

consist of cross-linked proteins (Waite, 1995). The cross-linking of eggshell proteins is considered to be essential for helminth eggshell sclerotization, and is dependent on the activities of tyrosinases (TYRs) (Smyth and Clegg, 1959; Smyth and Halton, 1983; Nollen, 1971; Colhoun et al., 1998), which are copper-containing enzymes that catalyze the *ortho*-hydroxylation of monophenols to *o*-diphenols (monophenol oxidase activity, MPO, EC 1.14.18.1), and the oxidation of *o*-diphenols to *o*-quinones (diphenol oxidase activity, DPO, EC 1.10.3.1) (Garcia-borrón and Solano, 2002). Schistosome TYR activities can be inhibited by phenol oxidase inhibitors. When cultured *in vitro* for 48 h in the presence of kojic acid, a DPO inhibitor, *Schistosoma mansoni* female adult worms have been shown to produce phenotypically abnormal eggs (Fitzpatrick et al., 2007). The activities of *S. japonicum* tyrosinases (*SjTYRs*) can also be inhibited by the phenol oxidase inhibitor, allyl thiourea. After treatment with allyl thiourea *in vivo*, the uteri of *S. japonicum* adult females were filled with granules instead of normal eggs due to a complete inhibition of the eggshell formation process (Cai et al., 2009).

Genes encoding two forms of TYRs in *S. japonicum* (*SjTYR1* and *SjTYR2*) and in *S. mansoni* (*SmTYR1* and *SmTYR2*) have been reported by Fitzpatrick et al. (2004, 2007). This group also examined the localization of DPO activities in these two trematodes using a modified *in situ* enzyme assay, and found that proteins containing DPO activities were mainly localized to the female eggshell-producing vitelline cells (Fitzpatrick et al., 2004, 2007). Previous work in our group showed that *SjTYR1* and *SjTYR2* share 38% of identity in amino acid sequence, and that *SjTYR* activities are not only localized to the vitelline cells but are present also in the shells of intra-uterine eggs (Cai et al., 2009). We also found that transcript levels of both *SjTYRs* were higher in adult female worms than in adult males, and that *SjTYR1* was more highly expressed than *SjTYR2* (Cai et al., 2009).

RNA interference (RNAi), which results in post-transcriptional gene silencing (PTGS) (Bosher and Labouesse, 2000) in a wide variety of organisms, was originally identified in *Caenorhabditis elegans* (Tabara et al., 1998), and has since been used in human parasitic worms, including schistosoma (Boyle et al., 2003; Mourão et al., 2009; Ndegwa et al., 2007; Cheng et al., 2009; Tchoubrieva et al., 2010; Zhao et al., 2008). In eukaryotic cells, small interfering RNA (siRNA) can be recognized by the RNA induced silencing complex (RISC), which effects degradation of the target mRNA, and abolishes expression of the corresponding protein (Zamore et al., 2000). siRNA duplexes, which can be synthesized in large quantities and transfected into target cells, are the most commonly used reagents for RNAi in cultured cells (Milhavet et al., 2003).

In the present study, we wished to define the roles of two *SjTYRs* in eggshell formation. *SjTYR* chromosomal gene segments were amplified according to the published mRNA sequences of two *SjTYR* genes (Fitzpatrick et al., 2004), and siRNA duplexes, respectively targeting *SjTYR1* and *SjTYR2*, were used in the *in vitro* RNAi experiments. We compared the effects of knockdown of either the *SjTYR1* or *SjTYR2* genes, or of both *SjTYR* genes in tandem, by determining *SjTYR* transcript levels and DPO activities of female adult worms, and by observing the morphological characteristics and amounts of intrauterine eggs.

2. Materials and methods

2.1. Parasites

The life cycle of *S. japonicum* (Chinese mainland strain) was maintained in *Oncomelania hupensis* snails and specific pathogen-free (SPF) BALB/c mice (female) from the Department of Animal, Hubei Academy of Medical Science, China. The mice were artificially infected with cercaria, 40 ± 2 cercariae per mouse. 42 days

post-infection, the adult worms were collected from the mice by dissecting the portal vein and mesenteric vein. A portion of the parasites was stored at –80 °C for further manipulation. The adult parasites for RNAi study were cultured in 6-well plates, which had 50 mated worms in each well with 4 ml of RPMI 1640 medium containing 10% fetal bovine serum (Gibco, USA), 100 U/ml penicillin G sulfate, 100 µg/ml streptomycin and 250 ng/ml amphotericin B, at 37 °C and 5% CO₂. During cultivation, the media along with siRNAs were replaced every 2 days.

2.2. Amplification of the chromosomal segments of *SjTYR1* and *SjTYR2*

Genomic DNAs were extracted from the *S. japonicum* adult worms using the Universal Genomic DNA Extraction Kit (Takara, Japan) according to the manufacturer's instructions. Chromosomal segments corresponding to *SjTYR1* and *SjTYR2* were amplified using the TaKaRa LA PCR™ Kit (Takara, Japan). PCR products were purified and sent to Sunny (Shanghai, China) for sequencing. The gene-specific primers for amplification of *SjTYR1* and *SjTYR2* are listed in Table 1.

2.3. siRNAs

SjTYR1 (GenBank accession No. AY815264) and *SjTYR2* (AY812904) were selected as the target genes for RNAi. One negative control (NC) siRNA against Firefly Luciferase, and three siRNAs targeting each of two *SjTYR* genes, were designed and chemically synthesized by Ribobio (Guangzhou, China). The species-appropriate genome database (www.ncbi.nlm.nih.gov/BLAST/) was used to confirm that the sequences share no significant homology with other genes. The sequences of siRNAs are shown in Table 2.

2.4. Evaluation of efficiency of siRNA transfection into schistosomes cultured *in vitro*

Cy3-labeled NC siRNA, also synthesized by Ribobio, at a final concentration of 200 nM, was added into 4 ml of culture medium, in which adult worms were incubated for 3 h. After incubation, worms were washed 5 times with phosphate buffered saline (PBS, 140 Mm NaCl, 2.7 mM KCl, 10 mM Na₂HPO₄, and 1.8 mM KH₂PO₄, pH 7.2), then placed on a glass slide and observed by a confocal laser scanning microscope (CLSM) (Leica, Germany).

Table 1
Sequences of primers.

Assay	Primer sequences	Size (bp)
<i>Amplification of chromosomal segments</i>		
<i>SjTYR1</i>	Forward 5'-GAT TAC ATC ACC AAC AAT AAT GTT C-3'	10,175
	Reward 5'-GGA CAA TAA TAT GCA CGT TGT CCA T-3'	
<i>SjTYR2</i>	Forward 5'-CAT TCT ACG TAA CAA TCA CTT CTG T-3'	6002
	Reward 5'-CTC TAT ATT TAG GAC CAC ATC TCA TG-3'	
<i>Semi-quantitative RT-PCR analysis</i>		
<i>SjTYR1</i>	Forward 5'-CAA CGT TCA ATT AAA GTA CGA CGT G-3'	618
	Reward 5'-CGT CTA TAT CTG GTA GAT CAC TTC-3'	
<i>SjTYR2</i>	Forward 5'-GAA TAT TGC TCT CCG CCA AC-3'	238
	Reward 5'-GAC GTA TTA GAA CCA GGA ATA G-3'	
<i>Sj-tubulin</i>	Forward 5'-CTA CTG TAG TGG ATG AAG TGC GAA C-3'	620
	Reward 5'-CAG CTG AAA TTA CTG GTG CAT AAG-3'	
<i>Quantitative RT-PCR analysis</i>		
<i>SjTYR1</i>	Forward 5'-GAA GTG ATC TAC CAG ATA TAG AC-3'	150
	Reward 5'-CTC ATA TTT GGA TAA GCA CCT G-3'	
<i>SjTYR2</i>	Forward 5'-ACC GAT AAC CTC TTG TT-3'	122
	Reward 5'-AGA ACC AGG AAT AGA AC-3'	
<i>Sj-tubulin</i>	Forward 5'-GTG CCT TCA TGG TAG ACA AC-3'	99
	Reward 5'-TGA CCA ATC AAG CGA TTC AG-3'	

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