1995; Sheehan et al., 2001; Hayes et al., 2005; Board and Menon, 2013). The universal function of GST enzymes is detoxification of chemicals by catalysing their conjugation to the thiol group of glutathione before removal from the cell (Sheehan et al., 2001; Hayes et al., 2005; Cole and Deeley, 2006; Deponte, 2013). The *T. circumcincta* GST identified in

this study is likely to be only one of the GSTs expressed in this species, as helminths are known to express homologues of most GST classes (Brophy and Pritchard, 1994; Sheehan et al., 2001; Markov et al., 2015; Bae et al., 2016; Matoušová et al., 2016); the genome of *C. elegans* contains around 50 different GST proteins (Markov et al., 2015). Database searches in the present study indicated that two of the top blast hits currently annotated as a hypothetical protein (locus tag EYC01088 of *A. ceylanicum*) and a proteins of unknown function (locus tag VDO85500 of *H. polygyrus*) can be assigned putative functions as GSTs. As more sequences become available for comparison, functions are likely to be progressively assigned to the large number (about 50%) of the protein-coding genes in helminth genomes of unknown function (Palevich et al., 2018).

TcGST appears to belong to the nu GST class (Fig. 1), which may be a nematode-specific class, or possibly a subfamily of the sigma class (Markov et al., 2015), based on observations that proteins in the same GST class have sequence identity of at least 40%, contrasting with less than 25% between classes (Hayes et al., 2005; Oakley, 2011). These haem-binding proteins, which also bind haematin, have been characterised in the nematodes *H. contortus* (van Rossum et al., 2004), *Onchocerca volvulus* (Perbandt et al., 2005) and hookworms of the genera *Necator* and *Ancylostoma* (Zhan et al., 2005; Goud et al., 2012). Modelling the protein structures of *TcGST* and *HcGST* (Fig. 2) revealed that the best structural models corresponded to the monomer of [2ON5](#), associated with *N. americanus* Na-GST-2 (Asojo et al., 2007). The searches of databases for other helminth GSTs allowed the assignment of a putative function as GSTs to two of the top blast hits currently annotated as a hypothetical protein (locus tag EYC01088 of *A. ceylanicum*) and a proteins of unknown function (locus tag VDO85500 of *H. polygyrus*). As more sequences become available for comparison, functions can become progressively assigned to the large number (about

50%) of the protein-coding genes in helminth genomes of unknown function (Palevich et al., 2018).

The universal function of GST enzymes is detoxification of chemicals by catalysing their conjugation to the thiol group of glutathione before removal from the cell (Sheehan et al., 2001; Hayes et al., 2005; Cole and Deeley, 2006; Deponete, 2013). Recombinant *Tc*GST conjugated the model substrate CDNB, with an optimum pH at 25 °C of pH 7 (Fig. 5), similar to those for nu class *H. contortus* and *A. caninum* GST, and with high activity ($V_{\max}$ 1535 nmoles.min⁻¹.mg protein⁻¹), similar to that of rHcGST-1 (van Rossum et al., 2004) and about twice that of Ac-GST-1 (Zhan et al., 2005).

GSTs have similar protein sequences (Fig. 1) containing a G-site, where glutathione binds, and the H-site, which is the non-specific substrate/chemical binding pocket where haem and haematin bind to nu class GSTs. These sites are shown in the proteins aligned in Fig. 1, where the triangles represent the largely conserved G-site and the asterisks the residues at the H-site. The molecular structures of nu class GSTs have been reported for HpoGSTN2-2 in *H. polygyrus* (Schuller et al., 2005), *Ov*-GST2 in *O. volvulus* (Perbandt et al., 2005) and *Na*-GST-2 and *Na*-GST-2 in *N. americanus* (Asojo et al., 2007) and compared with closely related sigma class GSTs, such as *Na*-GST-3 in *N. americanus* (Kelleher et al., 2013). The best structural models of *Tc*GST and *Hc*GST (Fig. 2) corresponded to the monomer of *N. americanus* *Na*-GST-2 with similar catalytic and active site residues within 4 Å of the substrate at Tyr-8, Phe-9, Trp-39, Lys-43, Gln-50, Leu-51, Pro-52, Gln-63, Ser-64 and Val-65. Like other nu class GSTs, the overall binding cavities were more open and probably therefore more accessible to diverse ligands than other GSTs.

Nu class GSTs participate in nematode haem metabolism through their ability to bind both haem and haematin. Nematodes are unable to synthesise haem and require

either an external source or a symbiont to supply haem, as well as transporters for its uptake across cell membranes and between tissues (Perally et al., 2008). Parasitic nematodes acquire haem from erythrocytes, host tissues and gut bacteria. A number of haem-responsive genes have been identified in nematodes, including the *C. elegans* transmembrane transporters *Ce-hrg-2*, expressed in the epidermis (Chen et al., 2012), and the *H. contortus* homolog *Hc-hrg-2*, which is expressed in all life cycle stages, but at the highest levels in L3 (Chen et al., 2012; Zhou et al., 2020). *A. ceylanicum* *Ace-GST*, a homolog of *Ac-GST* and *Na-GST-1*, is located in the epidermis, muscle and intestine of adult worms (Hang et al., 2020).

Recombinant helminth GSTs are showing promising results as vaccine antigens (Da Costa et al., 1999; Zhan et al., 2005, 2010; Preyavichyapugdee et al., 2008, Hang et al., 2020). Native *T. circumcincta* GST is highly antigenic and antibodies in both serum and saliva from field-immune sheep recognised recombinant *TcGST* in an ELISA (Fig. 7), suggesting it also may be a useful antigen for inclusion in further studies to assess the protective efficacy of recombinant *TcGST* in sheep and goats.

Acknowledgments

The authors would like to thank Dr Jacqui Knight for the initial database search and Drs Sandeep Gupta and Sofia Khanum for critically reviewing the manuscript. The financial support of AGMARDT (Grant No. P14003) is gratefully acknowledged.

References

Altschul, S.F., Madden, T.L., Schäffer A.A., Zhang, J., Zhang, Z., Miller, W., Lipman, D.J., 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25, 3389-3402.

Asojo, O.A., Homma, K., Sedlacek, M. Ngamelue, M., Goud, G.N., Zhan, B., Deumic, V., Asojo, O., Hotez, P.J., 2007. X-ray structures of *Na*-GST-1 and *Na*-GST-2 two glutathione s-transferase from the human hookworm *Necator americanus*. *BMC Struct. Biol.* 7, 42.

Bae, Y.-A., Kim, J.-G., Kong, Y., 2016. Phylogenetic characterization of *Clonorchis sinensis* proteins homologous to the sigma-class glutathione transferase and their differential expression profiles. *Mol. Biochem. Parasitol.* 206, 46-55.

Blocki, F.A., Ellis, L.B.M., Wackett, L.P., 1993. MIF protein are theta-class glutathione S-transferase homologs. *Prot. Sci.* 2, 2095-2102.

Board, P.G., Menon, D., 2013. Glutathione transferases, regulators of cellular metabolism and physiology. *Biochim. Biophys. Acta* 1830, 3267-3288.

Brophy, P.M., Barrett, J., 1990. Glutathione transferase in helminths. *Parasitology* 100, 345-349.

Brophy, P.M., Pritchard, D.I., 1994. Parasitic helminth glutathione S-transferases: an update on their potential as targets for immuno- and chemotherapy. *Exp. Parasitol.* 79, 89-96.

Campbell, A.M., Teesdale-Spittle, P.H., Barrett, J., Liebau, E., Jefferies, J.R., Brophy, P.M., 2001. A common class of nematode glutathione S-transferase (GST) revealed by the theoretical proteome of the model organism *Caenorhabditis elegans*. *Comp. Biochem. Physiol. B* 128, 701-708.

Chen, C., Samuel. T.K., Krause, M., Dailey, H.A., Hamza, I., 2012. Heme utilization in the *Caenorhabditis elegans* hypodermal cells is facilitated by heme-responsive gene-2. J. Biol. Chem. 287, 9601-9612.

Cole, S.P.C., Deeley, R.G., 2006. Transport of glutathione and glutathione conjugates by MRP1. Trend. Pharm. Sci. 27, 438-448.

Da Costa, A., Gaubert, S., Lafitte, S., Fontaine, J., Capron, A., Grzych, J-M., 1999. Egg-hatching in mice immunized with recombinant *Schistosoma bovis* 28kDa glutathione S-transferase. Parasit.e Immunol. 21, 341-350.

Deponte, M., 2013. Glutathione catalysis and the reaction mechanisms of glutathione-dependent enzymes. Biochim. Biophys. Acta 1830, 3217-3266.

Flanagan, J.U., Smythe, M.L., 2011. Sigma-class glutathione transferases. Drug Metab. Rev. 43, 194-214.

Goud, G.N., Deumic, V., Gupta, R., Brelsford, J., Zhan, B., Gillespie, P., Plieskatt, J.L., Tsao, E.I., Hotez, P.J., Bottazzi, M.E., 2012. Expression, purification, and molecular analysis of the *Necator americanus* glutathione S-transferase 1 (Na-GST-1): A production process developed for a lead candidate recombinant hookworm vaccine antigen. Protein Expr. Purif. 83, 145-151.

Hayes, J.D., Flanagan, J.U., Jowsey, I.R., 2005. Glutathione transferases. Annu. Rev. Pharmacol. Toxicol. 45, 51-88.

Hayes, J.D., Pulford, D.J., 1995. The glutathione S-transferase supergene family: regulation of GST and the contribution of the isoenzymes to cancer chemoprotection and drug resistance. Crit. Rev. Biochem. Mol. Biol. 30, 445-600.

Kelleher, A., Zhan, B., Asojo, O.A., 2013. Structure of monomeric Na-GST-3, a glutathione S-transferase from the major human hookworm parasite *Necator americanus*. Acta Crystallogr. F 69, 839-843.

Knight, J.S., Broadwell, A.H., Grant, W.N., Shoemaker, C.B., 2004. A strategy for shuffling numerous *Bacillus thuringiensis* crystal protein domains. J. Econ. Entomol. 9, 1805-1813.

Laskowski, R.A., Rullmann, J.A.C., MacArthur, M.W., Kaptein, R., Thornton, J.M., 1996. AQUA and PROCHECK-NMR: programs for checking the quality of protein structures solved by NMR. J. Biomol. NMR 8, 477–486.

Markov, G.V., Baskaran, P., Sommer, R.J., 2015. The same or not the same: lineage-specific gene expansions and homology relationships in multigene families in nematodes. J. Mol. Evol. 80, 18-36.

Matoušková, P., Vokrál, I., Lamka, J., Skálová, L., 2016. The role of xenobiotic metabolizing enzymes in anthelmintic deactivation and resistance in helminths. Trend. Parasitol. 32, 481- 491.

Morel, F., Aninat, C., 2011. The glutathione transferase kappa family. Drug Metab. Rev. 43, 281-291.

Oakley, A. 2011. Glutathione transferases: a structural perspective. Drug Metab. Rev. 43, 138-151.

Palevich, N., Britton, C., Kamenetzky, L., Mitreva, M., de Moraes Mourão, M., Bennuru, S., Quack, T., Scholte, L.L.S., Tyagi, R., Slatko, B. E. 2018. Tackling hypotheticals in helminth genomes. Trend. Parasitol. 34, 179-183.

Palevich, N., Maclean, P.H., Baten, A., Scott, R.W., Leathwick, D.M., 2019a. The genome sequence of the anthelmintic-susceptible New Zealand *Haemonchus contortus*. Genome Biol. Evol. 11, 1965-1970.

Palevich, N., Maclean, P.H., Baten, A., Scott, R.W., Leathwick, D.M., 2019b. The complete mitochondrial genome of the New Zealand parasitic roundworm

438 *Haemonchus contortus* (Trichostrongyloidea: Haemonchidae) field strain
439 NZ_Hco_NP. Mitochondrial DNA B, 4, 2208-2210.

440 Perally, S., Lacourse E.J., Campbell, A.M., Brophy, P.M., 2008. Heme transport and
441 detoxification in nematodes: subproteomics evidence of differential role of
442 glutathione transferases. J. Proteom. Res. 7, 4557-4565.

443 Perbandt, M., Hoppner, J., Betzel, C., Walter, R.D., Liebau, E., 2005. Structure of the
444 major cytosolic glutathione S-transferase from the parasitic nematode *Onchocerca*
445 *volvulus*. J. Biol. Chem. 280, 12630-12636.

446 Petit, E., Michelet, X., Rauch, C., Bertrand-Michel, J., Terce, F., Legouis, R., Morel, F.,
447 2009. Glutathione transferases kappa 1 and kappa 2 localize in peroxisomes and
448 mitochondria, respectively, and are involved in lipid metabolism and respiration in
449 *Caenorhabditis elegans*. FEBS J. 276, 5030-5040.

450 Preyavichyapugdee, N., Sahaphong, S., Riengrojpitak, S., Grams, R., Viyananay, V.,
451 Sobhon, P., 2008. *Fasciola hepatica* and *Schistosoma mansoni*: Vaccine potential of
452 recombinant glutathione S-transferase (rFgGST26) against infections in mice. Exp.
453 Parasitol. 119, 229-237.

454 Schuller, D.J., Liu, Q., Kriksunov, I.A., Campbell, A.M., Barrett, J., Brophy, P.M.,
455 Hao, Q. 2005. Crystal structure of a new class of glutathione transferase from the
456 model human hookworm nematode *Heligmosomoides polygyrus*. Proteins 61, 1024-
457 1031.

458 Sheehan, D., Meade, G., Foley, V.M., Dowd, C.A., 2001. Structure, function and
459 evolution of glutathione transferases: implications for classification of non-
460 mammalian members of an ancient enzyme superfamily. Biochem. J. 360, 1-16.

Sparkes, A., De Baetselier, P., Roelants, K., De Trez, C., Magez, S., Van Ginderachter, J.A., Raes, G., Bucalaf, R., Stijlemans, B., 2017. The non-mammalian MIF superfamily. *Immunobiology* 222, 473-482.

Umair, S., Ria, C., Knight, J.S., Simpson, H.V., 2013. Sarcosine metabolism in *Haemonchus contortus* and *Teladorsagia circumcincta*. *Exp. Parasitol.* 134, 1–6.

Van Rossum, A.J., Jefferies, J.R., Rijsewijk, F.A.M., LaCourse, E.J., Teesdale-Spittle, P., Barrett, J., Tait, A., Brophy, P.M., 2004. Binding of hematin by a new class of glutathione transferase from the blood-feeding parasitic nematode *Haemonchus contortus*. *Infect. Immun.* 72, 2780-2790.

Wiederstein, M., Sippl, M.J., 2007. ProSA-web: interactive web service for the recognition of errors in three-dimensional structures of proteins. *Nucleic Acids Res.* 35, W407–W410.

Yang, J., Yaan, R., Roy, A., Xu, D., Poisson, J., Zhang, Y., 2015. The I-TASSER Suite: Protein structure and function prediction. *Nat. Methods* 12, 7-8.

Zhan, B., Liu, S., Perally, S., Xue, J., Fujiwara, R., Brophy, P., Xiao, S., Liu, Y., Feng, J., Williamson, A., Wang, Y., Bueno, L.L., Mendez, S., Goud, G., Bethony, J.M., Hawdon, J.M., Loukas, A., Jones, K., Hotez, P.J., 2005. Biochemical characterization and vaccine potential of a heme-binding glutathione transferase from the adult hookworm *Ancylostoma caninum*. *Infect. Immun.*, 73, 6903-6911.

Zhan, B., Perally, S., Brophy, P.M., Xue, J., Goud, G., Liu, S., Deumic, V., de Oliveira, L.M., Bethony, J.M., Bottazzi, M.E., Jiang, D., Gillespie, P., Xiao, S., Gupta, R., Loukas, A., Ranjit, N., Lustigman, S., Oksov, Y., Hotez, P.J., 2010. Molecular cloning, biochemical characterization, and partial protective immunity of the heme-binding glutathione s-transferases from the human hookworm *Necator americanus*. *Infect. Immun.*, 78, 1552-1563.

486 Zhang, Y., Skolnick, J. 2004. Scoring function for automated assessment of protein
487 structure template quality, Proteins 57, 702-710.

488

Figure Legends

Fig. 1. Multiple sequence alignment of *TcGST* with homologues from *Ancylostoma ceylanicum* (EYC01088), *Ancylostoma duodenale* (GI: KIH60339), *Haemonchus contortus* (GI: AAF81283), *Heligmosomoides polygyrus* (GI: VDO85500), *Necator americanus* (GI: ACX53263), *Oesophagostomum dentatum* (GI: KHJ77903), *Nippostrongylus brasiliensis* (GI: VDL81310), *Ancylostoma caninum* (GI: AAT37718), *Caenorhabditis elegans* (GI: CCD62662), *Caenorhabditis briggsae* (GI: XP002631478), *Trichinella spiralis* (GI: ABA42914), *Dirofilaria immitis* (GI: AAA21585), *Ascaris lumbricoides* (GI: ATZ35993), *Onchocerca volvulus* (GI: CAA54568), *Fasciola gigantica* (GI: ACH88355), *Fasciola hepatica* (GI: ADP09370), *Schistosoma japonicum* (GI: 62738608), *Schistosoma bovis* (GI: RTG90762) and *Schistosoma mansoni* (GI: AAA29888) homologues. The % identity of the helminth GST with that of *T. circumcincta* is shown at the end of the alignment. The triangles represent the non-specific substrate/chemical binding pocket, the H-site and those with an asterisk (*) represent the GSH-binding G-site. The % homology of each sequence with *TcGST* is shown at the end of the alignment.

Fig. 2. The predicted tertiary structure of the *TcGST* and *HcGST* monomers. (A) Location of the C- and N-termini in the predicted tertiary structure of *TcGST*. (B) Superposition of the predicted tertiary structure of *TcGST* from *T. circumcincta* (red) and *H. contortus* GST (blue). (C) Location of the active site within *TcGST*. (D) The active site of *TcGST* (green) within 4Å of the superimposed 2CA8 (salmon) with polar bonds also shown in yellow.

Fig. 3. Purified recombinant *TcGST* on a NuPage™ 4 - 12% Bis-Tris protein gel stained with SimplyBlue safe stain. Lane 1: Seeblue™ plus 2 Pre-stained protein standard in Kda; Lane 2: Filtered soluble bacterial lysate; Lane 3: Unbound material to HisTrap column; Lane 4: Elution fraction (purified recombinant *TcGST* indicated by the black arrow).

Fig. 4. Effects of pH (top) and varying the substrate concentration at pH 7 (bottom) on the enzyme activity (mean $\pm$ SD, n = 2) of recombinant *TcGST* at 25 °C. Activity was calculated from the conjugation of L-glutathione and 1-chloro-2,4-dinitrobenzene, monitored spectrophotometrically at 340 nm.

Fig. 5. Recognition of recombinant *TcGST* by serially diluted immune serum (IgG) (top) or saliva (IgA) (bottom) (■), but not by parasite-naïve serum or saliva (●).

		1		60
			* * * * *	
	TcGST	MVHYRLLYFDGRGRAEVAR-QLFALANQEYVDV--	RI THEEWPKHKPEM--	PFGQLPVL
	<i>A. ceylanicum</i> GST	MVHYKLTYFNDRGAAEIIR-QLFVLADQEYEDV--	RL THEEWPKHKAEM--	PFGQLPVL
	<i>A. duodenale</i> GST	MVHYKLTYFDGRGAAEIIR-QVFALAGQEYEDV--	RLSFEWPKHKAEM--	PFGQLPVL
	<i>H. contortus</i> GST	MVHYKLTYFNDRGAAEIIR-QVFVLADQYEDV--	RL THEEWPKHKASM--	PFGQLPVL
	<i>H. polygyrus</i> GST	MVHYKLIYFNDRGAAEIIR-QLFVIAGKEYEDV--	RLTFEWPKYKPEM--	PFGQVPVL
	<i>N. americanus</i> GST	MVHYKLTYFDGRGAAEIIR-QIFVLADQEYEDI--	RLSHDEWPKYKNEM--	PFGQLPVL
	<i>O. dentatum</i> GST	-----MTYLC SRNLRLMSKEQIFALAGQDYEDV--	RYTFEWPKHKDEM--	PFGQMPVL
	<i>N. brasiliensis</i> GST	-----MNLKIFVLADQEYDDV--	RLSREEWPKIKAEM--	PFGQIPVL
	<i>A. caninum</i> GST	MVHYKLTYFNDRGLGECAR-QLFALADQQYEDI--	RVTHEDFPEIKPNL--	PFGQLPLL
	<i>C. elegans</i> GST	MVSYKLTYFNDRGAGEVSR-QIFAYAGQQYEDN--	RVTQEQWPALKETCAAPFGQLPFL	
	<i>C. briggsae</i> GST	MVAYKLTYFNDRGAGEVIR-QIFAHAGQDFEDV--	RVTMEQWPALKAGT--	PFGQLPYL
	<i>T. spiralis</i> GST	MPLYKLVYFPIRGLAEPIR-LLLHDQRVEFLDN--	RIQQKDWPEIKSQM--	LFGQVPCL
	<i>D. immitis</i> GST	-MSYKLTYFPIRGLAEPIR-LLLVDQGIKFTDE--	HIPKDDFVSIKSQF--	QFGQLPCF
	<i>A. lumbricoides</i> GST	-MGYKVITYFAIRGLAEPIR-LLLTDEIPFDDA--	RIKDLAEWQSVKHQF--	QFGQVPCL
	<i>O. volvulus</i> GST	-MSYKLTYFSIRGLAEPIR-LFLVDQDIKFIDD--	RIAKDDFSSIKSQF--	QFGQLPCL
	<i>F. gigantica</i> GST	-MPAKLGYWKIRGLQQPVR-LLLEYLDEEYEEHLYGRDDREKWLGDKFNMGDLPLNLPYY		
	<i>F. hepatica</i> GST	-MPAKLGYWKIRGLQQPVR-LLLEYLGEYEEHLYGRDDREKWLGDKFNMGDLPLNLPYY		
	<i>S. japonicum</i> GST	--SPILGYWKIKGLVQPTR-LLLEYLGEYEEHLYERDEGDKWRNKKFELGLEFPNLPYY		
	<i>S. bovis</i> GST	-----LVQPTR-LLLEYVGEVYEERLYDRNDGDVWRNEKFNGLGLEFPNLPYY		
	<i>S. mansoni</i> GST	-MAPKFGYWKVKGLVQPTR-LLLEHLEETYEERAYDRNEIDAWSNDKFKLGLEFPNLPYY		
		61		120
			* * *	
	TcGST	DVDGKLLGQSHAINRYLARQFGFAGKSPFEEALVDAFADQYRDFYTEAQPYLYAVWGFVK	Δ Δ Δ Δ	
	<i>A. ceylanicum</i> GST	EVDGKQLAQSFIVRFLARKFGFAGKCPFEEALVDSIADQYKDFINEVRPCLMVLMGFAE		
	<i>A. duodenale</i> GST	EVDGKQLAQSLAIVRFIARKFGFAGKCPFEEALVDSIADQHKDFINEIRPFLRVAMGFDQ		
	<i>H. contortus</i> GST	EVDGKQLPQSVIVRYRLARKFGYAGKSAWEEAVVDSIADQFKDFLNEVRPYFKVLLGMDQ		
	<i>H. polygyrus</i> GST	EIDGQKLAQSLAIVRYRLAREFGYAGKTPFEEALVDSIGDQYKDFVNEARPYFRVALGFQE		
	<i>N. americanus</i> GST	EVDGKKLAQSFIVRFLARKFGFAGKCPFEEALVDSITDQYKDFINEIRPFLRVAMGFAE		
	<i>O. dentatum</i> GST	EVDGKQLAQSFIVRFLARKFGFAGKTPFEEALVDSIADQFKDFSIECRPIAKVVMGFQE		
	<i>N. brasiliensis</i> GST	EVDGKKLAQSSAIVRYVARQFGYAGKNAFDEALVDSLVDQWKDFNEARPYFMVLLGFQE		
	<i>A. caninum</i> GST	NEDGKELAQSNAINRYRLARKFGFAGKTPFEEALVDSLADQMTDYRVEIKPFVYTAYGHQK		
	<i>C. elegans</i> GST	EVDGKKLAQSHAIARFLAREFKLNGKTAWEEAQVNSLADQYKDYSSSEARPYFYAVMGFGP		
	<i>C. briggsae</i> GST	EVDGKPLAQSHAIARYLAREFKLNGQCPWEEAQVNALSDQFKDYSSSEAKPYFYAKMGFGP		

<i>T. spiralis</i> GST	YEDDQPIVQSGAIMRHLGRRFGLYGNAE-EMTYVDQIYEGVVDLRLKYARLIYSD-----
<i>D. immitis</i> GST	YDGDQQIVQSGAILRHLARKFNLNGENNAETSYVDMFYEGIRDLHSHKYTRMIYEA-----
<i>A. lumbricoides</i> GST	HDDNEQIVQSGAILRHLARKHNLNGSNENEATYADMFYEGIRDLHMKYTKMIYHA-----
<i>O. volvulus</i> GST	YDGDQQIVQSGAILRHLARKYNLNGENEMETTYIDMFCEGVRDLHVKYTRMIYMA-----
<i>F. gigantica</i> GST	IDDKCKLTQSVAIMRYIADKHGMLGSTPEERARVSMIEGAAMDLMGMFVRVCYNP-----
<i>F. hepatica</i> GST	IDDKCKLTQSVAIMRYIADKHGMLGSTPEERARISMIEGAAMDLMGMFVRVCYNP-----
<i>S. japonicum</i> GST	IDGDVKLTQSMAILRYIADKHNLGGCPKERAIEISMLEGAVLDIRYGVSR IAYSK-----
<i>S. bovis</i> GST	IDGDVKLTQSMAILRYIADKHNLGGCPKERAIEISMLEGAILDIRLGVSR IAYNK-----
<i>S. mansoni</i> GST	IDGDFKLTQSMAILRYIADKHNLGACPKERAIEISMLEGAVLDIRMGVLR IAYNK-----

	121		180
<i>TcGST</i>			
<i>A. ceylanicum</i> GST	-GDVNALENEKFAPARDKFFNLMTKHLK--ASKSGFLVGDSVTWADLQLAE-LATFTEKY		
<i>A. duodenale</i> GST	-GDLEKLTKELLLPAKFFFGFMTKFLK--ESKSGYLVGDSLTFADLYLAETSAEFVKKF		
<i>H. contortus</i> GST	-GDVEKLAKELFLPAKFFFGFMTKFLK--ESKSGYLVGDSLTYADLYLAESSAEFAKKF		
<i>H. polygyrus</i> GST	-GDLKALEKDVFEPAKFFFTIVTKILK--ENKTGYLVGDSLTFADLYVAE-MTTFTEHY		
<i>N. americanus</i> GST	-GDEAALAKDVFLPAKFFFTFMTKFLN--QSKSGYLVGDSLTVADLVLAE-MAEVAKKV		
<i>O. dentatum</i> GST	-GDLEKLSNEVFLPAKFFFGFMTNFKL--ESKSGYLVGDSLTFADLYLAECASEFAKKT		
<i>N. brasiliensis</i> GST	-GDVEKLTKEVFNPAKFFFGYVTKFLK--ASKSGYLVGDSLTFADLYLAETTSEFVKKV		
<i>A. caninum</i> GST	-GDADAVAKQLVLPAREKFFFTFITKFIK--NSNSGFLVGDSVTWVDLIVAE-LATQYELV		
<i>C. elegans</i> GST	FGDLETLKKDVMLPARDKFLGFITKFLK--NNPSGFLVGDSVTWIDLALLAEHASDIQSKV		
<i>C. briggsae</i> GST	-GDVETLKKDIFLPAFEKFFYFGLVNFLK--ASGSGFLVGDSLTVIDLAVQAHSADLIAQG		
<i>T. spiralis</i> GST	--SFHESKGKFINEVLPDELAKFEKILT---GKKYILDDEITFADYALAEILLDVLILS		
<i>D. immitis</i> GST	---YETQKDPFIKNILPQELAKLEKLLATRDNGKNFILGDKISFADYVLFEELDVQQILD		
<i>A. lumbricoides</i> GST	---YETEKDSFIKDILPVELAKFEKLLPTRGGGAGYILGDKICFADYVLFEELDIMQILD		
<i>O. volvulus</i> GST	---YETEKDPYIKSILPGELAKFEKLLATRGNGRNLILGDKISYADYALFEELDVHQILD		
<i>F. gigantica</i> GST	--NFEEVKGDYLKE-LPKTLKMWSDFLG----DRQYLTGSSVSHVDFMVYEALDCIRYLA		
<i>F. hepatica</i> GST	--KFEEVKGDYLKE-LPTTLKMWSNFLG----DRHYLTGSSVSHVDFMVYEALDCIRYLA		
<i>S. japonicum</i> GST	--DFETLKVDFLSK-LPEMLKMFEDRLC----HKTYLNGDHVTHPDFMLYDALDVVLYMD		
<i>S. bovis</i> GST	--EFETLKVGFNLQ-LPGMLKMFENRLS----HKIYLNNGDNVTHVDFMLYDALDVVLYMD		
<i>S. mansoni</i> GST	--EYETLKVDFLNK-LPGRLKMFEDRLS----NKTYLNGNCVTHVDFMLYDALDVVLYMD		

	181	240	% identity
<i>TcGST</i>	ATLYVGFPEVKAHSEKVRSIPEIKKRIETRKNTPF-----		-
<i>A. ceylanicum</i> GST	PTIYDGFPEVKAHA EKVR SNPALKKWIETRPETKF-----		[68%]
<i>A. duodenale</i> GST	PSTYDGFPEVKAHA EKVR SNPSLKKWIETRPVTKF-----		[66%]
<i>H. contortus</i> GST	PKLYDGFPEVKAHA EKVR SNPKLKKWIETRPASKF-----		[64%]
<i>H. polygyrus</i> GST	PTLYDGFPEAKAHSEKIRSIPALAKWLQTRPETKF-----		[63%]
<i>N. americanus</i> GST	PTIFDGFPEIKAHA EKVR SNPALKKWIETRPETKF-----		[63%]
<i>O. dentatum</i> GST	PTLYDGFPEVKAHA EKVR SNPALKKWIETRPQTSF-----		[62%]
<i>N. brasiliensis</i> GST	PDFYKGFPEVKAHSEKVRSLPALKKWIETRPDTPF-----		[61%]
<i>A. caninum</i> GST	PEYLEGFPEVKAHMEKVR SI PKLKKWIETTPDTHF-----		[60%]
<i>C. elegans</i> GST	GD-FSKFPELKAHA EKIQAI PQIKKWIETRPVTPF-----		[55%]
<i>C. briggsae</i> GST	ID-FSKFQDLKAHSEKIQAI PQIKKWIDSRPETPF-----		[53%]
<i>T. spiralis</i> GST	SSCLENFTALTIYHSR FMNRP NLKRYLSSDIRKNAKINGNENK-----		[26%]
<i>D. immitis</i> GST	PHCLEKFPLLKA FHQR L G D K P K I K E Y C A K R N A S K M P V N G N G K Q -----		[26%]
<i>A. lumbricoides</i> GST	PHALDKFPTLKA FHQR M L D R P L I K A Y Y Q K R A E A K V P V N G N G K Q -----		[25%]
<i>O. volvulus</i> GST	PHCLDKFPLLKA FHQR M K D R P K L K E Y C E K R D A A K V P V N G N G K Q -----		[25%]
<i>F. gigantica</i> GST	PQCLNDFPKLKEFKSRIEDLPKI KAYMESEKFIKWPLNSWTASF GGGDAAPA-----		[23%]
<i>F. hepatica</i> GST	PQCLEDFPKLKEFKSRIEDLPKI KAYMESEKFIKWPLNSWSASF GGGDAAPA-----		[22%]
<i>S. japonicum</i> GST	PMCLDAFPKLVC FKKRIEAI PQIDKYLKSSKYIAWPLQG WQATF GGGDHPPKSDLVPR-----		[22%]
<i>S. bovis</i> GST	PKCLDAFPKLISFKQRIENLPPIKNYLNSDRHIKWPLQGWSAIF GGGDAPPK-----		[19%]
<i>S. mansoni</i> GST	SQCLNEFPKLVSFKKCIEDLPQIKNYLNSRYIKWPLQGW DATF GGGDTPPK-----		[19%]

Fig. 6. Recognition of recombinant *Teci*GST by serially diluted immune serum (IgG) (top) or saliva (IgA) (bottom) (■), but not by parasite-naïve serum or saliva (●).