Biochemical characterisation of the recombinant peroxiredoxin (FhePrx) of the liver fluke, *Fasciola hepatica*

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Received 16 May 2006; revised 31 July 2006; accepted 4 August 2006

Available online 22 August 2006

Edited by Judit Ovádi

Abstract  The parasitic helminth *Fasciola hepatica* secretes a 2-Cys peroxiredoxin (Prx) that may play important functions in host–parasite interaction. Recombinant peroxiredoxin (FhePrx) prevented metal-catalyzed oxidative nicking of plasmid DNA and detoxified hydrogen peroxide when coupled with *Escherichia coli* thioredoxin and thioredoxin reductase ($K_{cat}/K_m = 5.2 \times 10^3 \text{M}^{-1} \text{s}^{-1}$). Enzyme kinetic analysis revealed that the catalytic efficiency of FhePrx is similar to other 2-Cys peroxiredoxins; the enzyme displayed saturable enzyme Michaelis–Menten kinetics when assayed at low concentrations of substrate. FhePrx could not utilise reducing equivalents supplied by glutathione or glutathione reductase.

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Keywords: Peroxiredoxin; Thioredoxin peroxidase; *Fasciola hepatica*

1. Introduction

Peroxiredoxins (Prx) are a ubiquitous family of peroxidases that reduce hydrogen peroxide to water and alkyl hydroperoxides to alcohols [4,5,17,24,33]. At least in bacteria (AhpC), yeast (thioredoxin peroxidase), and trypanosomatids (tryparedoxin peroxidase) Prxs are central in the defence against reactive oxygen species (ROS) and protect these cells from oxidative stress [17,33]. More recent studies indicate that these enzymes also function intracellularly [32] and extracellularly [12] in the regulation of H$_2$O$_2$-mediated cell-signalling events in eukaryotes.

The catalytic cycle begins with oxidation by the peroxide substrate of the essential peroxidatic cysteine, the N-terminal proximal active site Cys, forming a Cys-sulfenic acid derivative. The intermediate is resolved by a condensation reaction when Cys-sulfenic acid reacts with a Cys in the C-terminal distal domain of a second inverted Prx molecule, thus forming a dimer linked by two disulfide bridges [17,33]. Reduction of the Prx dimer regenerates the Prx monomer and in most cases the physiological hydrogen donor is thioredoxin, but this may also be performed by tryparedoxin or glutathione [17]. Thioredoxin itself is maintained in the reduced state by electrons transferred from NADPH by thioredoxin reductase [4,5,21,33].

The liver fluke, *Fasciola hepatica*, is an important helminth pathogen of humans and livestock [8,11,22]. Infective parasites (metacercariae) excyst from a dormant state following ingestion and penetrate the intestinal wall before migrating to the liver. In this nutrient and oxygen rich environment the parasites undergo rapid growth and development, and energy is supplied by aerobic respiration [9,31]. As part of its antioxidative defence, *F. hepatica* expresses glutathione-S-transferase and superoxide dismutase, which detoxify ROS to hydrogen peroxide [1,2,21]. The pathway of hydrogen peroxide detoxification is unclear, since the liver fluke lacks catalase and exhibits little glutathione peroxidase activity [1,2,24]. Our laboratory was the first to describe the presence of Prxs in helminth parasites when we reported the isolation of a cDNA encoding this enzyme in *F. hepatica* [23]. Since these enzymes can detoxify hydrogen peroxide we suggested that Prx performs this function in *F. hepatica*, and other helminths that lack catalase [23,24].

Here we report the biochemical characterisation of a functionally active recombinant *F. hepatica* 2-Cys peroxiredoxin (FhePrx). We show its protective effects against hydrogen peroxide in a mixed-function oxidation assay, and by coupling FhePrx with *Escherichia coli* thioredoxin and thioredoxin reductase determined the specific activity and reaction kinetics of the enzyme. FhePrx displays saturable, Michaelis–Menten type kinetics when assayed at low concentrations of substrate but is sensitive, rather than robust, to over-oxidation by hydrogen peroxide. The FhePrx does not accept reducing equivalents from glutathione or glutathione reductase, which is in contrast to Prx from the related parasite *Schistosoma mansoni*.

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Abbreviations: Prx, peroxiredoxin; ES, excretory–secretory products


2. Materials and methods

2.1. Parasite materials, proteins and RNA extraction

Adult F. hepatica were recovered from the bile ducts of sheep experimentally challenged for 14 weeks with 200 infective metacercaiae. Soluble extracts were prepared by three cycles of freeze-thaw at −20 °C and sonication for 30 s in a soni-bath. Extracts were centrifuged at 14000 × g for 30 min, the supernatant decanted and stored at −80 °C. Excretory–secretory (ES) products were prepared by culturing parasites in RPMI-1640, containing 30 mM HEPES, 1% glucose and gentamicin (25 μg/ml) for 6 h. The culture medium was concentrated to 1 mg/ml on a Centricon (Amicon) with a 5000 Da molecular size cutoff. The cysteine protease inhibitor E-64 (final concentration 1 mM) was added to parasite extracts and ES products to prevent degradation by parasite cysteine proteases. Juvenile parasites were excysted from infective metacercariae as previously described [3,8]. Following a single freeze-thaw cycle at −80 °C, the parasites were homogenized in Tris-reagent (Sigma) and total RNA extracted according to the manufacturers’ specifications. For reverse transcription-PCR (RT-PCR), first strand cDNA was produced with oligo (dT) primers from 2 μg of total RNA by using avian myeloblastosis virus reverse transcriptase (Promega, Madison, WI) at 42 °C for 60 min. A 5-μl aliquot of the resultant cDNA was amplified by using primers specific for β-actin (mouse, Stratagene, La Jolla, CA) or Prx (FhePrx fwd and FhePrx rev, see Section 2.3) under the following conditions: 30 s denaturation at 95 °C and 12 s elongation at 72 °C for 40 cycles [13].

2.2. Preparation of anti-peroxiredoxin serum

Sheep were vaccinated three times with 100 μg of purified recombinant FhePrx at three week intervals using Quil A (100 μg per sheep) as an adjuvant. Antigen and adjuvant were formulated in 2 ml sterile phosphate buffered saline (PBS), pH 7.3, and injected sub-cutaneously in the neck region.

2.3. Cloning and functional expression of F. hepatica peroxiredoxin (FhePrx)

The FhePrx gene was PCR amplified from cDNA isolated from a 2gt 11 library immunoscreened with sera from cattle protectively vaccinated with a high molecular mass fraction from adult liver fluke (GenBank Accession No. U88577) [8,23]. The primers used to amplify the gene were FhePrx Forward: 5′-CCGGAATTCTAGTTGCTGCCGTTGCAGCCATGTTGCAGCCATGTTGCAGCCATGGTTGCAGCCATGGT-3′, which inserted an EcoRI site (underlined) proximal to the ATG start codon of the Prx open reading frame and FhePrx Reverse: 5′-CGGCTCGAGTCACTAGTGGCTGCTGAAA-3′ which inserted an XhoI site (underlined) proximal to a double stop codon. The full length cDNA corresponds to the 580 nucleotide open reading frame described in McGonigle et al., [23], initiating with the amino acid residues, MLQPN – and terminating with the residues – FSSAN, resulting in a polypeptide of 194 amino acid residues. The full length recombinant FhePrx protein was induced with IPTG (1 mM) and extracted using nant tobacco etch virus protease cleavage site.


The specific activity of FhePrx was determined by the reduction of H2O2 in a reaction containing E. coli thioredoxin and thioredoxin reductase (Sigma–Aldrich). The reaction mix contained 5 mM potassium phosphate, pH 7.0, 1 mM EDTA, 0.25 mM NADPH, 10 μM E. coli thioredoxin and 0.15 μM E. coli thioredoxin reductase in a total volume of 500 μl. Consumption of NADPH at 22 °C was monitored at A340 for 1 min in a spectrophotometer after adding hydrogen peroxide. The specific activity of the FhePrx was determined by the following products: units of Prx= mg of protein = ([(AAt × Vf)/ (6.22 × Vs × 1000)]/[protein] in mg/ml, where 6.22 = extinction coefficient of NADPH (mM·cm−1), Vf is the total reaction volume, Vs is the sample volume and 1000 is used to convert to nanomoles [4,5,19]. Steady-state kinetic analysis was performed using the same assay; however, concentrations of thioredoxin ranged from 5 μM to 20 μM and hydrogen peroxide ranged from 25 μM to 100 μM. Km and kcat values were determined using Enzpack for Windows, version 1.4 (Biosoft Software for Science).

3. Results and discussion

3.1. Purification of recombinant F. hepatica peroxiredoxin

Purified recombinant FhePrx migrated at an approximate molecular weight of 26 kDa when analysed by reducing SDS–PAGE, which agrees with the molecular weight of the FhePrx predicted from the deduced amino acid sequence, 21.6 kDa [23] plus the 6X His-tag (Fig. 1). When examined by SDS–PAGE under non-reducing conditions, the FhePrx enzyme migrated close to the 50 kDa molecular size marker indicating that the recombinant protein forms a dimeric enzyme containing a reactive center (Fig. 1B, lane 1). This was confirmed firstly by reduction of the inter-subunit disulfide bridges, and thereby splitting the two monomers, by addition of a small diethiol, DTT, to the sample prior to electrophoresis (Fig. 1B, lane 2). Addition of hydrogen peroxide to the recombinant FhePrx caused the dimer to migrate as two bands, one slightly slower than that seen in lane 1, presumably because either one or two covalent disulfide linkages were formed between the monomers with corresponding conformation rearrangements (Fig. 1B, lane 5) [16]. However, somewhat surprisingly, the addition of DTT before or after the addition of hydrogen peroxide to the recombinant FhePrx (Fig. 1B, lanes 3 and 4) did not increase the amount of monomeric form. It was expected that the reduced active site residues, Cys-SH, would react with the hydrogen peroxide to form the sulfenic acid derivative, Cys-SOH, which is resolved by dimerisation, and that addition of DTT before or after the addition of hydrogen peroxide to the recombinant FhePrx (Fig. 1B, lanes 3 and 4) did not increase the amount of monomeric form. It was expected that the reduced active site residues, Cys-SH, would react with the hydrogen peroxide to form the sulfenic acid derivative, Cys-SOH, which is resolved by dimerisation, and that addition of DTT before or after the addition of hydrogen peroxide to the recombinant FhePrx (Fig. 1B, lanes 3 and 4) did not increase the amount of monomeric form. It was expected that the reduced active site residues, Cys-SH, would react with the hydrogen peroxide to form the sulfenic acid derivative, Cys-SOH, which is resolved by dimerisation, and that addition of DTT before or after the addition of hydrogen peroxide to the recombinant FhePrx (Fig. 1B, lanes 3 and 4) did not increase the amount of monomeric form. It was expected that the reduced active site residues, Cys-SH, would react with the hydrogen peroxide to form the sulfenic acid derivative, Cys-SOH, which is resolved by dimerisation, and that addition of DTT before or after the addition of hydrogen peroxide to the recombinant FhePrx (Fig. 1B, lanes 3 and 4) did not increase the amount of monomeric form.
size of approximately 26 kDa in immunoblots of soluble
extracts co-migrated with the recombinant FhePrx protein
(1 and 2); this likely corresponds to a decameric form of the
FhePrx which is known to exist for other Prxs, and is impor-
tant in regulating the activity of the enzymes [17,33].

Using antibodies prepared against recombinant FhePrx we
identified a single band migrating at an apparent molecular
size of approximately 26 kDa in immunoblots of soluble
extracts of F. hepatica (Fig. 2A and B, lane 2) but is not a
major component of this preparation; the two major bands
observed in the ES products following Coomassie staining
are two previously characterised cathepsin L cysteine proteases
that have similar molecular sizes to FhePrx [7,8]. The native
FhePrx proteins detected in the parasite extracts and ES prod-
ucts co-migrated with the recombinant FhePrx protein
(Fig. 2A and B, lane 3) and also formed dimers under non-
reducing conditions (not shown). Pre-immune sheep sera did
not detect any bands (data not shown). Due to the paucity of
material that can be obtained from metacercariae we could
not detect FhePrx by immunoblotting; however, RT-PCR
using total mRNA isolated from these showed that the Prx
is expressed by this infective parasite stage (Fig. 2C).

These data suggest that FhePrx is abundant in F. hepatica
but whether the protein is actively secreted into the medium
by the parasite is not known. Prxs do not possess signal
sequences and are not normally secreted by mammalian cells
[17]; however, in certain infectious situations, such as severe
acute respiratory syndrome [6], HIV infection [16], and in
been detected in serum samples. Moreover, FhePrx may
appear in the ES products due to the continual sloughing
and replacement of the parasite tegumental and/or intestinal
cells [9]. We investigated the possibility that FhePrx is a non-
classically secreted protein using the SecretomeP 2.0 server
[www.cbs.dtu.dk/services/SecretomeP/, Ref. 14]. The analysis
of FhePrx returned a value of 0.527, compared to a threshold
value of 0.5, which indicates it is possible that the enzyme is
secreted without a signal peptide, but the probability is not
high. In contrast, a similar analysis of the schistosome egg
Prx (Genbank Accession No. AF121199) which is known to
be secreted returned a value of 0.622, indicating a higher prob-
ability of secretion. FhePrx is expressed by all stages of the
developing parasite, including the earliest infectious larvae,
and antibodies are detected in serum both during acute infec-
tion and at low levels in chronic disease (not shown).

3.2. Antioxidant activity of recombinant F. hepatica
peroxiredoxin

In the mixed-function oxidation assay, reactive oxygen spe-
cies are produced in the presence of FeCl₃, leading to strand
breaks in super-coiled plasmid DNA that can be visualised
by the formation of slower migrating nicked, open circular
plasmid in agarose gels [20] (Fig. 3A, compare lanes 2 and
3). Addition of recombinant FhePrx with DTT to the reaction
tube protected the plasmid from nicking (Fig. 3A, lane 4), since
this did not occur when DTT was substituted by ascorbic acid
(Fig. 3A, lane 5) the activity of FhePrx is, therefore, thiol-
dependent. The anti-nicking activity was FhePrx-specific, as
another F. hepatica recombinant protein, cathepsin L1 [7],
did not protect plasmid DNA from nicking (Fig. 3A, lane 6).
Although cathepsin L1 was expressed in the yeast Pichia pastoris, the active enzyme is His-tagged and was purified in an
identical manner to FhePrx. Also, incubation of the plasmid
DNA with another E. coli-expressed recombinant protein,
the surface antigen of Toxoplasma gondii, gave the same result
as the cathepsin L1 negative control. Our data supports that of
Salazar-Calderon and coworkers [28] who demonstrated that a
recombinant F. hepatica thioredoxin peroxidase fused to GST
was able to protect inactivation of glutamine synthetase and
enolase when subjected to FeCl₃-induced oxidative stress.

To determine the specific activity of recombinant FhePrx,
the enzyme was coupled with E. coli thioredoxin and thiore-
doxin reductase in an NADPH oxidation assay. In this
assay recombinant FhePrx exhibited a specific activity of
1200 nmole/min/mg. Exclusion of any of the three proteins
from the assay resulted in no significant consumption of
NADPH (Fig. 3B) although a low level of activity was
detectable with thioredoxin reductase and peroxiredoxin in the absence of thioredoxin.

Peroxiredoxins of the parasitic helminth *S. mansoni* (SmPrx 2 and SmPrx 3) can utilise glutathione and glutathione reductase in addition to the thioredoxin system to provide reducing equivalents [19,29]. Therefore FhePrx, which is 67% identical to SmPrx 2 on the amino acid level, was tested for glutathione affinity. We found that recombinant FhePrx was not active with glutathione (concentration ranging from 0.1 mM to 1 mM) and glutathione reductase (0.2 U) (Fig. 3B) as the addition of FhePrx failed to increase activity over the background rate of NADPH consumption. By preparing truncated recombinant versions of SmPrx 2 and SmPrx 3, Sayed and Williams [29] showed that the affinity for glutathione was dependent on the 22 amino acid C-terminal tail. In addition, another schistosome Prx, SmPrx 1, that lacks this C-terminal tail exhibited no affinity for glutathione [29]. In the Prx II group of peroxiredoxins, which includes SmPrx 2 and FhePrx, the C-terminus is known to form a well-ordered helix, which stabilizes the C-terminal arm and reduces mobility [29,33]. The FhePrx C-terminal tail contains the conserved Tyr-Phe motif at residues 89 and 90, and is predicted to form a helical structure from residues 183–194 by the PredictProtein server [www.predictprotein.org, Ref. 27]. However, the C-terminal tails of SmPrx 2 and FhePrx are only 55% identical on the amino acid level and this sequence variation between the *S. mansoni* and *F. hepatica* enzymes may account for the difference in C-terminal arm mobility, resulting in differences in glutathione affinity.

### 3.3. Steady-state enzyme kinetics and sensitivity to hydrogen peroxide

Prxs from various species can react with different hydroperoxides, although their efficiencies may differ between substrates [17]. FhePrx displayed saturable Michaelis–Menten type kinetics with the substrates hydrogen peroxide, cumene hydroperoxide and t-butyl hydroperoxide (Table 1). The $k_{cat}/K_m$ values for the substrates hydrogen peroxide and cumene hydroperoxide were similar, whereas the value for t-butyl hydroperoxide was slightly lower. The kinetic measurements for all three substrates were consistent with previously obtained data.
Table 1
Enzyme kinetics for recombinant FhePrx with various hydroperoxides

<table>
<thead>
<tr>
<th>Hydroperoxide</th>
<th>$K_m$ (µM)</th>
<th>$k_{cat}$ (s$^{-1}$)</th>
<th>$k_{cat}/K_m$ (M$^{-1}$ s$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cumene hydroperoxide</td>
<td>30.0</td>
<td>15.8</td>
<td>5.2 x 10$^5$</td>
</tr>
<tr>
<td>t-Butyl hydroperoxide</td>
<td>12.7</td>
<td>6.3</td>
<td>5.2 x 10$^5$</td>
</tr>
</tbody>
</table>

reported values for peroxiredoxins of mammals and other helminth parasites [17].

The steady-state kinetics of FhePrx were analysed by measuring initial rates of FhePrx activity using varying concentrations of substrates hydrogen peroxide and reduced thioredoxin. Two substrate enzyme reactions can be described by the equation of Dalziel (1) [10].

$$E/V_0 = \phi_0 + \phi_1/[A] + \phi_2/[B] + \phi_{1.2}/[A][B]$$

where $E$ is total enzyme molarity, $V_0$ is initial rate, $A$ is concentration of hydrogen peroxide, $B$ is concentration of thioredoxin, and $\phi_0$, $\phi_1$, $\phi_2$ and $\phi_{1.2}$ are constants associated with the enzyme–substrate affinity. The results were plotted as total enzyme molarity divided by initial rate versus the reciprocal of the hydrogen peroxide concentration (Fig. 4A). With typical peroxidase kinetics, regression lines of the primary data are parallel, however in Fig. 4A the lines are convergent. In secondary plots, the slopes and intercepts of the curves from the primary data were plotted against the reciprocal of the reduced thioredoxin concentration and values for constants $\phi_0$, $\phi_1$, $\phi_2$, and $\phi_{1.2}$ were derived [10]. The first order rate constant $\phi_0$ is the reciprocal of $k_{cat}$ in non-saturable kinetics, $k_{cat}$ approaches infinity, and the value of the reciprocal is zero. The $\phi_0$ value obtained for FhePrx is 0.0538 s and therefore finite, supporting previous conclusions that FhePrx is saturable and has Michaelis–Menten type kinetics. The constant $\phi_1$ refers to the affinity of the enzyme for the hydrogen peroxide substrate and $\phi_2$ refers to affinity of the oxidized enzyme for reduced thioredoxin. The value for $\phi_1$ for FhePrx is 0.105 µM s$^{-1}$ and is relatively low compared to that reported for Prx enzymes of schistosomes [28], bacteria and protozoa [16]. The significance of this relative low rate of association of reduced FhePrx for hydrogen peroxide is unknown, but these rates can differ by several orders of magnitude between Prxs of various species and may reflect differences in the levels of substrate in the particular microenvironment in which the enzymes function. Alternatively, the reported rates of association for hydrogen peroxide for Prxs of various sources may also be an artifact of recombinant protein production and/or the capacity of these proteins to form dimers or decamers. However, the $\phi_2$ constant of 0.173 µM s$^{-1}$ for the F. hepatica enzyme is similar to values for other peroxiredoxins, indicating that regeneration of the reduced enzyme likely occurs at a similar rate [17]. The third order rate constant $\phi_{1.2}$ was calculated as 12.42 µM$^2$ s$^{-1}$, it is surprising that our analysis yields a term for a ternary complex as nearly all kinetic evidence for reaction order in peroxiredoxins suggest that the detoxification of hydrogen peroxide occurs as two half reactions [17]. There are two possible explanations for deviation from a typical double displacement mechanism: (1) thioredoxin interacts with Prx before hydrogen peroxide can be attacked, in which case a type of ternary complex is formed. Thioredoxin certainly does interact with Prx, but all experimental evidence to date indicates that the function of thioredoxin is to provide reducing power in the regeneration of Prx [4] and no evidence of an intermediate in which Prx is interacting with both substrates simultaneously has been reported (2) Prx has an apparent single-displacement mechanism, which deviates from double displacement mechanism for a biologically significant reason. There is precedence for deviation from typical peroxidase
kinetics, the kinetics of S. mansoni Prx 2 and 3 [29] and the mitochondrial tpx of Leishmania infantum [17] do not conform to a double displacement mechanism. Reasons for a change in kinetic pattern could be (1) enzymatic activity is dependent on decameric versus dimeric conformation [17,33] and conformational changes of recombinant Prx versus native molecules are responsible, (2) sensitivity to hydrogen peroxide substrate, especially at higher concentrations of thioredoxin, alters the rates or (3) as the coupled enzyme reaction relies on the E. coli-derived thioredoxin and thioredoxin peroxidase, the use of the F. hepatica enzymes could result in a different pattern.

Many eukaryotic 2-Cys Prxs are sensitive to high levels of hydrogen peroxide due to over-oxidation of the peroxidatic cysteine to sulfenic acid, which cannot be rapidly reduced again, resulting in inactivation of the enzyme [17,32,33]. In the presence of high concentrations of hydrogen peroxide the effective concentration of the enzyme is reduced. We observed that FhePrx activity is subject to over-oxidation at hydrogen peroxide concentrations of 500 μM and greater (Fig. 4B). We further investigated the sensitivity of FhePrx to over-oxidation by determining the reaction rates of the enzyme at increasing hydrogen peroxide concentration. The rates of inactivation, determined by the ratio of the rate at each given time to the initial rate, were plotted against the concentration of hydrogen peroxide (Fig. 4C). The steep slope of the curve is consistent with an enzyme that is rapidly inactivated and is comparable to data reported for sensitive Prxs such as the schistosome Prx 2 and Prx 3 and human Prx 1 [29,32].

The data shows that, like other peroxiredoxins, the capacity of the FhePrx to scavenge hydrogen peroxide \( (k_{\text{cat}}/K_m = 5.2 \times 10^7 \text{M}^{-1} \text{s}^{-1}) \) is one or two orders of magnitude lower than other peroxidases. However, given that F. hepatica parasites lack catalase activity and express minimal levels of glutathione peroxidase [1,2,23] the Prx system must be a requirement for detoxification of metabolically-produced hydrogen peroxide in this parasite. The cells of the liver fluke may be under particular oxidative stress during migration in the host at which time (approximately 8 weeks) metabolic processes (catabolism of host proteins and anabolism of parasite proteins) result in growth from <1 mm to >1.5 cm in length [11]. The high affinity of FhePrx for hydrogen peroxide, the concentration required to obtain half maximal rate (\( K_m \)) is 30 μM, coupled with the high abundance of enzyme in parasite cells, is sufficient to maintain peroxide levels below toxic levels, 120–150 μM [25]. Recently, Sayed and Williams [30] demonstrated that knocking down Prx activity by interference RNA techniques in larvae of S. mansoni resulted in an increase in parasite mortality by seven-fold; although Prx 1 dsRNA was used for silencing, reduction in both Prx 1 and Prx 2 expression was observed.

Parasite Prxs are of further interest because of their possible function in maintaining the host–parasite relationship. The FhePrx is abundant in the parasite tissues, and is also secreted by the parasite [this study and references 13, 18 and 26], despite lacking a signal sequence, which suggests that the anti-oxidant functions outside the parasite. We and others have speculated that this function may include the inactivation of ROS released by immune effector cells such as eosinophils, neutrophils and macrophages, although there is no supporting evidence for this function [2,17,26]. However, we have recently shown that injection of partially purified native FhePrx or recombinant FhePrx into mice induced the recruitment of alternatively activated host macrophages [13]. The mechanism by which FhePrx exerts its function on macrophages needs to be elucidated but this may be via binding to specific surface receptors and/or drawing on emerging new functions of Prx in signal transduction [12], altering hydrogen peroxide levels on the extracellular surface of the cells.

Enzymes associated with antioxidant defence in parasites are considered targets at which new drug treatments could be developed, hence, it is important that we understand the biochemistry of these molecules. However, the high level of structural conservation between the Prx of F. hepatica and its hosts (approximately 65% at the overall amino acid levels and almost 100% in the catalytic motifs) and biochemical similarities do not augur well for selective chemotherapy. The alternative approach of disrupting the function of these molecules via vaccine-induced immune responses may prove more successful, particularly given the potential functions in host–parasite interaction.

Acknowledgements: Dr. Mary Sekiya was supported by Enterprise Ireland Research Innovation Fund Grant 2002/17. Dr. Colin Stack was supported by grants obtained from Enterprise Ireland, Republic of Ireland, and the Australian Research Council, Australia. Dr. Sheila Donnelly was funded by the National Health and Medical Research Council, Australia. Peter Collins and John Dalton were recipients of a Australian Department of Science, Education and Training (DEST) Endeavour Award. Prof. John Dalton is a recipient of a NSW Government BioFirst Award in Biotechnology which also supports Weibo Xu.

References